Public Health Environmental Surveillance Open Data Model (PHES-ODM) Documentation

2026-09-17

Table of contents

Introduction **1**
How to use the documentation . . . 2
Future documentation . . . 2
Quick start . . . 3
1. Get oriented to the ODM tables where you record results 3
2. View mandatory and optional data fields in the tables reference guide . . . 4
3. Try entering example data in ODM Excel templates . . . 4
4. Next steps . . . 5
Getting help . . . 7

Background **9**

Getting to know the ODM **11**
What are "Parts" and "Part Types"? . . . 11
"Sets" and the rationale behind sets . . . 12
Why MMA sets are a little different . . . 13
The "what" and "why" of Specimen IDs . . . 14
The "what" and "why" of Groups and Classes . . . 14
Tables and table types within the ODM . . . 15
Program description tables . . . 15
Results tables . . . 15
Look-up tables . . . 16
Measures, Methods, and Attributes: Key parts . . . 16
Measures . . . 16
Methods . . . 16

Attributes . . . 17
Data quality and reportability . . . 17
Time periods for samples and measures . . . 18
Dates within the ODM . . . 18
Translation and language capabilities . . . 19
Recording protocols . . . 20
Recommended formula for user-generated IDs . . . 22
Questions and online community . . . 27

How to use the ODM **29**
How-To guides . . . 29
1) How to use templates . . . 29
Conditional menus . . . 32
2) How to report Measures and Measure sets . . . 33
Quick Start . . . 33
`Measure report table` template . . . 33
Measure Sets Template . . . 35
Detailed description . . . 36
`Measures` template . . . 36
`Measure set report` template . . . 39
3) How to report samples and sample relationships: . . . 40
Quick Start . . . 41
Samples Template . . . 41
Sample Relationships Template . . . 42
Detailed Description . . . 43
`Sample report table` template . . . 43
`Sample relationships` template . . . 47
4) How to record a protocol . . . 48
Quick Start . . . 48
`Protocol steps` template . . . 49
`Protocols` template . . . 50
`Protocol relationships` template . . . 50
Detailed Description . . . 52
`Protocol steps` template . . . 52

Protocols template 53
Protocol relationships template 54
5) How to report metadata 55
Quick Start 55
Accession (or accessions) template 56
Address (or addresses) template 57
Contact (or contacts) template 58
Calculation (or calculations) template 58
Dataset (or datasets) template 59
Instrument (or instruments) Template 60
Organization (or organizations) template 61
Polygon (or polygons) template 62
Polygon Relationship (or polygonRelationships) template 63
Public Health Action (or phActions) template 64
Quality reports (or qualityReports) template 65
Sites (or sites) template 66
Accessions template 66
Address template 68
Contact template 69
Calculations template 70
Dataset template 72
Instrument template 74
Organization template 75
Polygon template 77
Polygon Relationships template 79
Public Helath Actions template 79
Quality reports template 81
Sites template 82
Notes regarding templates 84
Templates with conditional menus (Measure report and Protocol steps) 84

Templates with menus (all templates other than the `Measure sets`, `Protocols`, `Contact`, `Address` and `Dataset` templates) . . . 87

Sample Relationships **89**
Context . . . 89
Modelling sample relationships . . . 89
Implementation . . . 91

Long-format, wide-format, and wide-names **95**
Wide-format and long-format data . . . 95
Issues with moving between formats . . . 96
PHES-ODM approach to wide- and long-formats . . . 96

Wide-names **99**
Attributes . . . 99
Measures . . . 100
Protocol steps . . . 102
For combined long- and wide-formats . . . 103

Wide-name exceptions **107**
Attribute naming exceptions . . . 107
Measure and method naming exceptions . . . 108

Tutorials **109**
Building a wide-format ODM headers . . . 109
Building a wide-format ODM table . . . 112

How-To Guides **115**
Wide-name Templates . . . 115

I. Reference guide 117

Parts 121

16S Ribosomal Gene Sequencing . . . 122
a1306s delta-variant gene target . . . 122
a1918v delta-variant gene target . . . 122
a2710t omicron-variant gene target . . . 123
a63t omicron-variant gene target . . . 123
a67v omicron-variant gene target . . . 124
Omicron Variant a67v del69 and del70 mutations . . . 124
Atline Analyzer . . . 124
ABRicate Software . . . 125
Absolute humidity . . . 125
Absolute humidity unit set . . . 125
ABySS . . . 126
Accessions report table Shorthand . . . 126
Academic institution . . . 127
Accel-NGS 2S Plus DNA Library Kit . . . 127
Accessions Index ID . . . 127
accessions Table . . . 128
Accessions table column order . . . 128
Accessions table required headers . . . 129
Accession Number in Repository . . . 129
Acinetobacter . . . 129
Acinetobacter Group . . . 130
Number of active cases . . . 130
Number of active cases by Onset date . . . 130
Number of active cases by episode date . . . 131
Public health action . . . 131
Public health action datetime . . . 132
Public Health Action Group ID . . . 132
Public health action type . . . 132
Public Health Action Type Value Set . . . 133
Number of active cases by Report date . . . 133

Number of active cases by test date . . . 133
Active . . . 134
Address table Shorthand . . . 134
AdapterRemoval . . . 135
Analysis date . . . 135
Analysis date end . . . 135
Analysis date start . . . 136
Address Line 1 . . . 136
Address Line 2 . . . 136
Address table . . . 137
Addresses table column order . . . 137
Address table required headers . . . 138
Address ID . . . 138
Adenovirus (F40/41) . . . 138
Adenovirus Group . . . 139
Administrative regions . . . 139
Adenovirus 40 . . . 139
Adenovirus 41 . . . 140
Adenovirus F41 Fibre Gene Target . . . 140
Aeration tank . . . 141
Academic Free License v3.0 . . . 141
Afternoon . . . 141
AfterQC . . . 142
Air filter . . . 142
Aggregation . . . 142
Aggregation input (wide table) . . . 143
Aggregation name (wide table) . . . 143
Aggregations . . . 144
Aggregation scale . . . 144
Aggregation scales . . . 144
Aggregation set . . . 145
Aggregation sets . . . 145
GNU Affero General Public License v3.0 . . . 145
Agricultural activity . . . 146

Antimicrobial gradient test 146
Human Aichivirus (AiV) Group (Aichivirus A) 147
Air compartment 147
Air compartment set 147
Airplane 148
Airport 148
Airport lists worksheet 149
Airport Sheets Set 149
Airport Surveillance Template 149
Air and surface compartment set 150
Environmental temperature 150
Air and water compartment set 150
Aichivirus A (formerly Aichi virus) 151
Aichivirus B (Bovine kobuvirus) 151
Aichivirus C (Porcine kobuviru) 152
Aichivirus D (kagovirus from black cattles) 152
Aichivirus E (Rabbit picornavirus) 153
Aichivirus F (Bat kobuvirus) 153
Human Aichi virus P1 protein gene 154
Alias depreciated 154
Alias ID depreciated 154
AliView 155
Alkalinity 155
Alkalinity unit set 156
All Public Health Actions Set 156
All domains 156
Alleles class 157
Allele unit set 157
Access to all org 157
AllPaths-LG 158
Data Adjustment Standard Value Set 158
Assay Limit of Detection (LOD) 159
Aloh3 precipitation 159
The number of ambiguous bases (Ns) normalized 159

Assay method id default depreciated 160
Amicon ultrafiltration 160
Amicon filter, extract with MP96 161
Amplicon sequencing 161
Sequence Amplification Artifacts 161
Amplicon Size 162
Antimicrobial resistance (AMR) classification 162
Antimicrobial Resistance (AMR) Classification Value Set . 162
AMRFinderPlus Software 163
Anti-microbial resistance Group 163
AMR Analysis Software 164
AMR Software Set 164
Anaplasma Group 164
AND Boolean aggregation 165
Andes virus (ANDV) hantavirus 165
annealing/extension 166
Any compartment set 166
Any specimen set 166
Apache license 2.0 167
Anaplasma phagocytophilum 167
Apollo PrepX Library Preparation Kits 167
ARACHNE 168
Antibiotic Resistance Genes Database (ARDB) 168
Area proportional sample 169
A-Tier Region-level Aggregation at Site 169
ARG-ANNOT Annotation Tool 169
ARIBA 170
Arrival temperature 170
Artic V1 Primer Set 171
Artic V2 Primer Set 171
Use of the articV3 primer 172
Use of the articV4 primer 172
Artic V4.1 Primer Set 172
Artic V5 Primer Set 173

Artic V5.1 Primer Set 173
Artic V5.2 Primer Set, 1200bp 174
Artic V5.2 Primer Set, 400bp 174
Artic V5.3.2 Primer Set 174
Artistic license 2.0 175
Assay ID 175
Astrovirus 176
Astrovirus Group 176
Amies Transport Medium 176
Atropos 177
Attribute input (wide table) 177
Attribute name (wide table) 178
Attributes 178
Automatic composite sampling 178
Autosamplers 179
Automatic sequential sampling 179
Babesia 180
Babesia or Nuttallia Group 180
Bacterial culture 180
BacMet Database 181
Bacteroides 16S forward primer (HF183) (ABI) 181
Bacteroides 16S probe (BacP234) (ABI) 181
Bacteroides 16S reverse primer (BacR287) (ABI) 182
Bacteria unit set 182
Bacteroides Group 183
Bacteria and Fungus Class 183
Bacterial testing method 183
Bacterial testing method set 184
Miscellaneous bacteria group 184
Bag Mediated Filtration 185
BamQC (from Qualimap) 185
bamUtil Dedup 185
Bar screen 186
Base-pair unit set 186

BayesHammer (from SPAdes) 187
Bayesian Smoothing applied 187
BBDuk (from BBTools) 187
BBMap 188
BBMap Reformat 188
BBMap Suite 189
Bead beating, extract with MP96 189
Borrelia burgdorferi 190
Bcftools 190
bcov 190
bcov culture spike target 191
bcov spike target (unspecified) 191
bcov vaccine spike target 192
Bayesian Evolutionary Analysis by Sampling Trees (BEAST) Software 192
Beef extract flocculation 192
Is Before 193
Below LOD 193
Measured levels below LOQ 194
Beta 194
Beta Coronavirus Group 194
BIGSdb (Bacterial Isolate Genome Sequence Database) . . 195
Biologic 195
Fragment analyzers or bioanalyzers 196
BioEdit 196
Bioo Scientific NEXTflex Rapid DNA-Seq Kit 196
Digital droplet emulsification PCR 197
Biological replicate 197
Beta-Lactamase Anti-microbial resistance Group 198
Cephamycin Beta-Lactamase-Resistance gene target 198
CTX-M Beta-Lactamase-Resistance gene target 198
Impenemase (IMP) Beta-Lactamase-Resistance gene target 199
Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase-Resistance gene target 199

New-Delhi Metallo- (NDM) Beta-Lactamase-Resistance gene target . . . 200
OXA-type Beta-Lactamase-Resistance gene target . . . 200
SHV Beta-Lactamase-Resistance gene target . . . 201
BLASR (Basic Local Alignment with Successive Refinement) 201
TEM Beta-Lactamase-Resistance gene target . . . 201
Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase-Resistance-resistance gene target . . . 202
Binary Large Object (BLOB) data type . . . 202
BMTagger . . . 203
Breadth of coverage (>=5x depth) . . . 203
Bocaparvovirus Group . . . 203
Bocaparvovirus . . . 204
5-Day carbonaceous biochemical oxygen demand . . . 204
5-day total biochemical oxygen demand . . . 205
Boolean data type . . . 205
Boolean aggregation set . . . 206
Boolean value set . . . 206
Border closure . . . 206
Borrelia burgdorferi or Lyme Disease Group . . . 207
Body of water . . . 207
Bowtie2 . . . 207
Host Subtraction with Bowtie2 & SAMtools . . . 208
Base-pairs . . . 208
Buffered Peptone Water . . . 209
Bracken . . . 209
B-Tier Region-level Aggregation at Site . . . 210
Bovine respiratory syncytial virus group . . . 210
brsv culture spike target . . . 210
BRSV-N . . . 211
brsv vaccine spike target . . . 211
Brucella . . . 212
Brucella Group . . . 212
BSD Zero-Clause license . . . 212

BSD 2-clause “Simplified” license 213
BSD 3-clause “New” or “Revised” license 213
BSD 3-clause Clear license 214
BSD 4-clause “Original” or “Old” license 214
Boost Software License 1.0 214
Branch sewer pipleline 215
Building cleanout 215
Building-level Surveillance 216
Bundibugyo virus, Orthoebolavirus bundibugyoense 216
Bus 216
Bus Station 217
BWA (Burrows-Wheeler Aligner) 217
BWA for Host Filtering 218
BWA-MEM with Duplicate Marking 218
C28311T Omicron N1 Point Mutation 218
Cacipacore virus (Orthoflavivirus cacipacoreense) 219
Caffeine 219
Calculation Type 220
Calculation type set 220
Calculation ID 220
Calculations Table 221
Calculations table column order 221
Calculations table required headers 222
Calibration purpose 222
Calprotectin 222
Campylobacter 223
Campylobacter Group 223
Canal 224
Canu 224
Capacity class 224
Capacity unit set 225
CapsuleFinder 225
Capital city endonym 225
Capital city exonym 226

Comprehensive Antibiotic Resistance Database (CARD) . . 226
CARD Resistance Gene Identifier (RGI) 227
Case report date 227
Episode date of confirmed cases 227
Onset date of confirmed cases 228
Report date of confirmed cases 228
Test date of confirmed cases 229
Central average smoothing applied 229
Categorical data type 229
Categories 230
Candida auris 230
Candida auris Group 231
Carbonaceous Biochemical Oxygen Demand 231
Carbapenemase-encoding genes 232
Cary-Blair Transport Medium 232
Creative Commons Zero v1.0 Universal 232
Creative Commons Attribution 4.0 233
CC BY-NC 4.0 license 233
CC BY-NC-SA 4.0 license 234
Creative Commons Attribution ShareAlike 4.0 234
Long-term acute care hospital 234
Child day care 235
Sarbeco_E forward primer (IDT) 235
Sarbeco_E probe (IDT) 235
Sarbeco_E reverse primer (IDT) 236
2019-nCoV_N1 forward primer (IDT) 236
2019-nCoV_N1 probe (IDT) 237
2019-nCoV_N1 reverse primer (IDT) 237
2019-nCoV_N2 forward primer (IDT) 237
2019-nCoV_N2 probe (IDT) 238
2019-nCoV_N2 reverse primer (IDT) 238
2019-nCoV_N3 forward primer (IDT) 238
2019-nCoV_N3 probe (IDT) 239
2019-nCoV_N3 reverse primer (IDT) 239

CD-HIT . . . 239
Clostridium difficile . . . 240
Corynebacterium diphtheriae . . . 240
CeCILL Free Software License Agreement v2.1 . . . 240
Degrees Celcius . . . 241
Celera Assembler . . . 241
Population census . . . 242
Centrifugation . . . 242
Centricon ultrafiltration . . . 242
Centrifuges . . . 243
Centrifugation speed . . . 243
Ceres nanotrap . . . 243
Cesspit . . . 244
Colony Forming Units . . . 244
CFU per 100 ml . . . 245
Colony forming units per grams total solids . . . 245
Colony forming units per milliliter . . . 245
Changes column . . . 246
character length . . . 246
Chemical . . . 246
Chemical contaminant surveillance . . . 247
Chemagic viral dna/rna 300 kit . . . 247
ChewBBACA . . . 247
Chikungunya Group . . . 248
Chikungunya virus (CHIKV) . . . 248
Child relationship . . . 249
Chlamydia . . . 249
Chlamydia Group . . . 249
Circovirus Group . . . 250
City . . . 250
Campylobacter jejuni bacteria . . . 251
Composite Key . . . 251
Calculations Table Short Name . . . 251
Lineage- or Clade-analysis Software . . . 252

Lineage- or Clade-analysis Software Set 252
Clarified sample 253
CLARK 253
Class 253
Classes 254
CleanPlex DNA Library Prep Kit 254
ClermonTyping 255
Clinic 255
ClonalFrameML Software 255
Clostridium Group 256
Cloudy 256
BBMap's Clumpify 257
Clustal Omega 257
Centimetres 257
Contact table Shorthand 258
Carbon Dioxide 258
Chemical Oxygen Demand 259
Time from collection to storage 259
Colistin Anti-microbial resistance group 259
Collection group 260
Colistin resistance 260
Collection Approximate Time Period Set 260
Collection Approximate Time Period 261
Collection Date (time not included) 261
Collection date time 262
Collection date time end 262
Collection date time start 262
Sample collection set 263
Collection number 263
Collection period and number 264
Collection period 264
Sample collection type 265
Co-located relationship 265
Column name depreciiated 266

Commercial facility - not specified 266
Community-level Surveillance 266
Communitor 267
Composite sample - archival 267
Composite grab sample of 3 268
Composite grab sample of 3 depreciate 268
Composite 3hr grab sample 268
Composite 3hr grab sample depreciate 269
Composite 8hr grab sample depreciated 269
Composite 8hr grab sample deprecated 270
Compartment 270
Compartment input (wide table) 270
Compartment name (wide table) 271
Compartments 271
Compartment Set Header 272
Compartment sets 272
Composting toilet 272
Concentration measure 273
Is concurrent to 273
Sample volume after concentration 274
Water conductivity 274
Conductivity class 274
Conductivity unit set 275
Cone-shaped sampling 275
Number of confirmed cases 276
Number of confirmed cases by episode date 276
Number of confirmed Cases Onset date 276
Number of confirmed cases by report date 277
Number of confirmed cases test date 277
consensus genome length 278
Consensus Sequence Software 278
Consensus Sequence Software Set 278
Contact ID 279
Contact name 279

Contact table 279
Contacts table column order 280
Contact table required headers 280
Contact table set 281
Contamination 281
Control measure implementation 281
Control Measure Implementation Value Set 282
Control sample 282
Contact phone 283
Core sampling 283
Correctional facility 283
Cosavirus (CosaV) 284
Cosavirus Group 284
COSCa ball 285
Population count 285
Country-level Aggregation at Site 285
Countries look-up tables 286
Countries table column order 286
Counries table required headers 286
Country 287
Country endonym 287
Country exonym 288
Countries or sovereign states 288
Districts, counties, regions 288
Covid-19 289
SARS-CoV-2 measure 289
Covaris truXTRAC FFPE DNA Library Kit 290
SARS-CoV-2-B.1.1.7 290
SARS-CoV-2-B.1.351 290
SARS-CoV-2-E 291
SARS-CoV-2 M Gene target 291
SARS-CoV-2-N1 292
SARS-CoV-2-N2 292
SARS-CoV-2-N200 292

SARS-CoV-2-N3 293
SARS-CoV-2-P.1 293
SARS-CoV-2-RdRp 294
SARS-CoV-2 S Gene Target 294
SARS-COV-2 5' UTR Gene target 294
Clostridium perfringens 295
Covid-19 population measurement date 295
Cphd ID 296
Critical priority pathogen 296
Gene copies per well 296
crAssphage-N 297
Crassphage Standarized 297
Creatinine 297
Crosswalk table set 298
Cryptosporidium 298
Cryptosporidium Group 299
Cycle threshold or quantification cycle (Ct or Cq) 299
Cycle threshold per quantification cycle 299
CTFinder 300
Countries look-up tables Shorthand 300
Cumulative count 300
Cufflinks (with TopHat integration) 301
Custody Contact ID 301
Data custodian ID 302
Cutadapt 302
Circulating vaccine-derived poliovirus type 2 303
Number of cycles 303
D339H Mutation 303
d377y delta-variant gene target 304
d3g omicron-variant gene target 304
d63g delta-variant gene target 305
d796y omicron-variant gene target 305
d950n delta-variant gene target 305
DADA2 306

Daily count 306
Database and Data Repository Class 307
Data collection sector or organization 307
Host Data Repository or Bank 307
Data Repository Set 308
Dataset creation date 308
Dataset ID 308
Dataset table 309
Datasets table column order 309
Dataset table required headers 310
Data Type column (Reported) 310
Data types part type 310
Date data type 311
Date 311
Datetime data type 312
7-day smoothing of values 312
Days 312
DNA Data Bank of Japan (DDBJ) 313
ddcov_e sars-cov-2 gene target 313
ddcov_n sars-cov-2 gene target 314
Digital Droplet PCR (ddPCR) 314
Deaths 314
DeconSeq 315
DecontaMiner 315
Decreased surveillance 316
Deduplication Method 316
Deduplication Method Set 316
DeepARG Software 317
Dehosting Method 317
Dehosting Method Set 317
Omicron Variant 142-144 Deletion 318
del143/145 318
Delta Variant 156-157 Deletion 319
del 157/158 319

del2084/2084 . . . 319
del212/212 . . . 320
Omicron Variant 142-14431-33 Deletion . . . 320
del3674/3676 . . . 321
del69/70 . . . 321
Delayed Arrival or Prolonged Transit . . . 321
Delta . . . 322
SARS-CoV-2 Delta Variant Group . . . 322
Deltaretrovirus . . . 322
Deltaretrovirus Group . . . 323
Dengue Virus Type 1 . . . 323
Dengue Virus Type 2 . . . 324
Dengue Virus Type 3 . . . 324
Dengue Virus Type 4 . . . 324
denaturation . . . 325
Dengue . . . 325
depth of coverage threshold . . . 326
Depreciated . . . 326
Derived data . . . 326
Derived sample . . . 327
Description . . . 327
Description of change . . . 328
Desk or counter . . . 328
Dewatered solids . . . 329
Detected . . . 329
Access to details deprecated . . . 329
Detected Lineage or Clade Name . . . 330
De-escalated variant . . . 330
Development . . . 331
Dictionary reference table set . . . 331
Additional dictionary sheets . . . 331
Dictionary set type . . . 332
Dilution factor . . . 332
Point dillutions . . . 333

Dilution Class 333
Diphtheria Group 333
DISCOVAR de novo 334
Diseases (human) class 334
Dissolved gas concentration unit set 334
Dissolved oxygen 335
DNA Template 335
DNA Fragment Length 336
Nextera DNA Flex/DNA Prep Library Prep Kit 336
DNA/RNA Shield 336
Data Not Collected 337
Dengue Virus E Gene 337
Dengue Virus NS5 Gene 338
Dengue Virus prM Gene 338
Dobrava-Belgrade virus (DOBV) hantavirus 338
Depth of coverage 339
Domain 339
Domains 340
Domestic travel hub surveillance 340
Higher education domitory or residential building 340
Digital PCR (dPCR) 341
Digital PCR (dPCR) intruments 341
DDBJ sequence Read Archive (DRA) 341
Sewer (drain) 342
Drug surveillance 342
Dataset table Shorthand 343
Duration time of a method 343
e156g delta-variant gene target 343
e484a omicron-variant gene target 344
Enteroaggregative Escherichia coli (EAEC) 344
EAGER 345
EasySeq NGS Targeted Capture Kit 345
Orthoebolavirus Group 345
Ebola virus, Orthoebolavirus zairense 346

Epstein–Barr virus (EBV) 346
Educational Community License v2.0 347
Escherichia coli 347
Escherichia coli group 347
Eden V1 Primer Set 348
Educational facility 348
Education 349
Eastern equine encephalitis virus (EEEV) 349
Eastern equine encephalitis virus group 349
Efficiency 350
Wastewater Effluent - non-specified 350
Enterohemorrhagic Escherichia coli (EHEC) 351
Enteroinvasive Escherichia coli (EIEC) 351
Electrical potential unit set 351
Eluate/Resuspended filter material retained 352
Elution buffer 352
Contact email 352
Emboss Cons 353
Emergency targetted surveillance program 353
European Nucleotide Archive (ENA) 354
ENA Format 354
European Nucleotide Association Mapping Column 354
European Nucleotide Association (ENA) - notes 355
Enterobase archives 355
Enterovirus 355
Enterovirus Group 356
Enumeration for set values 356
Temperature and pH probes 357
Rainfall 357
Ground snow depth 357
Snowfall 358
Enteropathogenic Escherichia coli (EPEC) 358
Episode date 359
EpiWeek Mean 359

EpiWeek Number 359
EpiWeek Start Date 360
Year of the EpiWeek 360
Eclipse Public License 1.0 360
Eclipse Public License 2.0 361
Equation 361
ERD table set 362
Erythroparvovirus 362
Erythroparvovirus Group 362
Sarbecovirus-specific E sars-cov-2 gene target 363
ESBL-encoding genes 363
exclusions based sample preparation (ESP) 364
Estimated frequency of reads 364
Estimated data 364
Estuary, natural water body 365
Enterotoxigenic Escherichia coli (ETEC) 365
European Union Public License 1.1 365
European Union Public License 1.2 366
Ebola Virus Disease (EVD) 366
Evening 367
Exceptions Part Type 367
SARS-CoV-2 exoN gene (nsp14) 367
Extraintestinal pathogenic Escherichia coli (ExPEC) 368
Experiment Failed 368
Extraction Blank - Control 369
4s method 369
Nucleic acid extraction method 369
Extraction Recovery Percent 370
Nucleic Acid Extraction set 370
Extraction volume of sample 371
F456L Mutation 371
Fecal matter 371
Fast-flowing 372
Degree Fahrenheit 372

FALSE . . . 372
Farm . . . 373
FastMLST . . . 373
FASTP . . . 374
FastQC . . . 374
FASTQ Screen . . . 374
FastUniq . . . 375
FASTX Toolkit . . . 375
Male-specific (F+) coliphage - general . . . 376
F+ DNA coliphage . . . 376
Fecal coliform count . . . 376
Fecal-contamination . . . 377
Field sample . . . 377
Field sample replicate . . . 377
File location of polygon . . . 378
Filtration . . . 378
Filtration units . . . 379
First Nation . . . 379
Final volume . . . 379
First name of contact . . . 380
First released version . . . 380
Foreign key . . . 380
Foreign Key Alias ID . . . 381
AI - Inhibition present but addressed . . . 381
B - Trace levels of contamination . . . 382
FI - Inhibition present and unaddressed . . . 382
J - Weak signal extrapolation . . . 383
ND - Non-detect . . . 383
UJ - Trace signal extrapolation . . . 384
UQ - Unquantifiable . . . 384
Flavivirus (West Nile, Dengue, Zika) Group . . . 384
FLiRT/SLip Variant Group . . . 385
FLiRT Variants . . . 385
Float data type . . . 386

Flocculation 386
Flow-normalized mean 386
Floor 387
Flow rate 387
Flow proportional 24hr sample depreciated 388
Flow class 388
Flow meters 388
Flow proportional sample 389
Flow Standarized 389
Volume flow rate unit set 390
Flow volume 390
Influenza virus measure 390
Influenza A virus 391
Influenza virus A1 391
Influenza virus A1 and A2 combined 391
influenza virus A2 392
Influenza A Virus Group 392
Influenza virus B 393
Influenza B Virus Group 393
Influenza Virus General Group 393
Influenza A H5 hemagglutinin gene 394
Influenza A M gene 394
Fluidigm digital PCR 395
Influenza A N1 neuraminidase gene 395
Flye 395
First Nation Territory/Métis Settlement-level Aggregation at Site 396
Formazin nephelometric unit 396
Foggy 397
Feet 397
Fqtrim 397
Fraction analyzed 398
Fraction input (wide table) 398
Fraction name (wide table) 398

Sample fraction set . . . 399
FRCbam . . . 399
Freyja Script . . . 400
F-Specific RNA bacteriophages . . . 400
F+ RNA coliphage . . . 400
F-Specific RNA bacteriophages, G2 . . . 401
Sample frozen . . . 401
Field sample temperature . . . 401
Francisella tularensis . . . 402
Full dictionary sheets set . . . 402
Funder contact ID . . . 403
Funding agency ID . . . 403
Giardia 18S rRNA . . . 403
g215c delta-variant gene target . . . 404
g339d omicron-variant gene target . . . 404
g496s omicron-variant gene target . . . 405
g662s delta-variant gene target . . . 405
Gamma . . . 405
Gammaretrovirus . . . 406
Gammaretrovirus Group . . . 406
Gas class . . . 407
Gaussian distribution stanrdized/Normalized . . . 407
Gene copies . . . 407
Gene copies per copy of crAssphage . . . 408
Gene copies per day . . . 408
gene copies per day per 100,000 people . . . 408
Gene copies per gram solids . . . 409
Gene copies per L . . . 409
Gene copies per mL . . . 409
Gene copies per millilitre per 100,000 people . . . 410
Gene copies per PMMoV copy . . . 410
Gene copies per Reaction . . . 411
Giardia duodenalis . . . 411
GEM Mapper . . . 411

GenBank Archives 412
genome completeness 412
Geneious 413
Genetics unit set 413
General missingness set 413
GenoTyphi 414
Generic quality flag set 414
European Petroleum Survey Group Coordinates 415
Latitude 415
Longitude 415
Geographical Reference Missingness Set 416
Type of geography 416
Geographic set 417
Well-known text 417
GNU Free Documentation License v1.3 417
Giardia Group 418
Global Initiative on Sharing All Influenza Data (GISAID) archives 418
GitHub 418
Gram per kilogram 419
Gram per liter 419
10% Glycerol Solution 419
Gram per cubic metre 420
GMAP 420
Geometric mean 421
Nitrogen per total solids 421
Gonococcus Group 421
Government agency 422
Grams per total solids 422
GNU General Public License v2.0 422
GNU General Public License v3.0 423
Orthophosphate per total solids 423
Orthophosphate as phosphorus per total solids 424
Grab samplers 424

Grams 424
Gram stain 425
GraphMap 425
Gravity settling 426
Grab sample 426
Grit chamber 426
Gromstole 1.0 Script 427
Group 427
Groups 428
Growth in enrichment broth 428
Ground water 428
Genome Sequence Archive (GSA) 429
GSNAP 429
Guanidine Thiocyanate 430
Genomic Target Enrichment 430
Genomic Target Enrichment Methods Set 430
H5N1 avian influenza A virus (IAV) 431
Human mastadenoviruses (HAdVs) 431
Human mastadenovirus genotype group A 432
Human mastadenovirus genotype group B 432
Human mastadenovirus genotype group C 433
Human mastadenovirus genotype group D 433
Human mastadenovirus genotype group E 433
Human mastadenovirus genotype group F 434
Haemophilus Group 434
See Header for Aggregation 435
Human Aichi virus (AiV) 435
Human Aichi virus (AiV) Genotype A 436
Human Aichi virus (AiV) Genotype B 436
Human Aichi virus (AiV) Genotype C 436
Hand hygiene advisory 437
Orthohantavirus Group 437
Human bocavirus (HBoV) 438
Hank's Balanced Salt Solution (HBSS) 438

Healthcare activity 439
Healthcare facility 439
See Header for Compartment 439
Haemophilus ducreyi 440
Header 440
Health administration or planning agency 440
Health Region for a Site 441
Heat inactivated sars-cov-2 virus spike target 441
SARS-CoV-2 hel gene (nsp13) 442
Hepatitis A 442
Hepatitis B 442
Hepatitis C 443
Hepatitis E 443
hep g armored rna 443
hep g armored rna spike target 444
Hepatitis Group 444
Herpes Virus Group 445
HF183 Bacteriodes 16S 445
See Header for Fraction Analyzed 445
Hantavirus hemorrhagic fever with renal syndrome (HFRS) 446
Roseolovirus (Human Herpesvirus-6) 446
Human Herpesvirus-6A (HHV-6A) 447
Human Herpesvirus-6B (HHV-6B) 447
Roseolovirus (Human Herpesvirus-6) Group 448
5-hydroxyindoleacetic acid (5-HIAA) 448
High severity 449
Haemophilus influenzae 449
HISAT2 449
Human Immunodeficiency Virus (HIV) 450
HIV Group 450
Sewer Network Health Region 451
Hand Measurement 451
See Header for Measure 451
Human Metapneumovirus (HMPV) 452

Hollow fiber dead end ultrafiltration 452
Stay-at-home order 452
Horizontal grab sampling 453
General Hospital Admissions 453
Hospital Census 454
Hospital 454
Version of Data Hosting Platform/Repository 454
Holding tank wastewater depreciated 455
Hotel or motel 455
Hours 456
human parvovirus B19 (B19V) 456
Human Parechovirus (PeV) 456
Human Parechovirus-1 (HPeV1) 457
Human Parechovirus-3 (HPeV3) 457
Human Parainfluenza Virus (HPIV) 458
High priority pathogen 458
Hantavirus pulmonary syndrome (HPS) 459
Human Papiloma Virus (HPV) 459
Human Rhinovirus (HRV) 459
Human Rhinovirus (HRV) A 460
Human Rhinovirus (HRV) B 460
Human Rhinovirus (HRV) C 461
Rhinovirus Group 461
See Header for Specimen 461
Herpes Simplex Virus 462
Hantaan virus (HTNV) hantavirus 462
Holding tank wastewater 463
Holding tank 463
Human compartment 463
Human compartment set 464
Humidity class 464
General Humidity Unit Set 464
See Header for Unit 465
Animal husbandry 465

Hybrid Selection Method 465
i1566v omicron-variant gene target 466
i3758v omicron-variant gene target 466
i82t delta-variant gene target 467
Ibuprofen 467
International Classification of Diseases 467
Intensive care unit patients 468
IDBA-UD 468
Illumina DNA Prep with Enrichment 469
Instrument table Shorthand 469
Inch 469
Increased surveillance 470
Index 470
Industrial plant 470
Industrial activity 471
Industrial input 471
Influent equilibration 472
Influent pump station 472
Inhibition set 472
Inhibition measure 473
Inhibition method 473
Innovaprep ultrafiltration 474
Input 474
Omicron Variant ins214epe Insertion 474
International Nucleotide Sequence Database Collaboration (INSDC) Archives 475
Institution-level Surveillance 475
Instrument ID 476
Instrument table 476
Instruments table column order 476
Instrutment table required headers 477
Other instrument 477
Instrument Type 477
Describe other instrument type, if applicable 478

Instrument set 478
Integrase Anti-microbial resistance Group 479
Integer data type 479
Integrase Class I gene target 479
Intercept 480
Internal reference 480
International travel hub surveillance 480
Combined ip2 and ip4 sars-cov-2 gene target 481
IQ-TREE Software 481
ISC 482
ISO639-1 482
ISO639-2B 482
ISO639-2T 483
ISO639-3 483
ISO639-6 484
ISO 3166-1 alpha-2 country code 484
ISO 3166-1 alpha-3 country code 485
ISO 3166-2 code for country sub-domain 485
iVar 486
JN.1.7 Variant 486
JN.1 Variant 486
k856r omicron-variant gene target 487
KAPA HyperPrep Kit 487
Kaptive 488
Kilogram per cubic meter 488
Kilogram per second 488
Kilolitres 489
Klebsiella Group 489
Klebsiella pneumoniae 489
KneadData 490
Kobuvirus Group 490
KP.1.1 Variant 491
KP.1 Variant 491
KP.2 Variant 491

KP.3.1.1 Variant 492
KP.3 Variant 492
Kraken2 492
Litres 493
Omicron Variant l24s mutation 493
l452r delta-variant gene target 494
L455S Mutation 494
l981f omicron-variant gene target 494
Language Look-up table Shorthand 495
Laboratory 495
Lab ID default depricated 495
Laboratory duplicate 496
Label 496
Lab ID 497
Lachnospiraceae (Lachno3) 497
Low Average Genome Coverage 497
Lagoon system 498
Lake, natural water body 498
Lambda 498
Land-based Transit Hub 499
Language ID 499
Language family 500
Language name 500
National language script 500
Language Look-up table 501
Language table column order 501
Language table required headers 502
LAST (Large-Scale Alignment and Search Tool) 502
Last edited 502
Last name of contact 503
Last updated version 503
LaTeX expression 504
Latrine 504
LB.1 Variant 505

Low breadth of coverage 505
Laboratory control sample duplicate 505
Litres per day 506
Low depth of coverage 506
Leaked sample 507
Legionella 507
Legionella Group 507
Lentivirus Group 508
<10 people 508
10 - 100 people 508
10,000 - 100,000 people 509
1,000 - 10,000 people 509
100 - 1,000 people 510
100,000 - 1,000,000 people 510
GNU Lesser General Public License v2.1 510
GNU Lesser General Public License v3.0 511
Liter per hour 511
Link 511
Library preparation instruments 512
Library Preparation Kit 512
Library Preparation Kit Set 513
License 513
Data license set 513
Ligase-Dependent Library Prep Kits 514
LINEAGE Software 514
Linear scale aggregation set 515
Liquid fraction 515
Liquid/Supernatant retained 515
Liquid 516
Listeria 516
Listeria Group 516
List worksheet 517
List set 517
Liter per minute 518

Limit of Blank (LOB) 518
Access to local ha 518
Lockdown 519
Limit of detection (LOD) 519
Limit of detection (LOD) - sewage 520
log10 gene copies per g 520
log10 gene copies per L 520
log10 gene copies per mL 521
Log10 gene copies per 100 milliliter 521
Log10 gene copies per nanogram total DNA 521
log10 micrograms per g 522
log10 micrograms per L 522
Logarithmic scale aggregation set 522
Longitudinal, repeat sampling surveillance program 523
Dictionary tables 523
Limit of quantification (LOQ) 524
Low severity 524
Low Coverage of Characteristic Mutations 524
Lower limit of a 95% confidence interval 525
Low-quality Sequence 525
Low Signal-to-Noise Ratio 526
Low-volume sample 526
LP.8.1 Variant 526
Low Percent of Genome Captured 527
Omicron Variant LPPA24S mutation 527
LaTeX Project Public License v1.3c 527
Lactated Ringer's Solution 528
Liter per second 528
Long-term care facility 529
Long-term care - assisted living or retirement home 529
Other long-term care 529
Life technologies digital PCR 530
luminultra wastewater extraction kit 530
Lymphocryptovirus 530

Lymphocryptovirus Group 531
Lysis buffer 531
Cubic metres per day 532
Cubic metres per hour 532
Cubic meter per minute 532
Cubic metres per second 533
MAFFT 533
Magnetic nanobead binding 534
Magnetic separation racks 534
Plasmodium or Malaria Group 534
Shopping mall 535
Manual Composite Sample 535
Manufacturer 535
MapSplice 536
mash Software 536
Mask mandate 537
Mask recommendation 537
Human mastadenovirus Group 537
Maryland Super Read Celera Assembler (MaSuRCA) 538
Sample Material Characteristics 538
Sample Material Characteristics Set 539
Mate pair layout 539
Maximum length 539
Maximum value 540
Maximum value part support 540
Concentration Factor 540
MCR-1.1 Colistin-resistence gene target 541
Arithmetic mean 541
Measurement group 542
Measles 542
Measles Group 542
Other Measure 543
Measures quality set 543
Measure 544

Measure input (wide table) 544
Measure license 544
Measures 545
Measure name (wide table) 545
Measure Report ID 546
Measure report table 546
Measure set report set ID 546
Measure set report table 547
Measure sets table column order 547
Measure Set table required headers 548
Measures table column order 548
Measures table required headers 548
Meat processing plant 549
Median 549
Molecular Evolutionary Genetics Analysis (MEGA) 549
Mega-bases or Mega-base-pairs 550
MEGAHIT 550
MEGARes database 551
membrane filtration with addition of mgcl3 551
Normalized arithmetic mean 551
Other Measure Description 552
Milliequivalent per liter 552
Measures Part-type Shorthand 552
Effective Sample Size/Volume 553
Methods part-type Shorthand 553
Metabolite Group 554
MetAMOS 554
MetaPhlAn Software 554
Meter 555
Method 555
Concentration method 555
Concentration method set 556
Method input (wide table) 556
Method name (wide table) 557

Methods 557
Membrane filtration with acidification and mgcl2 557
Membrane filtration with acidification and mgcl2, membrane recombined with separated solids 558
Membrane filtration with addition of mgcl2 558
Membrane filtration with mgcl2 and separated solids 558
Membrane filtration with no amendment 559
Membrane filtration with no amendment, membrane recombined with separated solids 559
Membrane filtration with sample acidification 560
Membrane filtration with sample acidification, membrane recombined with separated solids 560
Millions of gallons per day (MG/D) 560
Mycoplasma genitalus 561
MGIEasy DNA Library Prep Kit 561
Milligrams per litre 562
Milligram per liter of calcium carbonate 562
Milligrams orthophosphate per liter 562
Milligrams orthophosphate as phosphorus per liter 563
Murine Hepatitis Virus 563
murine hepatitis virus (MHV) spike target 563
Multiple issues 564
Mid-level severity 564
Midnight and BC-CDC V1 Primer Set 564
Midnight and BC-CDC V2 Primer Set 565
Midnight and BC-CDC V3 Primer Set 565
Midnight and BC-CDC V4 Primer Set 566
Midnight scheme V1 Primer Set 566
Midnight scheme V2 Primer Set 567
Midnight scheme V3 Primer Set 567
Miniasm 568
Minimap2 568
Minimum length 568
minimum post-trimming read length 569

Minutes 569
Minimum value 570
Minimum value part support 570
Miscellaneous attribute group 570
Miscellaneous measure group 571
Missing data 571
Missingness 571
Missingness Set 572
Missingness sets 572
MIT 573
MIT No Attribution 573
MitoZ Deduplication 573
Mixed/homogenized sample 574
Millilitres 574
Megalitres per day (ML/d) 575
Method Limit of Detection (LOD) 575
MLST (Center for Genomic Epidemiology) 575
Millimetres 576
Measure, Method, or Attribute Set Header 576
Measure, method, or attribute sets 577
Millimho per centimeter 577
Model 578
monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) 578
Months 578
Moore swab passive sample 579
1,000,000+ people 579
Morning 579
Mozilla Public License 2.0 580
Most probable number per 100 milliliters 580
Most probable number per milliliter 580
Mpox 581
MPox Clade I Group 581
MPox Clade II Group 582

MPox Group 582
Medium priority pathogen 582
Metres per second 583
Metapneumovirus Group 583
Mpox B6R Gene Target 583
Clade I Mpox C3L Gene Target 584
Mpox Clade I 584
Mpox Clade II 585
Mpox & Orthopox E9L-NVAR Gene Target 585
Mpox & Orthopox E9L-OPX3 Gene Target 586
Mpox Clade I F3L Gene Target 586
Mpox G2R-G Gene Target 586
Mpox G2R-NML Gene Target 587
Clade II Mpox G2R-WA Gene Target 587
Mpox GT Molecular Gene Target 588
Measure report table Shorthand 588
MrBayes Software 588
Methicillin-resistant Staphylococcus aureus (MRSA) 589
Measure set report table Shorthand 589
ms2 coliphage 590
ms2 coliphage spike target 590
MilliSiemen per centimeter 590
Matrix spike duplicate 591
Microsoft Public License 591
Moore swab passive sample depreciated 591
Major sewer pipeline 592
Mycobacterium tuberculosis 592
Mu 593
murine coronavirus 593
murine coronavirus spike target 593
Multiple fraction 594
Mulan Permissive Software License, Version 2 594
Multi-Community-level Surveillance 595
Multiple Purpose 595

MultiQC 595
Mumps 596
Mumps Group 596
Municipalities or communes 596
Municipality 597
Municipality-level Aggregation at Site 597
Mutations class 598
Mutation panels class 598
MilliVolt 598
Mycoplasma Group 599
Mykrobe 599
N sars-cov-2 gene target 600
Combined N1 and N2 sars-cov-2 gene target 600
Omicron Variant n211i mutation 600
N50 601
Omicron Variant n679k mutation 601
Omicron Variant n856k mutation 602
Omicron Variant n969k mutation 602
Not applicable 602
Aggregation not applicable 603
Aggregation scale not applicable 603
Aggregation set not applicable 603
No amplification control 604
Class not applicable 604
Compartment not applicable 605
Compartment set not applicable 605
Domain not applicable 605
Group not applicable 606
Name 606
English name for countries 607
Official state name 607
Not a number 607
Nomenclature not applicable 608
NanoPlot 608

Specimen not applicable 609
Specimen set not applicable 609
Native Name 609
Unit not applicable 610
Unit set not applicable 610
NB.1.8.1 variant (Nimbus) 610
number of base-pairs sequenced 611
National Center for Biotechnology Information 611
NCBI Format 612
Nomenclaturre from the NCBI 612
NCBI - notes 612
NCBI's Pathogen Detection Isolates Browser 613
number of contigs 613
ncov-tools 614
University of Illinois/NCSA Open Source License 614
National Database of Antibiotic Resistant Organisms (NDARO) 614
NEBNext Ultra II DNA Library Prep Kit 615
New England Biolabs VarSKip V1a Long Primer Set 615
New England Biolabs VarSKip V1a short Primer Set 616
New England Biolabs VarSKip V2a Primer Set 616
New England Biolabs VarSKip V2b Primer Set 616
Negative experimental control 617
Neighbourhood 617
Local administrative units or neighborhoods 618
Neighbouring relationship 618
Neighbourhood-level Aggregation at Site 618
Population of newly vaccinated persons 619
NextClade nomenclature 619
Nextera XT DNA Library Preparation Kit 620
Nextstrain Software 620
Nanograms per liter 620
NGMLR (Next-Generation Mapping and Long-Read Alignment) 621

Normalized geometric mean 621
Neisseria gonorrhoeae 622
Next-Generation Sequencing (NGS) platforms or intruments 622
Ammonia and Ammonium as Nitrogen 622
Ammonium Nitrogen 623
Night 623
niid_2019-ncov_n sars-cov-2 gene target 623
SARS-CoV-2 Nimbus Variant Group 624
Nano-molar 624
No quality concerns 625
Sample not labelled 625
No liquid concentration, liquid recombined with separated solids 625
Nomenclature 626
Nomenclatures 626
No sample storage medium used 627
No rain 627
Purpose is normalization 627
Normalization Calculation Type 628
NORMAN 628
Norman Format 628
NORMAN - notes 629
Norovirus 629
Norovirus G1 630
Norovirus G2 630
Norovirus GI Group 630
Norovirus GII Group 631
Norovirus Group 631
No Seperation or Concentration 631
Notes 632
Sample missing time stamp 632
Novoalign 633
NovoPlasty 633
Number per 100 kilo-base-pairs 633

Not reported 634
Not reported, Not applicable missing set 634
MinusRT 635
Sarbecovirus-specific N sars-cov-2 gene target 635
SARS-CoV-2 nsp1 Gene target 635
SARS-CoV-2 nsp10 Gene target 636
SARS-CoV-2 nsp11 Gene target 636
SARS-CoV-2 nsp15 Gene target 636
SARS-CoV-2 nsp16 Gene target 637
SARS-CoV-2 nsp2 Gene target 637
SARS-CoV-2 nsp3 Gene target 638
SARS-CoV-2 nsp4 Gene target 638
SARS-CoV-2 nsp5 Gene target 638
SARS-CoV-2 nsp6 Gene target 639
SARS-CoV-2 nsp7 Gene target 639
SARS-CoV-2 nsp8 Gene target 639
SARS-CoV-2 nsp9 Gene target 640
Non-template control 640
NTC Amplification Detected 641
Control-plate Flag - NTCs 641
number of total reads 641
No target present 642
Nephelometric turbidity unit 642
Nuclisens automated magnetic bead extraction kit 643
nucleomag (ref. 744220.4) using kingfisher automated instrument 643
Nuclisens manual magnetic bead extraction kit 643
Null 644
ISO 3166-1 numeric country code 644
Number of NTCs per Run 645
number of unique reads 645
National Wastewater Surveillance System 645
US-CDC NWSS Format 646
NWSS - notes 646

NWSS - process 646
Water 647
coronavirus OC43 647
oc43 spike target 648
Ocean, natural water body 648
Other Collection depreciated 648
Odour Control Unit 649
Office 649
SIL Open Font License 1.1 650
Original Data Format Set 650
Lab Analysis 650
Omicron BA.1 651
Omicron BA.2 651
Omicron BA.2.75 651
Omicron BA.4 652
Omicron BA.5 652
SARS-CoV-2 Omicron Variant Group 652
Onset date 653
Online Sensor 653
Ontology reference 654
Value out of range 654
Open license not otherwise described 654
Orthophosphates 655
Optical calibrator sample 655
Surface water 656
Organization table Shorthand 656
Other residential building 656
OR Boolean aggregation 657
Sequence Order 657
SARS-CoV-2 orf10 Gene target 658
SARS-CoV-2 orf14 Gene target 658
ORF1a sars-cov-2 gene target 658
ORF1ab sars-cov-2 gene target 659
ORF1b sars-cov-2 gene target 659

SARS-CoV-2 orf3a Gene target 659
SARS-CoV-2 orf3b Gene target 660
SARS-CoV-2 orf6 (ns6) Gene target 660
SARS-CoV-2 orf7a Gene target 661
SARS-CoV-2 orf7b (ns7b) Gene target 661
SARS-CoV-2 orf8 (ns8) Gene target 661
SARS-CoV-2 orf9b Gene target 662
SARS-CoV-2 orf9c Gene target 662
Organism 663
Organization ID 663
Organization table 663
Organizations table column order 664
Organziation table required headers 664
Organization level 665
Organization level set 665
Organization sector 665
Organization sector set 666
Organization Type 666
Organization type set 666
Sample origin 667
Original Data Format 667
Sample Origin set 668
Oxidation reduction potential (ORP) 668
OrthoFinder Software 668
Orthopox Virus Group 669
Open Science Foundation (OSF) 669
Open Software License 3.0 670
Other Collection depreciated 670
Other aggregation scale 670
Other 671
Other aggregation set 671
Other aggregation depricated 672
Other (or proprietary) Format 672
Access to other prov depricated 672

Other report table set 673
Variants Other 673
Other Site - sample depreciated 674
Other Site - Site depreciated 674
Other Unit depricated 675
Value is an outlier 675
Outbreak declaration 675
End of Outbreak 676
Outbreak - on-going 676
Outbreak class 677
Outbreak declaration Value Set 677
Declared outbreak or Outbreak start 677
Overlapping relationship 678
Delta Variant p100l mutation 678
Omicron Variant p13l mutation 678
Delta Variant p2046l mutation 679
Delta Variant p2287s mutation 679
Omicron Variant p3395h mutation 680
Delta Variant p681r 680
Parts Look-up table Shorthand 680
polymerase activation 681
Paired Layout 681
Pangolin nomenclature 681
Pangolin Software 682
Papilomavirus Group 682
Paraxanthine (PARA) 683
Parainfluenza Group 683
Parapoxvirus Orf Virus Spike Target 683
Parent dataset ID 684
Parechovirus group 684
Parent sample ID 685
Parent Site ID 685
Part description 685
Part identifier 686

Part instruction 687
Parts Look-up table 687
Parts table column order 687
Parts table required headers 688
Part Support 688
Part type column (Reported) 688
Part type input (wide table) 689
Part type name (wide table) 689
Part types part type 690
Passive Sample - General 690
Pasteurized sample 690
Pathogenwatch 691
PATRIC/RAST Database 691
PBPfinder 692
Phosphate Buffered Saline (PBS) 692
Primary Clarifier Effluent depreciated 692
Postal or Zip Code 693
qPCR Class 693
PCR Action/Activity 694
PCR action/activity set 694
PCR Quanitification Cycles 694
PCR method 695
PCR quality set 695
PCR Sequencing Selection Method 695
PCR Method set 696
Primary Clarifier Sludge depreciated 696
Porcine Circovirus 1 (PCV-1) 697
Porcine Circovirus 2 (PCV-2) 697
Number of people 698
Primary clarifier effluent 698
Polyethyleneglycol (PEG) precipitation 698
PEHaplo 699
Percent 699
percent read contamination 699

Percent unit set 700
percent Ns across total genome length 700
Percent recovery 701
Persons for square kilometre 701
Persons per square mile 701
PGAP (Prokaryotic Genome Annotation Pipeline) 702
pH 702
Public Health Actions Report Table Shortname 703
PHA4GE Format 703
Access to phac 703
Public Health Action ID 704
Public Health Actions Report Table 704
Public health actions table column order 705
Public health actions table required headers 705
Public health advisory 705
Public Health Advisory Value Set 706
PHAGE 706
Bacteriophage Group 706
PHAGE - notes 707
Phagetyping Results 707
Phandango 708
Pharmaceutical manufacturing plant 708
pH class 708
Public health emergency (outbreak) 709
Phenol chloroform 709
PHES-ODM Version 1 Format 709
PHES-ODM Version 2 Format 710
PHES-ODM Version 3 Format 710
Pseudomonas virus phi6 711
phi6 spike target 711
Country national phone prefix 711
Total phosphorous 712
Total Phosphates 712
PHRED quality score 712

Physical property 713
PhyloPhlAn Software 713
PhyloSuite Software 714
PhyML Software 714
Physical class 714
Picard MarkDuplicates 715
Picobirnavirus 715
Picobirnavirus Group 716
Pipeline ID 716
PIQMIe 717
PiSeqQC 717
Primary key 717
Plasmodium 718
Platanus 718
Plumbing drain 719
PMMoV- and flow-normalized mean 719
PMMoV Group 719
PMMoV-normalized mean 720
PMMoV Standarized 720
PMMV forward primer (ABI) 721
PMMV probe (ABI) 721
PMMV reverse primer (ABI) 721
Polygon table Shorthand 722
Post-Grit depreciated 722
Polygon License 722
Policy and political sector or organization 723
Poliovirus Group 723
Polygon 723
Polygon ID 724
Polygon ID Object 724
Polgygon ID Subject 725
Polygon Relationships Table 725
Polygon relationships table column order 725
Polygon relationships table required headers 726

Polygon relationship ID 726
Polygon table 727
Polygons table column order 727
Polygon table required headers 727
Polyomavirus Group 728
Polygon Population 728
Polygon Relationship Set 728
Polygon or site specimen set 729
Polygon specimen set 729
Pooled 730
Population 730
Populated area type set 730
Populated area type 731
Population assessment method 731
Population Class 732
Type of date for case reporting depreciated 732
Population density 732
Population density unit set 733
Population equivalents 733
Population group 733
Population Interval Set 734
Population assessment method set 734
Population or polygon specimen set 735
Population Served 735
Population Served - Interval 735
Population unit set 736
Polygon Relationships Table Short Name 736
Porechop 736
Port or Harbour 737
Population or sample set 737
Positive experimental control 738
Population or site set 738
Population specimen set 738
PostgreSQL License 739

Percent positive 739
parts per million 740
PMMoV-CP 740
Percent positivity rate 740
Percent primary sludge 741
parts per thousand 741
Protocol relationships table Shorthand 741
Precipitation (from solution) 742
Precipitation - general 742
Precipitation class 743
Precipitation unit set 743
Storage temperature prior to concentration 743
Storage time prior to concentration 744
Predicted data 744
Predictive Modeling Calculation Type 745
Storage temperature prior to extraction 745
Storage time prior to extraction 745
preQC (from Meraculous) 746
presampling activity 746
Presampling activity category set 747
Pre-sampling weather 747
Pretreatment 747
Primary clarifer 748
Genetic primer 748
Genetic primer set 749
PRINSEQ 749
Prinseq-lite 749
Primate T-lymphotropic virus 1 750
Primate T-lymphotropic virus 2 750
Private sector 751
Private data - not for disemination 751
Protocols table Shorthand 751
Processing group 752
Environmental survey or profiling 752

Program decription tables 753
Prokka (with serotyping integration) 753
Prokka + Roary Pipeline (Nextflow) 753
promega automated tna kit 754
promega wastewater large volume tna capture kit - depreciated754
promega ht tna kit 755
promega manual tna kit 755
promega wastewater large volume tna capture kit 755
Proportion of total 756
Proportion of variant in sample 756
Proteins class 756
Protocol ID 757
Protocol ID container 757
Protocol ID object 757
Protocol ID subject 758
Protocol relationships table 759
Synthetic ID for the protocolRelationships table 759
Protocol relationships table column order 760
Protocol Relationship table required headers 760
Protocol Relationships set 760
Protocols table 761
Protocols table column order 761
Protocols table required headers 761
Protocol steps table 762
Protocol steps table column order 762
Protocol steps table required headers 763
Protocol table set 763
Protocol version 763
Access to prov ha 764
Provisional report 764
Province-level Aggregation at Site 765
Protocol steps table Shorthand 765
Pseudomonas 765
Pseudomonas Group 766

Primary clarifier sludge 766
Pumping station 766
Post-grit 767
Practical salinity unit 767
Pretreatment description - depreciated 768
Number of positive tests 768
Public Administration 768
Public Authority 769
Public health agency 769
Access to public 769
PubMLST 770
Puro virus 770
Puro virus spike target 771
Purpose 771
Purpose set 771
Puumala virus (PUUV) hantavirus 772
Poliovirus type 2 772
Peptone Water with Glycerol 773
Human Polyomavirus (PyV) 773
BK Polyomavirus (BKV) 773
JC Polyomavirus (JCV) 774
q19e omicron-variant gene target 774
q493r omicron-variant gene target 775
q498r omicron-variant gene target 775
q954h omicron-variant gene target 775
Quaility assurance method 776
QC3 776
Sequencing Quality Control Method 777
Quality concerns 777
qiagen allprep dna/rna kit 777
qiagen digital PCR 778
qiagen ez1 virus mini kit v2.0 778
qiagen allprep powerfecal dna/rna kit 778
qiagen allprep powerviral dna/rna kit 779

qiagen powerwater kit 779
qiagen qiaamp buffers with epoch columns 780
qiagen rneasy kit 780
qiagen rneasy powermicrobiome kit 780
qiagen allprep dna/rna kit depreciated 781
qiagen qiaamp dsp viral rna mini kit 781
QIAseq FX DNA Library Kit 781
Quantitative Real-Time PCR 782
qPCR instruments (quantitative PCR) 782
qProfiler2 783
Quality reports table Shorthand 783
Qualitative 783
Quality control 784
Quality flag 784
Quality indicators 785
Quality Indicator Set Header 785
Quality indicator sets 785
Quality report ID 786
Quality reports table 786
Quality rerpots table column order 786
Quality report table required headers 787
Quantitative 787
Quarantine recommendation 788
R squared 788
r203m delta-variant gene target 788
R346T Mutation 789
Raindance digital PCR 789
dPCR Rain Percentage 789
Rainy 790
Random sampling surveillance program 790
Random sequencing selection method 791
Ratio 791
Raw data 791
Raw wastewater 792

Raw Sequence Data Processing Method 792
Raw Sequence Data Processing Method Set 792
Raw sewage at site 793
Raw sewage downstream from a site 793
Raw sewage upstream from a site 794
RaxML Software 794
IP2 rdrp sars-cov-2 gene target 794
IP4 rdrp sars-cov-2 gene target 795
Sequencing read mapping software name 795
Sequencing read mapping software set 796
Date sample recieved 796
Recombinant Lineage Variant 796
Recovered patients 797
Redundans 797
Refugee camp 798
Reference link 798
Region 799
Regular Pathogen Surveillance 799
Regular reports table set 799
Relationship between entities 800
Measure relevance end date 800
Measure relevance start date 801
Relative humidity 801
Relative humidity unit set 802
Relationship Not Reported 802
General Relationship Set 802
Representative grab sample 803
Replicate Type set 803
replicate number 803
Primary reporting authority ID 804
Secondary reporting authority ID 805
Reportable 805
Report date 806
Reporter ID depreciated 806

Reporter table depreciated 806
Report table input (wide table) 807
Report table name (wide table) 807
Replicate Type 808
Reservoir 808
Resuspend COSCa filter collection 808
Research sector or organization 809
Research purposes 809
ResFinder Database 809
ResFinder Tool 810
Residents per square kilometre 810
Residents per square mile 811
Restaurant 811
Restricted data 811
Results tables 812
Resuspension method 812
Resuspension method set 813
Retained Element 813
Retained Element Set 813
Retention pond 814
Review of records 814
Rickettsia 814
Rickettsia Group 815
River, natural water body 815
RNA Template 816
rRNA Depletion Method 816
RNAlater 816
Ribonuclease P (RNase P) 817
Road 817
Roadside 817
Role of contact 818
Rotavirus 818
Rotavirus Group 819
Routine surveillance 819

Rate per 100,000 819
Revolutions per minute (RPM) 820
Raw post-pasteurized wastewater 820
Resistant strain identified 820
Respiratory syncytial virus A and B combined 821
Respiratory syncytial virus A 821
Respiratory syncytial virus B 822
Respiratory syncytial virus (RSV) Group 822
Respiratory syncytial virus 822
RSV N-gene 823
reverse transcription 823
RT-qPCR intruments 824
Rubella 824
Rubella Group 824
Rural 825
s2083i omicron-variant gene target 825
s371l omicron-variant gene target 825
s373p omicron-variant gene target 826
s375f omicron-variant gene target 826
s477n omicron-variant gene target 827
Sample 827
Saffold Virus Group 827
Saffold virus (SAFV) 828
Saffold virus 1 (SAFV-1) 828
Saffold virus 2 (SAFV-2) 829
Saffold virus 3 (SAFV-3) 829
Saffold virus 4 (SAFV-4) 829
Saffold virus 5 (SAFV-5) 830
Saffold virus 6 (SAFV-6) 830
Saffold virus 7 (SAFV-7) 831
Saffold virus 8 (SAFV-8) 831
Salivirus A (Salivirus aklasse) 831
Salivirus Group 832
Salinity 832

Salinity unit set 833
Salmonella 833
Salmonella Group 833
SalmonellaTypeFinder 834
Sample material 834
Sample concentrate 834
Sampling Event 835
Sample ID 835
Sample ID object 836
Sample ID subject 836
Sample material set 837
Sample quality set 837
Sample relationships table 837
Synthetic ID for the sampleRelationships table 838
Sample relationships table column order 838
Sample relationships table required headers 839
Sample relationships set 839
Sample report table 839
Sample shed 840
Samples table column order 840
Sample table required headers 841
Collection other depreciated 841
SAMtools rmdup 841
SAMtools 842
Sample volume 842
Sapovirus 843
Sapovirus Group 843
Sample relationships table Shorthand 843
SARS-CoV-2 844
Sample report table Shorthand 844
Sample specimen set 845
Sparse coverage 845
Secondary clarifier effluent depreciated 845
Standard curve frequency 846

School 846
School closure 846
sciencell viral rna isolation kit 847
Sequencing script version set 847
Genetic sequencing script version 848
Secondary clarifier sludge depreciated 848
Standard deviation 848
Normalized standard deviation 849
Sludge dryer 849
Sterile Distilled Water with Sodium Thiosulfate 849
Sets look-up table Shorthand 850
Sea, natural water body 850
Secondary clarifer 851
Seconds 851
See unit (aggregation scales) 851
See unit (data type) 852
See unit (value) 852
Secondary clarifier effluent 853
Access to self 853
Semi-solid 853
Date sample was sent 854
Seoul virus (SEOV) hantavirus 854
Septic tank wastewater 855
Septic tank 855
Sequence Assembly Software 855
sequence assembly length 856
Sequence Assembly Software Set 856
Sequence Contaminated 856
SeqKit rmdup 857
SeqKit stats 857
Sequencing Layout 858
Sequencing Layout set 858
SeqMan Pro (Lasergene) 858
Sequencing QC Pipeline 859

Sequencing QC Pipeline Set 859
Sequencing quality set 859
Sequencing selection method 860
Sequencing selection method set 860
SeqSero2 861
Sequencing Strategy 861
Sequencing Strategy set 861
seqtk 862
SeqTyping 862
Genetic sequences class 863
serial dillution 863
Serial dilution 863
Serotyping Method 864
Serotyping Method Set 864
SerotypeFinder 864
Serological Variant (Serovar) 865
Sewer Sediments Depreciated 865
Composite Set ID 866
Set ID 866
Sets look-up table 867
Sets table column order 867
Sets table required headers 867
Settled solids 868
Set type 868
Set Type Set 868
Severity indicator 869
Severity set 869
Sewage equivalent 870
Sewer network file link depreciated 870
Sewage travel time 870
Shaker aggitation speed 871
Shasta 871
Sampleshed set 871
Shigella 872

Shigella Group 872
Ship 873
Shipped on ice 873
ShortBRED Software 873
Short names 874
Read Lengths Shorter Than Expected 874
Shorthand or Short Name Set Type 874
Short Name Set 875
Sites table Shorthand 875
Sickle 876
Single 876
Single Layout 876
Singleplex, probe-based, one-step RT-qPCR 877
Site or sample specimen set 877
Site specimen set 877
Salmonella In Silico Typing Resource (SISTR) 878
Site 878
Site ID default 879
Site features group 879
Site ID 879
Level of Aggregation of a Sampling Site 880
Site Level Category Set 880
Site measure ID 881
Sites table 881
Sites table column order 881
Sites table required headers 882
Site Type 882
Site set 883
Skewer 883
Skimmed milk flocculation 883
Slow-flowing 884
Sample Limit of Detection (LOD) 884
slope 885
Wastewater Sludge - non-specified 885

Slurry 885
Siemens per meter 886
SMALT 886
SMARTer ThruPLEX Plasma-seq Kit 886
Skim Milk–Glycerol Medium 887
Smoothing Calculation Type 887
Snap 888
SNAPP Software 888
Sewer network file link depreciated 2 889
Snowy 889
Sin Nombre virus (SNV) hantavirus 889
Soap2 890
Soap3 890
SOAPdenovo 891
Social distancing measures 891
Software Class 891
Solid fraction (general) 892
Solid Fraction (Dry) 892
Solids/Pellet retained 892
Solid 893
Solid seperation 893
Solid separation set 894
Solid fraction (Wet) 894
SortMeRNA 894
Wide name source 895
Source Code 895
Source Protocol ID 896
Protocol step source ID 896
Sovereign status of a country 896
SPAdes 897
Specific humidity 897
Specific humidity unit set 898
Specifies 898
Specimen 898

Specimen input (wide table) 899
Specimen name (wide table) 899
Specimens 899
Specimen Set Header 900
Specimen sets 900
Spectrophotometers or fluorometers 901
Speed class 901
Speed Unit Set 901
Sucrose Phosphate Glutamate (SPG) Buffer 902
Spike matrix and recovery 902
Spike Concentration 902
SARS-CoV-2 Spike gene (orf2) 903
Spike material 903
Spike material set 904
Recovery efficiency spike target 904
Recovery efficiency spike target set 904
Sample spilled 905
Spring 905
Sequence Read Archive (SRA) 906
SRST2 Software 906
SSAKE 906
Streptococcus Serotyping Tool (SSI) 907
Secondary clarifier sludge 907
Social services shelter 908
Stabilization pond 908
Stagnant 908
Statistical Analysis of Metagenomic Profiles (STAMP) Software 909
Standard for Data Adjustment 909
Standard concentrations class 910
Standard curve class 910
Standardization Calculation Type 910
Staphylococcus Group 911
STAR (Spliced Transcripts Alignment to a Reference) . . . 911

StarAMR Software 912
Departments, states, or provinces 912
State, Province, or Region 912
Status 913
Status set 913
Standard sample 914
Standard concentration unit set 914
Standard Curve Calculation Method 914
Standard Curve Calculation Set 915
Shiga-toxin-producing Escheria coli (STEC) 915
Storage temp 915
Protocol Step ID 916
Step ID Object 916
Step ID Subject 917
Method step parent ID 917
Protocol step version 918
Standard Error 918
Stercobilin 918
Sample Storage Medium 919
Sample Storage Medium Set 919
Stormy Weather 920
Sewer network file blob 920
Storage time 920
Stream 921
Strain ID 921
StrainPhlAn Software 922
Streptococcus Group 922
Streptococcus pneumoniae 922
Sodium Thiosulfate Solution 923
Summary worksheet Shorthand 923
Subread 924
Subsample (General) 924
Suburban 924
Sub-variant or lineage 925

Sucralose . . . 925
Sudan virus, Orthoebolavirus sudanense . . . 926
Rolling sum of previous 14 days . . . 926
Summary . . . 926
Summary worksheet . . . 927
Sunny . . . 927
SureSelect XT HS2 DNA Library Preparation Kit . . . 928
Surface compartment . . . 928
Other surface . . . 928
Surface compartment set . . . 929
Surface and water compartment set . . . 929
Surface swab . . . 929
Surveillance alert . . . 930
Surveillance Alert Value Set . . . 930
Surveillance Level . . . 931
Surveillance Level Set . . . 931
Sewage truck . . . 931
Swift 2S Turbo DNA Library Kit . . . 932
Sewer sediment . . . 932
Sewer catchment area . . . 932
Synthetic sample . . . 933
t19r delta-variant gene target . . . 933
t3646a delta-variant gene target . . . 934
t547k omicron-variant gene target . . . 934
t9i omicron-variant gene target . . . 935
Tables . . . 935
Table column set . . . 935
Table Support . . . 936
Wide name measurement and linkage tag . . . 936
Taï Forest virus, Orthoebolavirus taiense . . . 937
Tanapox . . . 937
Tanapox Group . . . 938
TaqPath N sars-cov-2 gene target . . . 938
TaqPath S sars-cov-2 gene target . . . 939

Targeted surveillance program 939
Targetted surveillance initiated 939
Taxonium Software 940
Total Dissolved Solids (TDS) 940
Technical replicate 940
Sample temperature 941
Temperature class 941
Temperature unit set 942
Template Sheet Set 942
Template Set 942
Nucelic Acid Template Type 943
Nucleic acid template volume 943
Airport terminal 944
Test date 944
Number of tests performed 944
Protocol testing 945
Tetracycline Anti-microbial resistance Group 945
TetW Tetracycline-resistance gene target 945
Thermal cyclers 946
thermo magmax microbiome ultra nucleic acid isolation kit 946
thermo magmax viral/pathogen nucleic acid isolation kit . . 947
Threat designation 947
Threat designation Value Set 947
Public health threat targeted by action 948
ThruPLEX DNA-seq Kit 948
Transport hub - General 948
Time class 949
Time proportional sample 949
Time standardized 950
Time unit set 950
Total Kjeldahl Nitrogen 950
Country code top-level domain 951
Total Nitrogen 951
TopHat 952

Total amount or count - the sum 952
Time Proportional 24hr sample 952
Treponema pallidum 953
Translation look-up table Shorthand 953
Traditional Serotyping methods 954
Train 954
Synthetic ID for the translations table 954
Translation look-up table 955
Translation table column order 955
Translation table required headers 956
Transportation vehicle - general 956
Passive (trap) sampling 956
Travel ban 957
Travel hub surveillance - general 957
Travel warning 957
Treated 958
Treatment ID 958
TreeTime Software 959
Treponema Group 959
Trichomonas Group 959
TrimGalore! 960
Trimmomatic 960
Trinity 961
TE Buffer (Tris-EDTA) 961
Wastewater Triturator 961
trizol, zymo mag beads w/ zymo clean and concentrator . . 962
trizol, garnet bead beating, alcohol precipitation 962
trizol and RNA purification kit 962
Train Station 963
TRUE 963
TruSeq DNA PCR-Free Library Prep Kit 964
Total solids concentration 964
Tryptic Soy Broth (TSB) 964
Total suspended solids 965

Concentration of total suspended solids 965
Torque Teno Virus 965
Torque Teno Virus Group 966
Tuberculosis Group 966
Francisella tularensis (tularemia) Group 967
Turbidity 967
Turburdity class 968
Turbidity unit set 968
Trichomonas vaginalis 968
Tube weight empty 969
Tube weight full 969
Type other depreciate 969
Type other depreciate2 970
University campus 970
Ugene 971
Micrograms per gram 971
Micrograms per litre 971
Micrograms per milligram 972
Micro-litres 972
Ultracentrifuges 972
Micromho per centimeter 973
Unique Molecular Identifier (UMI) Tagging 973
UMI-tools 974
Undisclosed or Not Provided 974
Unicycler 974
Unique sample 975
Unit 975
Unit input (wide table) 976
Unitless measure 976
Unitless unit set 976
Unit name (wide table) 977
Units 977
Unit set 977
Unit sets 978

Unknown sample 978
The Unlicense 979
Ultracentrifugation 979
Untreated 979
Upper limit of a 95% confidence interval 980
Upstream sites 980
Urban 981
Ureaplasma 981
Ureaplasma Group 981
Urobilin or urochrome 982
Micro-Siemens per centimetre 982
Ultrafast Sample placement on Existing tRees (UShER) Software 983
U site measure ID 983
Coordinated universal time (UTC) zone 983
Coordinated universal time (UTC) zone in daylight savings 984
Utilities sector or organization 984
Universal Transport Medium (UTM) 985
V1104L Mutation 985
v2930l delta-variant gene target 985
Vacuum sludge sampling 986
Validation study 986
Value Treatment 986
Value treatment value set 987
Value 987
VanA-A Vancomycin-resistance gene target 988
Vancomycin Anti-microbial resistance Group 988
Vancomycin resistance 988
Variable character data type 989
Frequency of variants detected 989
Variants class 989
Varicella 990
Varicella Group 990
Population with 1 dose of vaccine 991

Proportion of population with 1+ vaccine dose(s) 991
Population with 1+ dose(s) of vaccine 991
Population with 2 or more doses of vaccine 992
Proportion of population with 2+ vaccine doses 992
Population with 2+ or more doses of vaccine 993
Population with 3 or more doses of vaccine 993
Proportion of population with 3+ vaccine doses 993
Population with 3+ or more doses of vaccine 994
Population with 4 or more doses of vaccine 994
Proportion of population with 4+ vaccine doses 995
Population with 4+ or more doses of vaccine 995
Change to Vaccine Schedule 995
Velvet 996
ODM V1 category 996
ODM V1 location 997
ODM V1 table 997
ODM version 1 to 2 changes 997
ODM V1 variable 998
Vertical grab sampling 998
Vibrio 998
Vibrio Group 999
Viral passage experiment 999
Miscellaneous viruses group 999
Variant of concern 1000
Variant of interest 1000
Size in volume 1001
Volume proportional sample 1001
Volume unit set 1002
Volatile suspended solids 1002
Volatile suspended solids - ignition 1002
Vesicular stomatitis virus (VSV) target 1003
VSV forward primer (ABI) 1003
VSV probe (ABI) 1004
VSV reverse primer (ABI) 1004

Vesicular Stomatitis Virus (VSV) Group 1004
Verotoxin-producing Escherichia coli (VTEC) 1005
Viral Transport Medium (VTM) 1005
variant under monitoring 1005
Water compartment 1006
water concentrating buffer (R2042-1) 1006
Water depreciated 1007
Water compartment set 1007
Water Quality Group 1007
Water-based Transit Hub 1008
Wastewater temperature 1008
Weather (time of sampling) 1008
Weather class 1009
Weather set 1009
Weeks 1010
Well 1010
West Nile 1010
Whole genome sequencing 1011
WHO nomenclature 1011
Wide 95% interval 1011
Specified attribute (wide table) 1012
Compartment set for wide names 1012
Fraction set for wide names 1013
Measure identification (wide table) 1013
Wide Name 1013
Wide name table 1014
Wide name table order 1014
Wide name table required 1014
Wide name type 1015
Specified protocol (wide table) 1015
Speciment set for wide names 1016
Wind Speed 1016
Wind speed unit set 1016
Whole Metagenome Sequencing 1017

Wide name table Shorthand 1017
Sample stored incorrectly 1017
Sample stored at wrong temperature 1018
World Sphere (W-SPHERE) 1018
wSphere Format 1019
World Sphere (W-SPHERE) notes 1019
Delta Variant wt214 gene target 1019
Wastewater Treatment Agency 1020
WTDBG (aka wtdbg2) 1020
Do What The F*ck You Want To Public License { #wtfpl } 1020
Wastewater Treatment Plant Operator 1021
Whole Virome Sequencing 1021
Weight for weight 1022
Wastewater aerobic digestion 1022
Wastewater anaerobic digestion 1022
wastewater comminution process 1023
Wastewater sludge removal 1023
Wastewater sludge dewatering 1023
Wastewater sludge drying 1024
Wastewater filtration 1024
Wastewater grit removal 1025
Wastewater microbial treatment 1025
Wastewtaer primary sedimentation 1025
Wastewater screening process 1026
Wastewater secondary sedimentation 1026
Wastewater treatment plant 1026
Wastewater treatment efficiency assessment 1027
Back-up wastewater treatment site 1027
Wastewater treatment plant designed capacity 1028
Industrial wastewater treatment plant 1028
Municipal wastewater treatment plant for combined sewage 1028
Municipal wastewater treatment plant for sanitary sewage only 1029
Wastewater treatment 1029

XEC Variant . . . 1030
Relative Centrifugal Force (RCF) or x g units . . . 1030
y505h omicron-variant gene target . . . 1030
Years . . . 1031
Yersinia enterocolitica . . . 1031
Yersinia Group . . . 1032
Zenodo . . . 1032
Zika . . . 1032
zLib License . . . 1033
Zones look-up table Shorthand . . . 1033
English name of country sub-domains . . . 1033
Zones look-up table . . . 1034
Zones table column order . . . 1034
Zones table required headers . . . 1035
zymo quick-rna viral kit #r1035 . . . 1035
zymo quick-rna viral 96 kit #r1041 . . . 1035
zymo environ water rna kit (cat. r2042) . . . 1036
zymo quick-rna fungal/bacterial miniprep #r2014 . . . 1036
zymo environ water rna kit (cat. r2042) - depreciated . . . 1036

Sets **1039**
Public Health Action Type Value Set . . . 1039
Aggregations . . . 1040
Aggregation scales . . . 1043
Aggregation sets . . . 1043
Boolean aggregation set . . . 1044
Linear scale aggregation set . . . 1044
Logarithmic scale aggregation set . . . 1046
Aggregation set not applicable . . . 1047
Other aggregation set . . . 1047
Aggregation sets . . . 1049
All Public Health Actions Set . . . 1050
Data Adjustment Standard Value Set . . . 1053
Antimicrobial Resistance (AMR) Classification Value Set . . . 1054

AMR Software Set 1055
Attributes 1056
Bacterial testing method set 1082
Boolean value set 1083
Calculation type set 1084
Categories 1084
Lineage- or Clade-analysis Software Set 1177
Classes 1180
Collection Approximate Time Period Set 1183
Sample collection set 1184
Compartments 1186
Compartment sets 1187
    Air compartment set 1187
    Air and surface compartment set 1187
    Air and water compartment set 1188
    Any compartment set 1188
    Human compartment set 1189
    Compartment set not applicable 1189
    Surface compartment set 1189
    Surface and water compartment set 1189
    Water compartment set 1190
    Compartment set for wide names 1190
Compartment sets 1191
Consensus Sequence Software Set 1192
Control Measure Implementation Value Set 1194
Data Repository Set 1195
Data types part type 1197
Deduplication Method Set 1198
Dehosting Method Set 1200
Additional dictionary sheets 1201
Domains 1202
Exceptions Part Type 1202
Nucleic Acid Extraction set 1203
Sample fraction set 1207

Geographic set 1207
Groups 1208
Genomic Target Enrichment Methods Set 1220
Inhibition set 1220
Instrument set 1221
Library Preparation Kit Set 1223
Data license set 1226
Sample Material Characteristics Set 1231
Measures 1232
Concentration method set 1284
Methods 1287
Missingness 1292
Missingness sets 1293
General missingness set 1293
Geographical Reference Missingness Set 1294
Not reported, Not applicable missing set 1294
Missingness sets 1294
Measure, method, or attribute sets 1295
Nomenclatures 1303
Original Data Format Set 1304
Organization level set 1305
Organization sector set 1306
Organization type set 1307
Sample Origin set 1308
Outbreak declaration Value Set 1308
Part types part type 1309
PCR action/activity set 1314
PCR Method set 1314
Public Health Advisory Value Set 1315
Polygon Relationship Set 1316
Populated area type set 1317
Population Interval Set 1317
Population assessment method set 1318
Presampling activity category set 1319

Genetic primer set 1321
Protocol Relationships set 1326
Purpose set 1327
Quality indicators 1329
Quality indicator sets 1333
    Generic quality flag set 1333
    Measures quality set 1334
    PCR quality set 1337
    Sample quality set 1338
    Sequencing quality set 1340
Quality indicator sets 1342
Raw Sequence Data Processing Method Set 1342
Sequencing read mapping software set 1346
General Relationship Set 1349
Replicate Type set 1351
Resuspension method set 1353
Retained Element Set 1354
Sample material set 1354
Sample relationships set 1356
Sequencing script version set 1357
Sequence Assembly Software Set 1358
Sequencing Layout set 1360
Sequencing QC Pipeline Set 1361
Sequencing selection method set 1364
Sequencing Strategy set 1364
Serotyping Method Set 1365
Set Type Set 1369
Severity set 1371
Sampleshed set 1371
Shorthand or Short Name Set Type 1376
    Short Name Set 1376
Site Level Category Set 1380
Site set 1381
Solid separation set 1386

Specimens . . . 1387
Specimen sets . . . 1388
Any specimen set . . . 1388
Specimen set not applicable . . . 1388
Polygon or site specimen set . . . 1389
Polygon specimen set . . . 1389
Population or polygon specimen set . . . 1389
Population or sample set . . . 1390
Population or site set . . . 1390
Population specimen set . . . 1390
Sample specimen set . . . 1391
Site or sample specimen set . . . 1391
Site specimen set . . . 1391
Speciment set for wide names . . . 1392
Specimen sets . . . 1392
Spike material set . . . 1394
Recovery efficiency spike target set . . . 1394
Status set . . . 1396
Standard Curve Calculation Set . . . 1397
Sample Storage Medium Set . . . 1397
Surveillance Alert Value Set . . . 1400
Surveillance Level Set . . . 1400
Tables . . . 1401
Table column set . . . 1405
Template Set . . . 1406
Threat designation Value Set . . . 1407
Units . . . 1407
Unit sets . . . 1422
Absolute humidity unit set . . . 1422
Alkalinity unit set . . . 1423
Allele unit set . . . 1423
Bacteria unit set . . . 1424
Base-pair unit set . . . 1425
Capacity unit set . . . 1426

Conductivity unit set 1427
Dissolved gas concentration unit set 1427
Electrical potential unit set 1428
Volume flow rate unit set 1428
Genetics unit set 1429
General Humidity Unit Set 1432
Unit set not applicable 1433
Percent unit set 1433
Population density unit set 1433
Population unit set 1434
Precipitation unit set 1438
Relative humidity unit set 1439
Salinity unit set 1439
Specific humidity unit set 1440
Speed Unit Set 1440
Standard concentration unit set 1441
Temperature unit set 1443
Time unit set 1443
Turbidity unit set 1444
Unitless unit set 1445
Volume unit set 1445
Wind speed unit set 1446
Unit sets 1446
Value treatment value set 1449
Weather set 1450
Fraction set for wide names 1451

Tables **1453**
Table types 1454
Header roles 1455
Mandatory, optional, mandatoryIf 1456
Table list 1456
accessions Table 1458
Address table 1458

Calculations Table 1459
Contact table 1460
Countries look-up tables 1461
Dataset table 1463
Instrument table 1464
Language Look-up table 1465
Measure report table 1466
Measure set report table 1468
Organization table 1468
Parts Look-up table 1469
Public Health Actions Report Table 1481
Polygon Relationships Table 1482
Polygon table 1482
Protocol relationships table 1484
Protocols table 1484
Protocol steps table 1485
Quality reports table 1486
Sample relationships table 1486
Sample report table 1487
Sets look-up table 1489
Sites table 1490
Translation look-up table 1492
Wide name table 1492
Zones look-up table 1494

Introduction

Dictionary v3.0.1 Documentation v3.0.1

> Facilitating the Collection and Sharing of High-Quality, Interoperable Environmental Surveillance Data: A Community Open Science Project.

The Public Health and Environmental Surveillance Open Data Model (PHES-ODM or ODM) is an open-source data model and set of tools aimed at promoting global collaboration and use of environment and public health data. The ODM model facilitates interoperable environmental surveillance and research by improving quality reporting data, enhancing data management, and supporting data provenance and sharing.

This documentation is intended for those who want to understand how the ODM model works, its organizational structure, and how to use it effectively for their program. It is also a useful resource for those who currently use a different data dictionary and wish to share their data with a program that uses the ODM. If you need to share your data with another program that uses a different data dictionary, this documentation can help you compare and create a common cross-walk between dictionaries. The ODM starts as a conceptual model that represents real-world processes through data elements and data relationships, which are common to all environmental and public health surveillance systems.

How to use the documentation

There are six document sections, each with a different purpose.[1]

Background provides some additional context and explanation about the history and guiding principles of the PHES-ODM project. This section is not as important for users trying to get started with the model.

Getting to know the ODM is oriented to understanding the ODM. This section explains the ODM, its structure, and how the model was designed and developed.

How to use the ODM are step-by-step guides to help you use different aspects of the ODM such as report templates.

Sample relationships provides a deeper overview of sample relationships and sample provenance, and how to record it accurately in the ODM.

Long-format, wide-format, and wide-names is an overview of the differences between "long" and "wide" formatted data, and how the ODM can be used in both formats. It also provides instructions on how to alternate reproducibly between the two.

Reference guide is a description of each part of the ODM. It serves as a reference for the other sections, and the definitive record of each part, table and set – along with their attributes.

Future documentation

Video tutorials and explanations are available in our vimeo library, with new videos and tutorials still in development. Tutorials will help newcomers get started. Further documentation and lessons that are still forthcoming include items on how to:

[1] David Laing and Divio's Grand Unified Theory of Documentation.

- Describe a protocol using protocol tables.
- Use of the `accessions`, and `calculations` tables.
- Further guidance and walk-throughs on how to use ODM tools

Quick start

You can get to know the ODM by imaging how to record a polymerase chain reaction (PCR) test result for SARS-CoV-2 from a wastewater sample.

1. Get oriented to the ODM tables where you record results

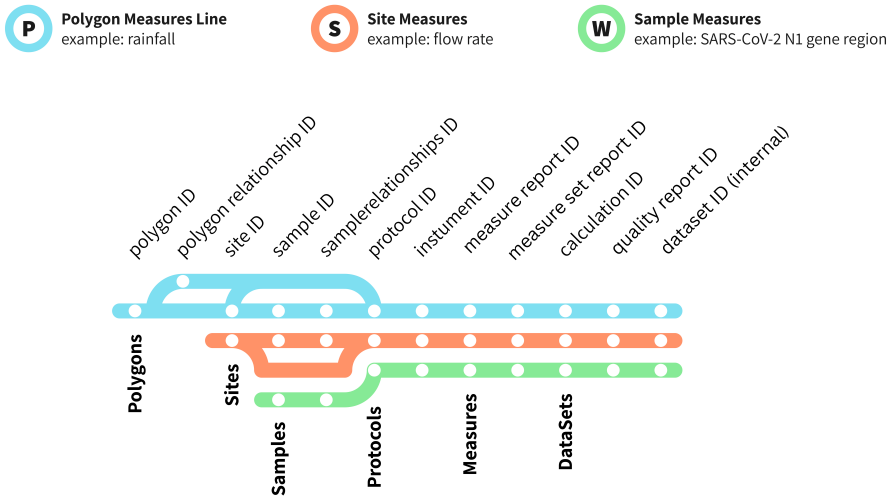


Figure 1.: **Figure 1 - Key ODM tables for recording data**

The `Sample report table` (samples) and the `Measure report table` (measures) are where you record information about samples and measures.

If you want to go deeper, the `Sites report table`(Sites) will capture data about where samples are collected, and the `Polygons report table`(Polygons) will record information about the regions that are represented by environmental samples.

2. View mandatory and optional data fields in the tables reference guide

You can view mandatory and optional data field here: (samples) and (measures). 'Mandatory' means they are fields are needed to ensure interoperablity.

> What are ODM parts and how to find them?
>
> In the ODM, tables are an example of a part. A part name can be identified by its text style like `this`. The part identifier often follows the part in parenthesis, with a link to the part in the reference section. So, `Sample report table` is the part name, and (samples) is the part ID and link to the documentation for that part.
> You can find out more about parts on the reference guide section.

3. Try entering example data in ODM Excel templates

Keep in mind, ODM templates are only examples of how to use the ODM dictionary to record data. Templates are available at the PHES-ODM OSF.io repository. The 'How to use the ODM" section describes how to enter information into tables.

Storing sample data in an ODM template

A `sample` (sampleID) is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. The sample template stores one sample per row. The `Sample report table` has seven mandatory fields that are listed in the reference] for the table.

https://vimeo.com/802349692

Storing measure data in an ODM template

A `measure` (measure) is an observation or measurement of any substance, including biological, physical, or chemical substances, obtained from a specimen such including a site, sample, person, or population. Each measure is stored in the `Measures table` template as a separate row, following the "long" table format, which is the primary method for storing measures. For example, if you recorded PCR results for two SARS-CoV-2 regions, covN1 and covN2, you would record each measurement on a separate line. Alternatively, you can use a "wide" table format to store multiple measures in a single row or create tables that combine both long and wide headers. The European Union supersites template is a hybrid template that exemplifies this (found in the "supersites - FKA airports" folder).

(Video)

4. Next steps

In addition to recording measures from samples, you can also record measures for a specific site, such as wastewater flow rate (flowRate), or the population served by the site, such as the Covid-19 hospitalization rate for a wastewater treatment plant's wasteshed or municipality. **Figure**

2 illustrates the these three types of measurements: `sample`, `site`, and `polygon`.

The "who, where, and why" of these measurements are stored in the contact information tables, geospatial tables, and data source & processing tables; while the "how," which refers to the measurement protocol or method, is stored in the protocol or methods tables, and the results tables.

The "who, where, and what else" are extended in version 3 to also integrate public health actions and external dataset linkages. These are included as optional extensions for programs that want to incorporate these items, and operate at this level of detail.

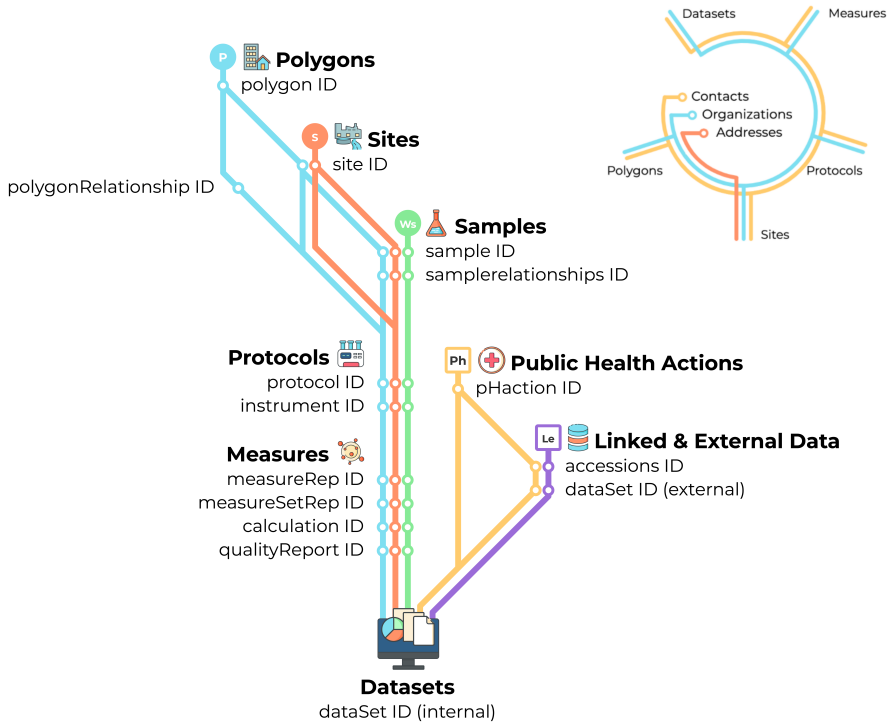


Figure 2.: **Figure 2 - ODM tables and 'subway' lines for storing measures**

Getting help

We hope that the documentation serves its purpose and that you find it useful in figuring out how to best use the ODM and its suite of tools. If you do encounter any issues or questions that do not seem to have an easy answer, please create an issue on our GitHub repository or consult our Discourse page.

Background

Dictionary v3.0.1 Documentation v3.0.1

The ODM is designed to support a broad range of users in the field of environmental surveillance, including wastewater laboratories, municipalities, public health agencies, researchers, and citizen scientists. Its goal is to provide a comprehensive and extensible approach to data collection and management across the lifecycle of environmental surveillance, from sample collection and analysis to public reporting.

The ODM dictionary includes provisions for a wide range of biological, chemical, and physical properties, such as antimicrobial resistance, drugs, and toxins, as well as metadata for laboratory protocols that may affect measurement consistency across laboratories. The ODM supports laboratory information and management systems (LIMS) with measure to describe ensure data quality control and provenance.

To support the open science principle of FAIR data (Findable, Accessible, Interoperable, and Reusable), the ODM strives to make its data easily discoverable, accessible, and usable by all stakeholders.[2] It also adopts an open-source approach, allowing anyone to inspect, modify, and enhance the codebase in a transparent and collaborative manner on platforms like GitHub.

While the ODM is a complex dictionary, it includes tools to support its use, such as data validation, input templates, and SQL database definitions for data storage. Additionally, it supports collaborations among different

[2] FAIR Priniciples.

organizations seeking to share and combine samples and measurements. As an open model, third parties can extend the model, such as the European Union Digital European Exchange Platform (EU4S-DEEP) data templates for wastewater surveillance at airports, European Union Digital European Exchange Platform (EU4S-DEEP) data templates for wastewater surveillance at airports, the CETO Epidemiologic platform, and Ottawa Automatic Data Pipeline to analyse qPCR data and transform it to ODM format.

Overall, the ODM aims to support the evolving field of environmental surveillance and science by providing a standardized, extensible approach to data collection and management.

Getting to know the ODM

Dictionary v3.0.1 Documentation v3.0.1

What are "Parts" and "Part Types"?

Within the ODM, every component or element of the model and the dictionary is called a "part". Parts are grouped into "part types".

Because the term "parts" refers to every component of the ODM, "part types" are a way to differentiate between parts which have different functions and structures. The three most important part types are:

- **Measures**: A measurement or observation of any substance including a biological, physical or chemical substance.
- **Methods**: A procedure for collecting a sample or performing a measure.
- **Attributes**: A description of the who, where, when, and why of environmental surveillance.

See the parts reference document for more details.

There are additional part types to support the dictionary including:

- Aggregations
- Aggregation scales
- Aggregation sets
- Categories

- Classes
- Compartments
- Compartment sets
- Data types
- Additional dictionary sheets
- Dictionary set type
- Domains
- Exceptions Part Type
- Groups
- Missingness
- Missingness sets
- Measure, method, or attribute sets
- Nomenclatures
- Part Support
- Part types
- Quality indicators
- Quality indicator sets
- Short names
- Shorthand or Short Name Set Type
- Specimens
- Specimen sets
- Tables
- Table Support
- Units
- Unit sets

For information and details about all the part types, please see the parts reference document.

"Sets" and the rationale behind sets

"Sets" are a way of grouping together different possible categorical inputs within the ODM. The purpose behind sets is to group options together

so that users only need to check a few options from a drop-down menu, rather than scroll through a long list. Sets are also designed so that a single part can be used in multiple sets, which avoids the need to create multiple versions of this part for these different use contexts. For example, if you're taking a measure of concentration, that measure will likely populate the unit choice drop-down list with units from the "standard concentration unit set". Units in this set include Milligrams per litre, parts per million, and Percent Primary Sludge. Similarly, if one were measuring the amount of oxygen in a wastewater sample they would be offered units from the "dissolved gas unit set". The units in this set include parts per million, and Milligrams per litre. You see here how Milligrams per litre is used twice across the sets, but exists still as a single part in the parts list. Unit sets are only one type of set, with the others being:

- Aggregation sets
- Compartment sets
- Dictionary sets
- Missingness sets
- Measure, method, or attribute sets
- Quality indicator sets
- Shorthand or Short Name Sets
- Specimen sets

Details about these sets are their similar - but unique - applications can be found in the at their individual links. Importantly, "Measure, method, or attribute sets", or "MMA sets" are a little different. See the section below for an explanation of this difference.

Why MMA sets are a little different

One of the reasons why "sets" are set up and organized the way that they are, is to allow for the re-use of parts in multiple sets. "Measure, method, or attribute sets", or "MMA sets" are, however, an exception to

this rule because the categories that make up a category set are - in general - used in only one set. Furthermore, the general sets are needed for almost every measure or method (which require unit, aggregation, quality, and compartment information), while MMA sets are used only in specific circumstances for specific fields. These are things such as collection metadata (example: Sample collection category set), dictionary metadata and model architecture (example: Data Type Category Set), or more detailed types of certain methods (example: Nucleic Acid Extraction Category Set). MMA sets are also a distinct part type, and more information about them can be found in the entry for Measure, method, or attribute sets.

The "what" and "why" of Specimen IDs

Specimen IDs indicate the level at which a measure is being done. This can be: a site measure, ie. a measure at a site such as temperature or weather; a sample measure, ie. a laboratory measurement on a sample, such as gene copies of SARS-CoV-2 per mL; a polygon measure, ie. case numbers within a health region's polygon; or a population measure, ie. an aggregate measure of a population, such as the number of confirmed cases of a given illness. The reason specimen IDs were created was so that there could be a single manner in which measures and methods are recorded, regardless of the level at which they were performed, while still maintaining the possibility to collect site, sample, and population measures as a distinct types of metadata.

The "what" and "why" of Groups and Classes

Groups and classes, similar to sets, are ways of grouping together different measures within the ODM. Given that the ODM aims to be as robust as possible and has a very long list of possible measures, groups and classes were designed to give shorter lists of measures in the drop down lists

by specifying details about the kind of measure that a user is recording. Groups and classes can work together to further specify what kinds of measures are being reported. For example, the group `sarsCov2` contains many measures, but by specifying that the class is an `allele` or `variant`, the list of possible measures is pared down. Alternatively, class can be said to be non-applicable, paring down the measures in the `sarsCov2` group to only be unspecified measures of the quantity of the virus.

Tables and table types within the ODM

Within the ODM there are three types of tables: program description tables, results tables, and look-up tables. These table types exist to differentiate the function of these tables and to highlight these differences to users. The different tables take different types of inputs and maintenance from users, so understanding the differences can be important.

Program description tables

Program description tables (represented in yellow in the ERD) are tables used to record metadata on the organizations, locations, methods, and appurtenance. These tables help to describe surveillance and testing programs, and are intended to be updated infrequently.

Results tables

Results tables (represented in blue in the ERD) are the tables used to record details on samples and measures. These tables record the main outcomes data and are updated daily, if not more frequently.

Look-up tables

Look-up tables (represented in green in the ERD) are the tables that are pre-programmed and pre-populated in the ODM. These hold information on sets, all parts, languages, and translation abilities. These are only updated by the ODM team in version updates.

Measures, Methods, and Attributes: Key parts

While there are many part types, there are three main part types users should be most familiar with: measures, methods, and attributes. These three have parallels with the three table types, and the differences and details of these parts are useful to understand.

Measures

Measures are actually types of measures that can be performed. These can range from temperature to the number of gene copies in a sample. The measure, or `measurement`, can be selected from a drop down in the templates and it specifies the kind of measure you intend to record. The actual value of the measure is then recorded in the `value` field of the `measures` table, with units and aggregation specified in the `unit` and `aggregation` fields.

Methods

Similar to measures, methods are types of methods that can be performed to accomplish a measurement. These can be diverse, ranging from incubation, qPCR, or nucleic acid extraction. The method itself (`method`) is selected from a drop down in the templates, specifying in general terms the kind of method the user wishes to record. From there, the `value` field of the

`protocolSteps` table can be populated by one of the inputs from the category set associated with that `method`. This provides a higher level of detail for a given method. For example, the `method` might be `solidSep` for solid separation of a sample. The value field might then be populated with `cent` for centrifugation, indicating more details about how the sample settling was done.

Attributes

Attributes are the largest category of part type, as these refer to most of the fields in the ODM. Attributes are fields for metadata within the ODM and range greatly in the use. They comprise everything from collection dates, to sampling period, to names.

Data quality and reportability

Within the ODM there is a `qualityFlag` field located in the `qualityReports` table. Each row of this table has a unique ID (`qualityReportID`) which can then be linked to specific measures, measure sets, and/or samples in the `measures`, `measureSets`, or `samples` tables. This field serves to highlight whether or not there is a quality issues with the sample or the measure(s). The quality flag also allows a user to specify the type of quality issue. This is managed through the use of quality sets, which are the sets that contain the possible quality flags for a given measure or for samples. The idea is that this provides data on any issues with a sample and an indication of the nature of that issue. Having data about the nature and presence of a quality issue is often not sufficient for decision makers who are trying to use and interpret the data. As such, there is also a `reportable` field which is a Boolean indicator of whether or not data can or should be reported or included in final reports and decisions, and a `severity` indicator with a "traffic light" style reporting to indicate how serious the issue is. In previous versions of the ODM,

`qualityFlag` was included as an attirubute in the `measures` and `samples` tables. Separating it out like this allows for multiple flags to be noted on the same measure/sample, and a higher level of detail on the quality issues identified. It can be added back to be reported with measures, however, using a wide table template.

Time periods for samples and measures

For measures, there is a field `aDateStart` and `aDateEnd` which specify the date and time that an analysis was begun and finished. This allows for the recording of greater detail around timelines for especially long, multi-day analyses. For shorter analyses, which will likely make up the bulk of reported measures, the same date can be inputted into both fields. The idea is to have the reporting tables for measures be as robust as possible to allow for various kinds of timelines.

For samples, there is `collDT`, `collDTStart`, and `collDTEnd`. The first field is for the collection date and time of a single grab sample, so start and end are not necessary and the other two fields can be left blank. For composite or pooled sample, the start and end date and time for collection is crucial information to know. When these two fields are populated, the `collDT` field can be left blank.

Dates within the ODM

There are a number of date fields within the ODM which all serve different purposes. Collection datetime (`collDT`) is the date a sample was collected, used only for grab samples. This field is left blank if the collection datetime start and end fields (`collDTstart` and `collDTEnd`) have been populated instead. Inversely, collection datetime start and end fields should be left blank if the collection datetime filed has been populated. Similarly, analysis

datetime start and analysis datetime end (`aDateStart` and `aDateEnd`) are used to report the date and or timeline of an analysis for a measure.

Date fields that are more related to data processing and laboratory infrastructure are: the last edited date (`lastEdited`) which indicates the last time a table, or a measure or sample details, were last edited or updated; the sent date (`sentDate`), or date that a sample was sent to the lab from the field; the received date (`recDate`), or the date the sample was received in the lab; and the report date (`repDate`), or the date that the analysis results or measures were reported. These give a greater indication of how up to date data is, but also on the speed and efficiency of the pipeline between sampling and reported results. Dates should be reported in day/month/year format to accommodate the most popular global convention.

Translation and language capabilities

The default language of the ODM is English, but French translations of all descriptive elements of the data model dictionary are also available. Beta versions of Spanish and Portuguese translations are also available. As additional nation states and partners adopt the ODM, we anticipate that these fields will be translated into other languages as well. The translation capacities are managed through the language look-up table (`languages`), the translation look-up table (`translations`), and the parts table (`parts`). When a translation for a given part is not available, the dictionary will default to the English term. The language look-up table stores linguistic and classification codes for spoken human languages, with the most recent ISO639 code being the language ID (`languageID`). In the translation table, the language ID is paired with every part ID (`partID`), along with the label (`partLabel`), description (`partDesc`), and instructions (`partInstr`) translated to that language. The part IDs are linked to the full parts list which otherwise contains metadata that is coded in variables and requires no further translation.

Recording protocols

When analyzing data from various sources, it is important to understand how the data was produced. The PHES-ODM recognizes this and includes protocols as one of its entities. To store protocols efficiently in database tables, several challenges must be addressed:

1. Protocols are comprised of a collection of steps.
2. Protocol steps can consist of two entries:
    - They can prescribe the use of a specific quantity of something. This can be described using the different measures found in the PHES-ODM dictionary and assigning them a prescribed value and unit of measurement.
    - They can prescribe an action. The PHES-ODM calls this a method.
3. Protocol steps must be organised in the right order to convey the meaning of the protocol.
4. Steps may follow each other, or they can be done concurrently.
5. Measures found inside a protocol specify the quantity of reagents, supplies and conditions involved in the realization of a method.
6. Different protocols may use some of the same steps, but in a different order.
7. Protocols may have steps that consist in one or several (sub)protocols.
8. Protocols can be updated with new versions, or they can reference and build from other protocols.

To solve these constraints, the PHES-ODM stores a protocol (e.g., what it does, who developed it, when it was developed) separately from its constituent steps. These protocol steps are stored in the `Protocol Steps` table. The entries in the steps table are either methods or measures.

The protocol steps are linked together in their own `Protocol Relationships` table. Rows in the relationship table have four

main attributes. The first is the protocol identifier. The three other attributes define a relationship between two steps in the protocol. The relationship is expressed in the form:

```
subject → relationship → object
```

Where the subject and the object can either be a protocol step or subprotocol. The available relationships (e.g., `is_before`, `specifies`, `is_concurrent_with`, etc.) allows one to organize the protocol in a more semantically meaningful way than by simply using a sequential order.

This flexible structure allows protocol steps and subprotocols to be reused in any number of protocols. The relationships between protocols, protocol orderings, and protocol steps are shown in Figure A.

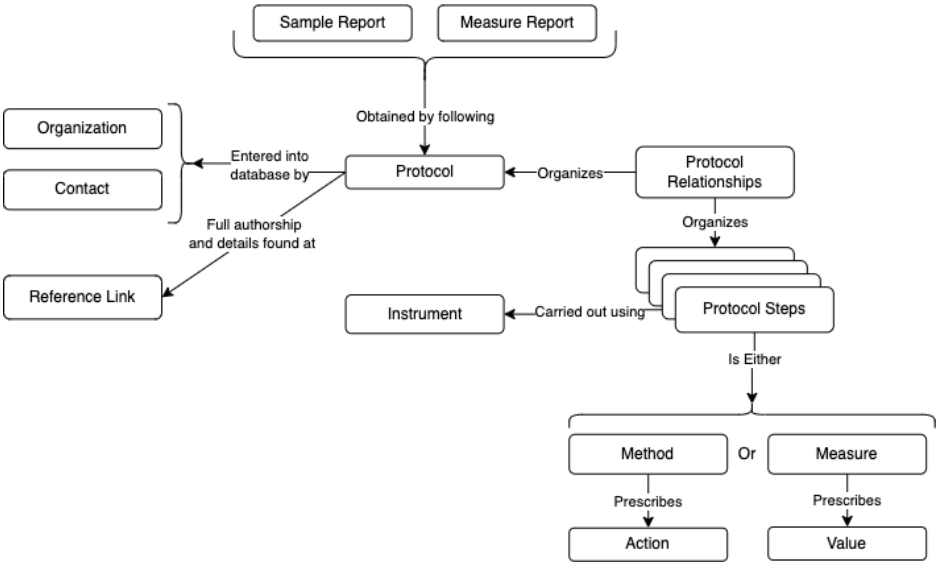


Figure 3.: Figure A: Main entities and relationships used to represent protocols

Recommended formula for user-generated IDs

There are 18 user-generated IDs used in the ODM. These IDs are necessary unique identifiers used to organize observations and metadata. The ODM is not opinionated about IDs, and users are free to use whatever formula or naming convention they prefer for these IDs. We have prepared a recommended formula for these IDs, however, which users are free to use. These are the formulas used by the ODM tools to machine generate IDs where one hasn't been provided. For a quick breakdown, see the below table:

User ID	Formula	Example
Accessions Index ID	datahost + accessNum	sraPRJNA788395
Address ID	country code + province code + 2-3 letters of municipality + row	caOnOtt002
Calculation ID	pipelineID + treatmentID	standardiza-tionpmmov15stan-dardizationpm-mov1
Contact ID	orgID + first 3 letters of role	caOnOtt002UniRes
Dataset ID	datasetID = orgID	caOnOtt002Uni
Instrument ID	first 3 letters of manufacturer + first 3 letters of name + first 3 letters of model + index	fisHanHan
Organization ID	addID + first 3 letters of name	caOnOtt002Uni
Pipeline ID	First Treatment ID in the pipeline + # treatments in the pipeline	standardiza-tionpmmov15
Polygon ID	orgID + siteID	caOnOtt002Uni-CaOnOttOtt
Protocol ID	first 5 letters of name + protocolVersion	pmmov1

Recommended formula for user-generated IDs

User ID	Formula	Example
Protocol Step ID	orgID + last 3 letters of part ID of method/measure	caOnOtt002UniIon
Public Health Action ID	actionType + action + threatTarget + actionDT	survAlerttargSurvsarsCov228022027
Quality Report ID	quality flag part ID + either the measure report ID, the sample ID, or measure set report ID that the quality report is for	flagJcaOnOttOttawasite1202008021000covN1002
Measure report ID	sampleID + part ID of measure + row number	caOnOttOtt20200802Covn1002
Measure set report ID	Report ID of first measure in the set + # measures in the set	caOnOttOtt20200801Covn1002003
Sample ID	siteID + collDT/collDTEnd (not including time) + index (if applicable)	caOnOttOtt20200801
Site ID	country code (ISO) + province code (ISO) + first 2-3 letters of municipality + 3 first letters of site name	caOnOttOtt
Treatment ID	calcType + standard + order	standardizationpmmov1

To go into greater detail, the *Accessions Index ID* is a unique ID for each row in the `accessions` table, and is made by concatenating the value of the `dataHost` field and the `accessNum` field. For example, an SRA entry with the accession index number of PRJNA788395 would give an accessions index ID of sraPRJNA788395.

The *Address ID* uses the recipe country code + province code + 2-3 letters of municipality + row. So it's built using pieces of the metadata fields for the given address' entry in the addresses table, and the row it

occupies in that table. For example, the ID for an address in Ottawa would use Country Code = Canada, Province Code = Ontario, Municipality = Ottawa-Carleton, and lets say it's recorded in the second row of the table, so Row = 002. This gives us an address ID of caOnOtt002.

For the *Calculation ID*, as a composite key, will just be generated by concatenating the pipelineID and the treatmentID of a given row. For example, if a row contains the pipeline ID "standardizationpmmov15" and the treatment ID "standardizationpmmov1", the calculation ID would be standardizationpmmov15standardizationpmmov1.

The *Contact ID* in the contacts table uses the recipe organization ID + first 3 letters of role, again building the ID from pieces of the metadata. So if, for example, we are building a contact ID for a research associate at an organization with the ID caOnOtt002Uni, the contact ID would be caOnOtt002UniRes.

For the *Dataset ID*, we recommend it be the same as the *organization ID* (see below). So if, for example, we looked at our organization with the ID caOnOtt002Uni, the dataset ID would also be caOnOtt002Uni.

Instrument ID uses the same approach of building using metadata, with the recipe of first 3 letters of manufacturer + first 3 letters of name + first 3 letters of model + index to generate the ID. For example, if we wanted to record a HandyStep S Repeating Pipetter (name), manufactured by Fisherbrand, and is of the model HandyStep S Mechanical, the recommended ID that is generated would be fisHanHan.

Our recommended recipe for *Organization ID* uses the address ID for an organization (see above for explanation) + the first 3 letters of the name. So if the organization in Ottawa described in the address ID section was the University of Ottawa, the ID would be caOnOtt002Uni.

The *Pipeline ID* recommended recipe is to use the treatment ID of the first data treatment in the pipeline, and concatenate that with the number of treatments in the pipeline as a whole. For example, if the first treatment in a

pipeline has the ID "standardizationpmmov1" and there are five treatments in the pipeline, the pipeline ID would be standardizationpmmov15.

For the *Polygon ID*, the recipe uses associated IDs to generate the final product. Specifically, we recommend organization ID + site ID. So for a polygon managed by an organization using the ID caOnOtt002Uni and covering a site with the ID caOnOttOtt, for example, the polygon ID would be caOnOtt002UniCaOnOttOtt.

The *Protocol ID* is generated using the first 5 letters of the name + the protocol version. For example, if using generating a protocol ID for a first version of a protocol called "PMMoV Process", the ID would be pmmov1.

For the *Protocol step ID*, we recommend constructing combining the organization ID + last 3 letters of the part ID for the method or measure used in the step. For example, a nucleic acid extraction method (partID = extraction) step from our university of Ottawa example lab with the organization ID caOnOtt002Uni would generate the protocol step ID of caOnOtt002UniIon.

For the *Public Health Action ID*, we recommend concatenating the value for the actionType field, the action field, the threatTarget, and the actionDT field (just the numbers). So if, for example, a surveillance alert (survAlert) action was taken to have targeted surveillance (targSurv) roll out for SARS-CoV-2 (sarsCov2) on February 28, 2027, the public health action ID would be survAlerttargSurvsarsCov228022027.

Quality Report ID ia generated using the recipe of part ID for the given quality flag + either the measure report ID, the sample ID, or measure set report ID for which the quality report is being generated. Generating an example, if we are reporting the qulaity flag J - Weak signal extrapolation (partID = flagJ) for a measure report with the ID caOnOttOttawasite1202008021000covN1002, we get the quality ID of flagJcaOnOttOttawasite1202008021000covN1002.

The *Measure Report ID* is built using sampleID + part ID of measure + row number. For example, taking a measure of the SARS-CoV-2 N1 gene

region (partID = covN1) from a sample with the ID caOnOttOtt20200801, recorded in the second row of the table, we get the measure report ID of caOnOttOtt20200802Covn1002.

The recommended recipe to generate a *Measure Set Report ID* is to use the Measure Report ID of the first measure in the set + the number of measures in the set. So for a set of 3 measures that starts with the same SARS-CoV-2 N1 gene region measure as described above (caOnOttOtt20200801Covn1002), you get the measure set report ID of caOnOttOtt20200801Covn1002003.

Sample ID is generated by combining the siteID for the sample + the collection Datetime OR the end of collection datetime fields (excluding the time and only using the date) + the index value (if applicable). So for a composite sample taken at a site with the ID caOnOttOtt, which finished collection on 2020-08-01 10:00:00, with no index, the sample ID would be caOnOttOtt20200801.

A *Site ID* can be generated by combining the country code (ISO) for the site + the province code (ISO) for the site + first 2-3 letters of municipality + 3 first letters of site name. So to generate a site ID for the wastewater treatment plant in Ottawa, Canada, we would take the ISO code for Canada (ca), for Ontario (on), The first three letters of Ottawa-Carleton (Ott) and the first three letters of the site name, where the name is Robert O. Pickard Environmental Centre (Rob). This gives us the recommended site ID of caOnOttRob.

Lastly, a *Treatment ID* can be generated using the recipe of concatenating the value from the calcType field, the standard field, and then the value for the order in a pipeline. For example, if a data treatment that standardizes to circulating levels of pepper mild mottle virus (PMMoV) and is the first step in a data pipeline, its treatment ID would be standardizationpmmov1.

Questions and online community

If any users have additional questions or issues with the ODM, we invite them to check out our Discourse Page for discussion boards and community support. For larger issues, and to ask the ODM team to add additional fields or variables into the model, we encourage users to visit the project's GitHub repository and to create and issue there so that a team member can respond.

How to use the ODM

Dictionary v3.0.1 Documentation v3.0.1

How-To guides

1) How to use templates

ODM Excel report templates provide you with an easy way to enter your wastewater and other environmental data into the relevant PHES-ODM tables (more information about the tables can be found in the getting-to-know and tables sections). The templates also serve as an interactive way to get to know the ODM and can be found at the OSF.io PHES-ODM reference file folder.

The guides below will walk you through each of the report templates. In these guides, "field" refers to a column in the template, and "entry" refers to a row of information that you entered. The guides also provide definitions and explanations for some terms; more complete information can be found in the Reference Guide - Parts document. If you have any questions or comments, you can post them on our Discourse forum.

As a starting point:

- `Sample report table` and `Measure report table` are used for day-to-day reporting. You can record information about a sample in the `Sample report table`. Measures (or measurements) are recorded in

the `Measure report table`. A measure is "measurement or observation of any substance including a biological, physical or chemical substance".

- There are four optional tables that support the reporting of samples and measures:
  - `Sample relationships table` is used only when you have samples that are pooled or split.
  - `Measure set report table` can be used to link measures together.
  - `Quality reports table` is used for detailed quality assurance and control reporting (you can, and should, record a quality flag attribute for each measure or sample in the `Measure report table` and `Sample report table`).
  - `Public health actions report table` is for recording information on public health actions that are related to a given measure; whether a measure led to increased surveillance, or increased surveillance led to the measure is not made clear. The causality is specifically left ambiguous, but it illustrates the material connection between surveillance and action.
- Typically, there is a one time initial setup where you will need to enter information into the `Sites table`, `Address table`, `Organization table`, and `Contact table`.
  - `Sites table` is mandatory and records information about where testing is performed.
  - `Address table`, `Organization table`, and `Contact table` optionally provide additional context, metadata, and contact information for sites and entities such as laboratories.

- There are other optional supporting tables, such as `Protocols table` and `Instrument table`, where you can use the templates to record information about how samples are taken and how measures are reported. The `Calculations table` also helps in this regard, as it is where you can store information on the calculations or data treatments used to generate certain measurement values. You only need to compete these tables once and then update them as needed.

```
-   `Protocol steps table` and `Protocol relationships table` are used alongside the `Protoc
```

- Other supporting tables include `Polygon table`, which stores information about the sample shed, and `Polygon relationships table`, which describes relationships (such as overlap, co-location) of sample shed or other polygon areas. `Dataset table`, which stores information about the data custodian and owner of the data, and `Accessions table`, which stores linkages to external databases for things like sequencing data, help ensure that data is correctly linked and cited.

The templates contain four main types of fields; in these how-to guides they are colour-coded for instructional purposes:

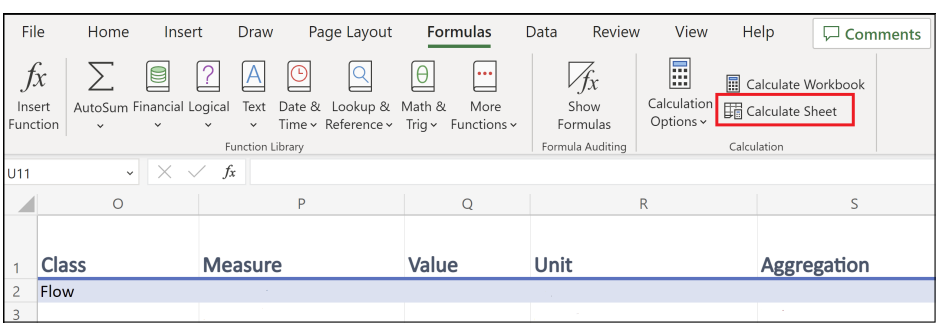
- **Identifier and unique identifier (red):** In these fields you will create a value that will be used to identify something. For instance, `Sample ID` is used to identify each unique sample. An identifier can be repeated between entries, while an unique identifier cannot. There is usually only one unique identifier per template sheet, and they correspond to the name of the template. For example, `Measure Report ID` for the `Measure report table` template, and `Contact ID` for the `Contact table` template.

- **Drop-down and conditional drop-down menus (green):** These fields have a drop-down menu which contain the values that you can either select **or** type in. In conditional drop-down menus, the values may depend on what you entered in a previous field.

- **Date fields (purple):** Dates are entered in these fields and must be in the form of the ISO 8601 format: `yyyy-mm-dd`. All datetime fields also support entries for hours, minutes, and seconds: `2022-01-01T06:11:54` and `2022-01-01T06:11:54+13:30`
- **Free form fields (blue):** In these fields, you can enter your data in any format that you wish. Any restrictions will be specified in the relevant sections. Keep in mind, different measures may have different data types that cannot be validated in Excel. The data type of a measure can be checked in the reference list for the measure. For example, the data type for Sample temperature is a real number.

Conditional menus

Conditional menus use the FILTER function (which is present in Excel 2019 and later) and are only functional in the first three rows of their respective templates. In addition, the auto-calculation has been disabled. Thus, you will need to press the "Calculate Sheet" button, which is in the "Formulas" tab after entering the value in the field upon which the conditional menu is based upon; this button is outlined in red in the image below (the image is for Excel Online). For example, for the `Measure` conditional menu in the `Measure report` template, you would select a value in the `Class` field, press "Calculate Sheet" and then the correct values will show up in the menu of the `Measure` field.



All of this was done because, in an online environment (such as Excel Online), the code for the conditional menus work can cause the templates to run very slowly. You can reactivate the auto-calculation if you wish. For further information about how to expand these menus to additional rows and other aspects of the templates, see Notes regarding templates.

2) How to report Measures and Measure sets

In this guide you will learn how to record data in the `Measure report table` (or `measures` Excel tab) and the `Measure set report table` (or `measureSets` tab) templates. In the `Measure report table` template, each row represents a measure. Along the same lines, in the `Measure set report` template, each entry represents a collection or set of measures.

You can find additional information regarding terms and the colour-coding of columns at the beginning of this document (How-To guides) and the Reference Guide - Parts document.

Quick Start

Below you will find the mandatory fields for the `Measure report table` and `Measure set report table` templates. You will also find definitions of these fields and examples of entries of data. A more detailed description of some of the key concepts can be found in the following section, Detailed description.

`Measure report table` template

1. **Mandatory fields**

- **`Measure report ID`**: Unique identifier for the `Measure report table` template. Each value represents a measure.
- **`Sample ID`**: Identifier for the sample that is associated with each measure.
- **`Site ID`**: Identifier for the location where a sample was taken.
- **`Analysis Date End`**: Date the measure was completed.
- **`Specimen`**: Substance or thing upon which the observation was made. Specimens include `Population`, `Sample`, and `Site`. This field is only mandatory if there is more than one specimen type that is collected in the dataset.
- **`Fraction analyzed`**: the fraction or portion of the wastewater that was analyzed (for example "liquid", "solid", "mixed").
- **`Measure`**: A measurement or observation of any substance including a biological, physical or chemical substances.
- **`Value`**: Value of the measure.
- **`Unit`**: Units of a value.
- **`Aggregation`**: Statistical measure that the measure represents (for example "mean", "single").

2. **Examples**

	A	B	C	D	E	F	G	H	I	J
1	Measure Report ID	Sample ID	Site ID	Analysis date end	Specimen	Fraction analyzed	Measure	Value	Unit	Aggregation
2	o.04.08.20covN11	o.04.08.20	Ottawa-1	2020-04-08	sa	solid	covN1	0.00026	gcPMMoV	meanNr
3	o.04.08.20covN12	o.04.08.20	Ottawa-1	2020-04-08	sa	solid	covN1	9.5E-05	gcPMMoV	sdNr
4	o.04.08.20covN23	o.04.08.20	Ottawa-1	2020-04-08	sa	solid	covN2	0.00013	gcPMMoV	meanNr
5	o.04.08.20covN24	o.04.08.20	Ottawa-1	2020-04-08	sa	solid	covN2	4.4E-05	gcPMMoV	sdNr
6	o.04.08.20nPPMoV5	o.04.08.20	Ottawa-1	2020-04-08	sa	solid	nPPMoV	27.35	Ct	mean
7	o.04.24.20covN16	o.04.24.20	Ottawa-1	2020-04-24	sa	solid	covN1	0.00015	gcPMMoV	meanNr
8	o.04.24.20covN17	o.04.24.20	Ottawa-1	2020-04-24	sa	solid	covN1	6.2E-05	gcPMMoV	sdNr
9	o.04.24.20covN28	o.04.24.20	Ottawa-1	2020-04-24	sa	solid	covN2	2E-05	gcPMMoV	meanNr
10	o.04.24.20covN29	o.04.24.20	Ottawa-1	2020-04-24	sa	solid	covN2	4.7E-06	gcPMMoV	sdNr

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

Measure Sets Template

1. **Mandatory fields**

- `Measure Report set ID`: Unique identifier for the `Measure set report` template. Each value represents a group of related measures.

note: the reason that the ID is the only mandatory field is because the value is referenced as a foreign key in the `Measure report table`, and as such the linkage can be found in that table rather than this one.

3. **Examples**

	A
1	Measure Set Report ID
2	o.04.08.20cov
3	o.04.24.20cov
4	o.05.10.20cov
5	o.05.26.20cov

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

4. **Full example**

	A	B	C	D	E	F	G	H	I	J	K
1	Measure Report ID	Sample ID	Site ID	Measure set report II	Analysis date end	Specimen	Fraction analyzed	Measure	Value	Unit	Aggregation
2	o.04.08.20covN11	o.04.08.20	Ottawa-1	o.04.08.20cov	2020-04-08	sa	solid	covN1	0.0002601	gcPMMoV	meanNr
3	o.04.08.20covN12	o.04.08.20	Ottawa-1	o.04.08.20cov	2020-04-08	sa	solid	covN1	9.523E-05	gcPMMoV	sdNr
4	o.04.08.20covN23	o.04.08.20	Ottawa-1	o.04.08.20cov	2020-04-08	sa	solid	covN2	0.000127	gcPMMoV	meanNr
5	o.04.08.20covN24	o.04.08.20	Ottawa-1	o.04.08.20cov	2020-04-08	sa	solid	covN2	0.0000436	gcPMMoV	sdNr
6	o.04.08.20nPPMoV5	o.04.08.20	Ottawa-1	o.04.08.20cov	2020-04-08	sa	solid	nPPMoV	27.35	Ct	mean
7	o.04.24.20covN16	o.04.24.20	Ottawa-1	o.04.24.20cov	2020-04-24	sa	solid	covN1	0.0001537	gcPMMoV	meanNr
8	o.04.24.20covN17	o.04.24.20	Ottawa-1	o.04.24.20cov	2020-04-24	sa	solid	covN1	6.219E-05	gcPMMoV	sdNr
9	o.04.24.20covN28	o.04.24.20	Ottawa-1	o.04.24.20cov	2020-04-24	sa	solid	covN2	1.988E-05	gcPMMoV	meanNr
10	o.04.24.20covN29	o.04.24.20	Ottawa-1	o.04.24.20cov	2020-04-24	sa	solid	covN2	4.722E-06	gcPMMoV	sdNr

The above examples takes the previous example table, and adds the `Measure set report ID` column, to organize grouped measures together. In this case, mean and standard deviation measures of the SARS-CoV-2 N1 and N2 gene regions, and the PMMoV fecal biomarker standard, all from the same samples. The most basic `Measure set report table` would look the same as in the example at point 3 above, but optionally could include additional metadata about the set.

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

Detailed description

`Measures` template

1. **Columns A to I**

	A	B	C	D	E	F	G	H
1	Measure Report ID	Protocol ID	Sample ID	Purpose	Polygon ID	Site ID	Dataset ID	Measure set report
2								
3								

```
i)  Columns A-C, and E-H

    -   These are identifier fields.
```

- `Measure Report ID` (column A) is the unique identifier for this template, and it ca

- You can repeat the other fields between entries (if needed). For instance, if you en

- You may have already created these identifiers in another template. For instance, yo

ii) Column D

- `Purpose` has a drop-down menu. If you are unsure what to put, select `Regular` for
odm.org/sets.html#purposeSet).

iii) Column I

- `Name` is a free text and optional field for providing a general name for a measure

2. **Columns J to P**

	J	K	L	M	N	O	P
1	Analysis date	Analysis date end	EpiWeek Start Date	EpiWeek Number	Year of the EpiWeek	Measure relevance start date	Measure relevance end date
2							
3							

i) Columns J to P
- These are date fields where you can enter the dates associated with your measure in
mm-dd. Including hours and minutes is optional, but all date-
entries in columns J, K, L, and P use the ISO 8601 format. `2022-
01-01T06:11:54` or `2022-01-01T06:11:54+13:30`

ii) Columns M and N
- M records the epi week of a measurement. Epi weeks are a way of standardizing time t

iii) Columns O and P
- These measure relevance date fields were added in version 3.0.0 to better contextual
style data. For measures like population counts, for example, which may have time constraint

3. **Columns Q to AA**

	Q	R	S	T	U	V	W	X	Y	Z	AA
1	Report date	Compartment	Specimen	Fraction analyzed	Group	Class	Measure	Value	Unit	Aggregation	Value Treatment
2											
3											

i) Columns R, S, and T
- `Compartment`, `Specimen` and `Fraction analyzed` have drop-
down menus. In general these fields are optional, but are recommended (see ne
- `Compartment` is only truly necessary to report if you are reporting
- `Specimen` is mandatory when the ensemble of data you are entering ha
- `Fraction analyzed` applies only for water and wastewater samples. Yo
- Of note is that if you generate wide names, these three fields are al

ii) Columns U and V
- `Group` and `Class` help organize the `Measure` field by making speci
down menu and are optional.
- Leave these fields **blank** if you do not use them.

iii) Column W
- `Measure` is where you select what is being measured. A measure in OD

iv) Column X
- `Value` is where you enter the value of your measure. For instance,
- Note: While the value you enter into this field can be of any data t

v) Column Y
- `Unit` is where you enter the unit of your measure.

vi) Column Z
- `Aggregations` is where you enter the aggregation of your value using
down menu. For instance, does your value represent a mean, median, etc.

vii) Columnn AA
- `Value treatment` is a dropdown menu option that acts as a flag to de

odm.org/sets.html#valTreatSet).

4. **Columns AB to AK**

	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK
1	Pipeline ID	Nomenclature	Index	Measure license	Reportable	Organization ID	Contact ID	Last edited	Reference link	Notes
2										
3										

i) Columns AB, AC, and AD
- AB is an identifier field used for connecting to detailed calculations or data treat
down menus, and AD is a free text field.
- `Nomenclature` is used when reporting a variant or disease to specify which naming c
- `Index` (column AD) is used if you have multiple entries with the same values in mos

ii) Column AE and AF
- These are fields which contain drop-down menus.
- `Measure license` (column V) refers to the access and use licensing of the measure t
odm.org/sets.html#licSet).
- `Reportable` (column W) is where you can indicate if the measure should not be used

iii) Column AG and AH
- These are identifier fields that are used to indicate the organization and contact

iv) Column AI, AJ, and AK
- `Last edited` is where you can indicate the date when the entry was last updated. Th
- `Reference link` is used to point out to an external reference for a single measure,
- `Notes` is free text field for recording any additional details that users may feel

Measure set report template

1. **Columns A to G**

	A	B	C	D	E	F
1	Measure set report set ID	Protocol ID	Name	Organization ID	Contact ID	Last edited
2						
3						

```
i)     Columns A, B, D and E

    -   These are identifier fields.

    -   `Measure set report set ID` (column A) is the unique identifier for t

    -   For the rest, you can repeat the identifier between entries (if neede

    -   You may have already created these identifiers in another template. I

ii)    Columns C and G

    -   These are free form fields in which you can enter the indicated infor

iii)   Column F

    -   `Last edited` is a date field in which you can enter the date when th
```

You have now entered your data in the `Measure report` and `Measure set report` templates, congratulations!

3) How to report samples and sample relationships:

In this guide you will learn how to enter information about samples and sample relationships into their respective templates. In the `Sample report`

`table` (or `samples` tab) template, each entry represents a sample. A sample is the wastewater that you collected so that measures can be made - but it may also be a sample from a surface, from air, or other environmental material. Along the same lines, each entry in the `Sample relationships table` (or the `sampleRelationships` tab) template represents an interaction (or relationship) between two samples in the form "subject - relationship - object". So, to specify that Sample A is a field sample replicate of Sample B, you would enter `Sample ID` of A - `Field sample replicate` - `Sample ID` of B.

You can find additional information regarding terms and the colour-coding of columns at the beginning of this document (How-To guides) and the Reference Guide - Parts document.

Quick Start

Below you will find the fields that are mandatory for the `Sample report` and `Sample relationships` templates. You will also find definitions of these fields and examples of entries of data. A more detailed description of some of the key concepts can be found in the following section, Detailed Description.

Samples Template

1. **Mandatory fields**

- **`Sample ID`**: Unique identifier for the `Sample report` template. Each value represents a sample.
- **`Site ID`**: Identifier for the location where a sample was taken.
- **`Sample material`**: Type of material that the sample is made of.
- **`Sample collection type`**: Method used to collect the sample.

- **`Collection period`**: The time period over which the sample was collected, in hours.
- **`Collection number`**: The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling.
- **`Collection date time`**: The date, time and time zone the sample was taken.

2. **Examples**

	A	B	C	D	E	F	G
1	Sample ID	Site ID	Sample material	Sample collection type	Collection period	Collection number	Collection date time
2	o.04.08.20	Ottawa-1	pSludge	timePr	24	24	2020-04-08
3	o.04.24.20	Ottawa-1	pSludge	timePr	24	24	2020-04-24
4	o.05.19.20	Ottawa-1	pSludge	timePr	24	24	2020-05-19

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

Sample Relationships Template

1. **Mandatory fields**

- **Synthetic ID for the sampleRelationships table**: A unique identifier for each row of the `Sample relationships table`. Can be any combination of characters, as long as there are fewer than 30.
- **`Sample ID object`**: The object (or one of the samples) of a relationship between two samples. This will always be a `Sample ID` that was previously created in the `Sample report` template.
- **`Relationship`**: Describes the relationship between two samples. For the list of possible relationships, please refer to sampleRelSet.

- **`Sample ID subject`**: The subject (or one of the samples) of a relationship between two samples. This will always be a `Sample ID` that was previously created in the `Sample report` template.

2. **Examples**

	A	B	C	D
1	Synthetic ID for the sampleRelationships table	Sample ID subject	Relationship between entities	Sample ID object
2	.20achil0mas	o.04.08.20a	child	o.04.08.20mas
3	.20bchil0mas	o.04.08.20b	child	o.04.08.20mas
4	.20afiel.20b	o.05.19.20a	fieldReplicate	o.05.19.20b

Detailed Description

`Sample report table` template

Columns A to J

	A	B	C	D	E	F	G	H	I	J
1	Sample ID	Protocol ID	Organization ID	Contact ID	Site ID	Purpose	Sample material	Dataset ID	Sample origin	Replicate Type
2										
3										
4										

```
i)  Columns A to E, and H:

    -   These are identifier fields.

    -   `Sample ID` (column A) is the unique identifier for this template and cannot be repe

    -   For the rest of the fields, you can repeat values between entries. For instance, if

    -   The sample logic applies for sampling protocols (`Protocol ID`), for the individual

    -   You may have already created these identifiers in another template. For instance you
```

ii) Columns F to G:

- These are fields that contain drop-down menus where you can enter ini
odm.org/sets.html#purposeSet)) and `Sample material` (column G, [sampleMatSet
odm.org/sets.html#sampleMatSet)) of your sample.

ii) Columns I to J:

- These are fields that contain drop-down menus where you can enter ini
odm.org/sets.html#originSet)) and the `Replicate type` (column J, [replicateS
odm.org/sets.html#replicateSet)) of your sample.

2. **Columns K to Q**

	K	L	M	N	O	P	Q
1	Sample collection type	Collection period	Collection number	Pooled	Collection date time	Collection date time start	Collection date time end
2							
3							
4							

i) Columns K, N:

- These fields contain drop-down menus and are related to various chara

- `Sample collection type` (column K, [collectSet](https://docs.phes-odm.org/sets.html#collectSet)) refers to the collection technique you used to

- `Pooled` (column O, [booleanSet](https://docs.phes-odm.org/sets.html#booleanSet)) refers to whether or not the sample that you a

ii) Columns L to M:

- These are free form fields.

- `Collection period` (column L) refers to the number of hours that you took to colle

- `Collection number` (column M) refers to the number of subsamples that were used to

iii) Columns O to Q:

- These fields are datetime fields to record details about when exactly a sample was c
mm-dd. Including hours and minutes is optional, but all date-
entries use the ISO 8601 format. `2022-01-01T06:11:54` or `2022-
01-01T06:11:54+13:30.`

- For single collection or grab samples, users can use `Collection date time` (Column

- For composite or agragated samples, users can use `Colelction date time start` (Colu

3. **Columns R to V**

	R	S	T	U	V
1	Collection Date (time not included)	Approximate Time	EpiWeek Start Date	EpiWeek Number	Year of the EpiWeek
2					
3					
4					

i) Columns R and T:

- These are optional date fields that are related to your sample. These dates will be
mm-dd. Including hours and minutes is optional, but all date-
entries use the ISO 8601 format. `2022-01-01T06:11:54` or `2022-
01-01T06:11:54+13:30.`

- `Collection Date (time not included)` (Column R) is where you can enter the date of

- `EpiWeek Start Date` (Column T) is an optional date field used when recording [epiWe

ii) Column S:

- `Approximate Time` (column S) is an optional time field when using `(
odm.org/sets.html#collAppxSet).

iii) Columns U and V:

- These are optional free-text fields to be used as accessories to a da

- `EpiWeek Number` (collumn U) specifies the number of the EpiWeek (bet

- `Year of the EpiWeek` (column V) specifies the year of the epiWeek.

- In order for epiWeek information to be useful, **all three pieces (`E

4. **Columns W to AA**

	W	X	Y	Z	AA
1	Date sample was sent	Date sample recieved	Reportable	Last edited	Notes
2					
3					
4					

i) Columns W, X, and Z:

- These fields are datetime fields to record details about when exactly
mm-dd. Including hours and minutes is optional, but all date-
entries use the ISO 8601 format. `2022-01-01T06:11:54` or `2022-
01-01T06:11:54+13:30.`

- `Date sample was sent` (column W) records when a sample leaves the co

- `Last edited` (Column Z) is where you can enter the date when the en

ii) Columns Y and AA:

- `Reportable` (column U, [booleanSet](https://docs.phes-odm.org/sets.html#booleanSet)) is a drop-down menu field where you can indicate if the sampl

- `Notes` (column W) is a free form field where you can indicate anything of interest.

Sample relationships template

1. **Columns A to F**

	A	B	C	D	E	F
1	Synthetic ID for the sampleRelationships table	Sample ID subject	Relationship between entities	Sample ID object	Last edited	Notes
2						
3						
4						
5						

i) Columns A, B, and D:

- These are identifier fields.

- `Synthetic ID for the sampleRelationships table` is a unique identifier for each row

- Both of the identifiers for subject (Column B) and object (Column D) are `Sample ID`

ii) Columns B:

- `Relationship` (Column C, [sampleRelSet](https://docs.phes-odm.org/sets.html#sampleRelSet) is a drop-down menu field where you can select the type of r

iii) Columns E and F:

- These are a date field (column E) and a free form field (column F) where you can en

- `Last edited` (column E) is where you can enter in the date when the

- `Notes` (column F) is a free form field where you can indicate anythi

You have now entered your data in the `Sample report` and `Sample relationships` templates, congratulations!

4) How to record a protocol

In this guide you will learn how to enter protocols, protocol steps and protocol relationships into their respective templates. A protocol is "A procedure for collecting a sample or performing a measure". Each entry in the `Protocols table` (or protocols) template represents a unique protocol. A protocol is made up of protocol steps. In the `Protocol steps table` (or protocolSteps) template, each entry is one of these steps. Finally, protocols and protocol steps can be linked to each other. Each entry in the `Protocol relationships` (or protocolRelationships) template represents one of these relationships in the form, "subject - relationship - object". So, for example, if you want to specify that Protocol step A needs to be done before Protocol step B, you would enter the `Protocol step ID` of A - `Is Before` - `Protocol Step ID` of B.

You can find additional information regarding terms and the colour-coding of columns at the beginning of this guide (How-To guides) and the Reference Guide - Parts document.

Quick Start

Below you will find the fields that are mandatory for the `Protocols`, `Protocol steps` and `Protocol relationships` templates. You will also

find definitions of these fields and examples of entries of data. A more detailed description of some of the key concepts can be found in the following section, Detailed Description.

`Protocol steps` template

1. **Mandatory fields**

- `Protocol Step ID`: The unique identifier for the `protocol steps` template. Each value represents a protocol step.
- `Measure`: A measurement or observation of any substance including a biological, physical or chemical substance.
- `Method`: A procedure for collecting a sample or performing a measure.
- `Value`: Value of the entry. This is only mandatory if the entry is a measure.
- `Unit`: The units of the value. This is only mandatory if the entry is a measure.
- `Aggregation`: Statistical measures used to report a measure (for example, "mean"). This is only mandatory if the entry is a measure.

2. **Examples**

	A	B	C	D	E	F
1	Protocol Step ID	Method	Measure	Value	Unit	Aggregation
2	April_N1-N2_MP.inhibition	inhibMeth		serialDilution		
3	April_N1-N2_MP.surrogateRecovery		percRec	nr		
4	April_N1-N2_MP.sampleSize		samVol	0.1	l	sin
5	April_N1-N2_MP.slod		slod	1	gcMl	
6	April_N1-N2_MP.sloq		loq	5	gcMl	
7	April_PMMoV-229e_MP.inhibition	inhibMeth		serialDilution		

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Protocols` template

1. **Mandatory fields**

- `Protocol ID`: The unique identifier for the `Protocols` template. Each value represents a protocol.

2. **Examples**

	A
1	protocolID
2	AssayMethod N1-01
3	AssayMethod N2-01
4	AssayMethod PMMoV-01
5	AssayMethod N1-01_Solids

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Protocol relationships` template

1. **Mandatory fields**

- `Synthetic ID for the protocolRelationships table`: A unique identifier for each row of the `Protocol relationships table`. Can be any combination of characters, as long as there are fewer than 30.

- `Protocol ID container`: The unique identifier for the `Protocol relationships` template. Each value represents a protocol, and the step(s) and other protocol(s) that make it up. This identifier should also be a `Protocol ID` that was created using the `Protocols` template.

- `Protocol ID object`: Identifier of the object of a relationship between a protocol, and a protocol step or protocol. This is only mandatory if the object is a protocol.

- `Step ID Object`: Identifier of the object of a relationship between a protocol step, and a protocol step or protocol. This is only mandatory if the object is a protocol step.

- `Relationship between entities`: Describes the relationship between the subject and object.

- `Protocol ID subject`: Identifier of the subject of a relationship between a protocol, and a protocol step or protocol. This is only mandatory is the subject is a protocol.

- `Step ID Subject`: Identifier of the subject of a relationship between a protocol step, and a protocol step or protocol. This is only mandatory is the subject is a protocol step.

2. **Examples**

Synthetic ID for the protocolRelationships table	Protocol ID container	Protocol ID object	Step ID Object	Relationship between entities	Protocol ID subject	Step ID Subject
settling.storage4	settling		storage4	specifies		settle
settling.time1	settling		time1	specifies		settle
pgsSolids.NA	pgsSolids	settling		before		pellet
lliquidPrep.NA	lliquidPrep	settling		before		liquid
lliquidPrep.liquid	lliquidPrep		liquid	before		filter1
lliquidPrep.filter1	lliquidPrep		filter1	before		filter2

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

Detailed Description

`Protocol steps` template

1. **Columns A to G**

	A	B	C	D	E	F	G
1	Protocol Step ID	Method	Measure	Summary	Protocol step source ID	Protocol step version	Reference link
2							
3							
4							

```
i)  Column A and E:
    -   These are identifier fields.
    -   `Protocol step ID` (column A) is the unique identifier field for this
    -   `Protocol step source` (column E) specifies the protocol step that yo
ii) Columns B to C:
    -   These are fields with drop-down menus.
    -   You only need to enter a value into `Method` (column B) *or* `Measure
iii) Columns D, F and G:
     -   These are free form fields.
     -   `Summary` (column D) is a short description of the protocol step tha
     -   `Protocol step version` (column F) specifies the version of a given
     -   `Reference link` (column G) is used to report a URL or hyperlink to
```

2. **Columns H to O**

	H	I	J	K	L	M	N	O
1	Organization	Contact ID	Instrument ID	Value	Unit	Aggregation	Last edited	Notes
2								
3								
4								

```
i)  Columns H to J:
    -   These are identifier fields.
```

- You can repeat values between entries. For instance, if you are entering two differe

ii) Column K:

- `Value` is a free form field where, if the protocol step is a measure, you can enter
- Of note, for some measures and methods, they can take enumerated values, so this fie

iii) Columns L and M:

- These fields contain conditional drop-down menu fields.
- `Unit` (column L) depends on what you entered in `Measure` (column C). This field i
- `Aggregation` (column M) depends on what you entered in `Unit` (column L). This fie

iv) Columns N and O:

- These are a date field (column N) and a free form field (column O) where you can ent
- `Last edited` (column N) is where you can enter the date when the entry was last upd

mm-dd. Including hours and minutes is optional, but all date-
entries use the ISO 8601 format. `2022-01-01T06:11:54` or `2022-
01-01T06:11:54+13:30.`

Protocols template

1. **Columns A to J**

	A	B	C	D	E	F	G	H	I	J
1	Source Protocol ID	Protocol ID	Name	Summary	Reference link	Organization ID	Contact ID	Protocol version	Last edited	Notes
2										
3										
4										

i) Columns A and B; F and G

- These are identifier fields.
- `Protocol ID` (column B) is the unique identifier for this template, and *cannot be
- `Source Protocol ID` (column A), `Organization ID` (column F), and `Contact ID` (col
- `Source Protocol ID` (column A) is where you can enter the `Protocol ID` of the prot
- `Organization ID` (column F) records the linked organization who created or designed
- `Contact ID` (column G) records the ontact information for questions about the proto

ii) Columns C to E:

- These are free form fields in which you can enter the indicated infor
- `Name` (column D) refers to the name that you have decided to give yo
- `Summary` (column D) and `Reference link` (column E) record a narrati

iii) Columns H, J:

- These are free form fields.
- `Protocol version` (column I) is where you can indicate the version o
- `Notes` (column J) records any additional details about the protocol

vi) Columns I:

- `Last edited` is a date field where you can enter the date when the

Protocol relationships template

1. **Columns A to I**

	A	B	C	D	E	F	G	H	I
1	Synthetic ID for the protocolRelationships table	Protocol ID container	Protocol ID object	Step ID Object	Relationship between entities	Protocol ID subject	Step ID Subject	Last edited	Notes
2									
3									
4									

i) Columns A to D; F and G:

- These are identifier fields.
- `Synthetic ID for the protocolRelationships table` is a unique, auto
- All the remaining identifiers (columns B to D; F and G) are either `
- You should only enter a value for one of the two `object` columns (co
- An example will be given in point (ii) below.

ii) Column E:

- `Relationship` contains a drop-down menu; it is where you can select

```
    -   For example, pretend you wanted to enter a relationship stating that Protocol step A

iii) Columns H and I:

     -   These are a date field (column G) and a free form field (column H) where you can en
     -   `Last edited` (column G) is where you can enter the date when the entry was last up
```

You have now entered your data in the `Protocol steps`, `Protocols` and `Protocol relationships` templates, congratulations!

5) How to report metadata

In this guide you will learn how to enter in the metadata of your wastewater data through a series of templates. Each entry in a template will usually represents what is found in the title of the template. For instance, in the `Organizations` template each row will represent an organization. In the context of the PHES-ODM, metadata is anything that gives general information about the data that you are entering and is not found in the templates related to measures, protocols and samples.

You can find additional information regarding terms and the colour-coding of columns at the beginning of this guide (How-To guides) and the Reference Guide - Parts document.

Quick Start

Below you will find the fields that are mandatory for the metadata-related templates. You will also find definitions of these fields and examples of entries of data. A more detailed description of some of the key concepts can be found in the following section, Detailed Description.

`Accession` (or `accessions`) template

1. **Mandatory fields**

- `Accessions Index ID`: The unique indentifier for each row, used to reference an external data linkage.
- `Measure Report ID`: An identifier for a measure. This is only mandatory if the entry is related to a measure.
- `Measure Set Report ID`: An identifier that links together a group of related measures. This is only mandatory if the entry is related to a measure set.
- `Public Health Action ID`: An identifier for a public health action. This is only mandatory if the entry is about a public health action.
- `Host Data Repository or Bank`: The hosting website or organization where the external data being referenced is permanently stored. This is availbale as an enumerated value.
- `Accession Number in Repository`: The unique reference code or number used for the external data being linked in the repository provided.

2. **Examples**

	A	B	C	D	E	F
1	Accessions Index ID	Measure Report ID	Measure Report ID	Public Health Action ID	Host Data Repository or Bank	Number in Repository
2	rawwwSeq120421	NA	shapiro 120431	NA	sra	PRJNA788395
3	covidSeq120421	NA	shapiro 120431	NA	gisaid	EPLISL_3098106
4	vchoSeq240821	cholera240821	NA	NA	genbank	PRJNA668606

this semi-fictional example data is generated from open data generated by the Shapiro lab from the following papers: Levade, I., Khan, A. I., Chowdhury, F., Calderwood, S. B., Ryan, E. T., Harris, J. B., LaRocque, R. C., Bhuiyan, T. R., Qadri, F., Weil, A. A., & Shapiro, B. J. (2021). A combination of

metagenomic and cultivation approaches reveals hypermutator pheno-types within Vibrio cholerae–infected patients. mSystems, 6(4), e00889-21. https://doi.org/10.1128/mSystems.00889-21
N'Guessan, A., Tsitouras, A., Sanchez-Quete, F., Goitom, E., Reiling, S. J., et al. (2022). Detection of prevalent SARS-CoV-2 variant lineages in wastewater and clinical sequences from cities in Québec, Canada [Preprint]. medRxiv. https://doi.org/10.1101/2022.02.01.22270170

`Address` (or `addresses`) template

1. **Mandatory fields**

- `Address ID`: The unique identifier for the `Address` template. Each value represents an address.
- `Dataset ID`: The identifier of the dataset that stores information for measures, samples and other reporting tables.
- `Address line 1`: Line 1 (the street name, number and direction) for a given address of a site or organization.
- `City`: The city where a site or organization is located; part of the address.
- `State, province or region`: The state, province, or region where a site or organization is located; part of the address.
- `Country`: The country where a site or organization is located; part of the address.

2. **Examples**

	A	B	C	D	E	F	G	H	I
1	Address ID	Address Line 1	Address Line 2	City	State, Province, or Region	Postal or Zip Code	Country	Last edited	Notes
2	CACA-ONOtt1	nr	nr	Ottawa	CA-ON	nr	CA		
3	CACA-ONGue2	nr	nr	Guelph	CA-ON	nr	CA		
4	CACA-ONGue3	nr	nr	Guelph	CA-ON	nr	CA		
5	CACA-ONSud4	nr	nr	Sudbury	CA-ON	nr	CA		

this example data is pulled from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Contact` (or `contacts`) template

1. **Mandatory fields**

- `Contact ID`: The unique identifier for the `Contact` template. Each value represents a contact person.
- `Organization ID`: An identifier for the organization to which the contact person is affiliated.
- `Email`: Contact e-mail address.

2. **Examples**

	A	B	C	D	E	F	G	H	I
1	Contact ID	Organization ID	First name of contact	Last name of contact	Contact email	Contact phone	Role of contact	Last edited	Notes
2	CarletonU R1	CU Lab1	Chanchal	Yadav	chanchalyadav@email.ca	123-456-7891	nr	2021-04-21	No longer working at CU
3	CarletonU R2	CU Lab1	Richard	Kibbee	richard.kibbee@email.ca	123-456-7891	nr		Responsibe for generating, analyzing and reporting the data
4	DK	LG	Devita	Kireina	dkireina@email.ca	123-456-7891	nr		

this example data is adapted from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Calculation` (or `calculations`) template

1. **Mandatory fields**

- `Calculation ID`: A unique identifier for each row in the `calculations` table, it is typocally generated by concatenating the pipeline and treatment IDs together.
- `Pipeline ID`: A unique identifier for the data pipeline, or seuence of calculations/data treatments applied to the data.
- `Treatment ID`: A unique identifier for each treatment or step in the calcution or data pipeline that generated the reported measure.
- `Calculation Type`: An ennumerated field to explain the purpose/nature of a single calculation/data treatment.

2. **Examples**

	A	B	C	D
1	**Calculation ID**	**Pipeline ID**	**Treatment ID**	**Calculation Type**
2	labWork1pmmovStd	labWork1	pmmovStd	standardization
3	labWork1predict321	labWork1	predict321	predictiveModels
4	weekSmoothsmooth12	weekSmooth	smooth12	smoothing

this example data is invented data intended to showcase usecases of the `calculations` table.

`Dataset` (or `datasets`) template

1. **Mandatory fields**

- `Dataset ID`: A unique identifier for the `Dataset` template. Each value represents a dataset.
- `License`: The license of the dataset.
- `Data custodian`: The data custodian of the database. This is represented by an `Organization ID` and would have been created in the `Organization` template.

2. **Examples**

	A	B	C
1	**Dataset ID**	**License**	**Custody Contact ID**
2	OntarioConsortiumData	ccby40	DeGroot
3	modelEAUxMiCELxPolytech	ccby40	vanrolleghem.modeleau_lab
4	Ottawa-1	ccby40	delatollaLab

this example data is adapted from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium, centrEAU, and the Delatolla Lab

`Instrument` (or `instruments`) Template

1. **Mandatory fields**

- `Instrument ID`: The unique identifier for the `Instrument` template. Each value represents an instrument.
- `Model`: Model number or version of the instrument.
- `Instrument type`: The type of instrument used to perform the measurement.

2. **Examples**

	A	B	C
1	**Instrument ID**	**Model**	**Instrument Type**
2	HSNRI_qPCR_1	AriaMX	rtqPCRinst
3	RTqPCR	CFX96	rtqPCRinst
4	RTqPCR_QS	QuantStudio 5	rtqPCRinst

this example data is adapted from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Organization` (or `organizations`) template

1. **Mandatory fields**

- `Organization ID`: The unique identifier for the `Organization` template. Each value represents an organization to which the reporter is affiliated.
- `Address ID`: An identifier for the address of the organization.

2. **Examples**

	A	B
1	**Organization ID**	**Address ID**
2	CU Lab1	CACA-ONOtt1
3	LG	CACA-ONGue2
4	MH	CACA-ONGue3

this example data is adapted from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Polygon` (or `polygons`) template

1. **Mandatory fields**

- `Polygon ID`: The unique identifier for the `Polygon` template. Each value represents a polygon.
- `Type of geography`: Type of geography that is represented by the polygon.
- `Well-known text`: Well-known text of the polygon.
- `European Petroleum Survey Group Coordinates`: A code that specifies a given geospatial area.

2. **Examples**

	A	B	C	D
1	Polygon ID	Type of geography	European Petroleum Survey Group Coordinates	Well-known text
2	qc_01_swrcat	swrcat	nr	POLYGON ((-71.252979 46.915
3	qc_02_swrcat	swrcat	nr	POLYGON ((-71.2782469 46.93
4	prov_qc_hlthreg_capitale-nationale	hlthreg	nr	MULTIPOLYGON (((-69.805511

this example data is adapted from open data sources using the ODM at centrEAU

`Polygon Relationship` (or `polygonRelationships`) template

1. **Mandatory fields**

- `Polygon Relationship ID`: A unique identifier for each row of the `Polygon relationships table`. Can be any combination of characters, as long as there are fewer than 30.

- `Polygon ID Object`: Identifier of the object of a relationship between polygons. Relationships are read as "`polygon object` is `relationship ID` of `polygon subject`". `relationship ID` is technically not mandatory, as simply naming the related polygon IDs implies a relationship, even without more details.

- `Polygon ID Subject`: Identifier of the subject of a relationship between polygons. Relationships are read as "`polygon object` is `relationship ID` of `polygon subject`". `relationship ID` is technically not mandatory, as simply naming the related polygon IDs implies a relationship, even without more details.

2. **Examples**

	A	B	C
1	**Polygon relationship ID**	**Polgygon ID Subject**	**Polygon ID Object**
2	hrlovaces	hr1	wwtpAces
3	hrlovhearts	hr1	wwtpHearts
4	hr1chityg	hr1	cityG
5	hr2ovhearts	hr2	wwtpHearts

this example data is invented data intended to showcase usecases of the `calculations` table.

`Public Health Action` (or `phActions`) template

1. **Mandatory fields**

- `Public Health Action ID`: Unique identifier for public health actions, one for each row in the `phActions` table.
- `Measure Report ID`: Unique identifier for a measurement linked to a public health action. This is only mandatory if the entry is related to a measure.
- `Measure set report set ID`: Unique identifier that links together a group of related measures, linked to a public health action.This is only mandatory if the entry is related to a measure set.
- `Public health action type`: The type of public health action being taken. This is only mandatory if the entry/row is *not* operating as an action group.

2. **Examples**

	A	B	C	D
1	Public Health Action ID	Measure Report ID	Measure set report set ID	Public health action type
2	maskCityAJune26	xXJuneFluMeasure	NA	contMeasImp
3	jRSVoutbCityA jRSVoutbCityAsubA	NA	yyJuneRSVMeasureSet	survAlert
4	jRSVoutbCityA jRSVoutbCityAsubB	NA	xxJuneRSVMeasureSet	outb

this example data is invented data intended to showcase use cases of the `Public Health Actions` table.

`Quality reports` (or `qualityReports`) template

1. **Mandatory fields**

- `Quality report ID`: The unique identifier for the `Quality reports` template. Each value represents a quality issue that you wish to report.
- `Measure Report ID`: An identifier for a measure. This is only mandatory if the entry is about a measure.
- `Sample ID`: An identifier for a sample. This is only mandatory if the entry is about a sample.
- `Measure Set Report ID`: An identifier that links together a group of related measures. This is only mandatory if the entry is related to a measure set.
- `Quality flag`: A field for reporting any quality concerns for a sample or measure.

2. **Examples**

	A	B	C	D	E
1	Quality report ID	Measure Report ID	Sample ID	Measure set report set ID	Quality flag
2	flagND11792_ORANGE24921_covN1_2_2021-09-24	11792_ORANGE24921_covN1_2_2021-09-24	NA	NA	flagND
3	flagB8107_TPKL230315_2_nPMMoV_3_2023-03-24	8107_TPKL230315_2_nPMMoV_3_2023-03-24	NA	NA	flagB
4	flagUJ9945_TPMOOS221023_1_covN1_2_2022-11-04	9945_TPMOOS221023_1_covN1_2_2022-11-04	NA	NA	flagUJ
5	flagJ17969_TPTIMM230215_1_covN2_3_2023-02-17	17969_TPTIMM230215_1_covN2_3_2023-02-17	NA	NA	flagJ

this example data is adapted from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium

`Sites` (or `sites`) template

1. **Mandatory fields**

- `Site ID`: The unique identifier for the `Sites` template. Each value represents the site where a wastewater sample was taken.
- `Site type`: Type of site where a sample was taken.
- `Sample shed`: A geographic area, physical space, or structure. A sample is taken from a sample shed for a representative measurement of a substance.
- `Contact ID`: An identifier for a given contact person.
- `Latitude`: Latitude in decimal coordinates of the site.
- `Latitude`: Longitude in decimal coordinates of the site.
- `European Petroleum Survey Group Coordinates`: A code that specifies a given geospatial area.

2. **Examples**

	A	B	C	D	E	F	G
1	Site ID	Site Type	Sample shed	Contact ID	Latitude	Longitude	European Petroleum Survey Group Coordinates
2	Site O1800	upstream	uCampus	CarletonU R2	45.38279363	-75.69583527	nr
3	ACT	wwtpMuC	nr	DK	43.628685	-80.02066618	nr
4	MAP	upstream	corFcil	DK	43.52563205	-79.8982342	nr
5	MH	wwtpMuC	nr	DK	43.420464	-79.731517	nr
6	WWTP	wwtpMuC	nr	DK	43.628685	-80.264376	nr
7	TPKL	wwtpMuC	nr	Jknockleby	46.46572	-81.03262	nr
8	Barrie	wwtpMuS	nr	Islam G	44.375947	-79.690186	nr

this example data is adapted from open data sources using the ODM at the Ontario Wastewater Surveillance Consortium ## Detailed Description

`Accessions` template

1. **Columns A to F**

	A	B	C	D	E	F
1	Accessions Index ID	Measure Report ID	Measure set report set ID	Public Health Action ID	Host Data Repository or Bank	Organization ID
2						
3						
4						

i) Columns A to D, and F:

- These are identifier fields.

- `Accessions Index ID` (column A) is the unique identifier for each row of the `acces

- `Measure report ID` (column B), `Measure set report ID` (column C), and `Public Heal

- `Organization ID` (column F) is an field to link the organization who made the publi

ii) Column E:

- `Host Data Repository or Bank` (column E) is the field for listing the name of the r
odm.org/sets.html#dataRepoSet) for more information.

2. **Columns G to J**

	G	H	I	J
1	Accession Number in Repository	Version of Data Hosting Platform/Repository	Last edited	Notes
2				
3				
4				

i) Columns G, H, and J:

- These are free form fields in which you can enter various informatio

- `Accession number in Repository` (column G) should be the unique refe

- `Version of Data Hosting Platform/Repository` (column H) sets the ve

- `Notes` (column J) is a free text field to record additional comment

ii) Columns I:

- `Last Edited` (column I) is a date field where you can enter the da

Address template

1. **Columns A to E**

	A	B	C	D	E	F	G	H	I
1	Address ID	Address Line 1	Address Line 2	City	State, Province, or Region	Postal or Zip Code	Country	Last edited	Notes
2									
3									
4									

i) Columns A:

- This is the identifier field.

- `Address ID` (column A) is the unique identifier for this template, a

ii) Columns B to D, and F:

- These are free form fields in which you can enter various informatio

- `Address Line 1` (column B) and `Address Line 2` (column C) record s

iii) Columns E and G:

- These are categorical fields that take predetermined ennumerated values.

- The values for `State, Province, or Region` (column E) are the ISO 3166-2 code for country sub-domainm, which can be found in the [`Zones table`](https://docs.phes-odm.org/tables.html#zones)

- The values for `Country` (column G) are the ISO 3166-1 alpha-2 country codes, which can be found in the [`Countries table`](https://docs.phes-odm.org/tables.html#countries).

iv) Columns H to I:

- `Last edited` (column H) is a date field where you can enter the date when the entry

- `Notes` (column I) is for any extr comments or information.

Contact template

1. **Columns A to E**

	A	B	C	D	E	F	G	H	I
1	Contact ID	Organization ID	First name of contact	Last name of contact	Contact email	Contact phone	Role of contact	Last edited	Notes
2									
3									
4									

i) Columns A to B:

- These are identifier fields.

- `Contact ID` (column A) is the unique identifier for this template, a
- For the rest of the fields, you can repeat the values between entries
- You may have already created these Identifiers in another template. I

ii) Columns C and G:

- These are free form fields in which you can enter the name(s) and var

iii) Columns H to I:

- `Last Edited` (column H) is a date field where you can enter the date
- `Notes` (column I) is for any extr comments or information.

Calculations template

1. **Columns A to G**

	A	B	C	D	E	F	G
1	Calculation ID	Pipeline ID	Treatment ID	Name	Calculation Type	Standard for Data Adjustment	Summary
2							
3							
4							

i) Columns A to C:

- These are identifier fields.
- `Calculation ID` (column A) is a unique identifier for each row in th
- `Pipeline ID` (column B) is a unique identifier for the data pipeline

- `Treatment ID` (column C) is a unique identifier for each treatment or step in the c

ii) Columns D and G:

- These are free-text fields.

- `Name` (column D) is a name used for a given data treatment, while `summary` (column

iii) Columns E and F:

- These are categorical or enumerated fields.

- `Calculation Type` (column E) is An ennumerated field to explain the purpose/nature
odm.org/sets.html#calcTypeSet).

- `Standard for adjustment` (column F) is used for smoothing or standardisation calcul
odm.org/sets.html#measurements)

2. **Columns H to M**

	H	I	J	K	L	M
1	Sequence Order	Equation	Reference link	Source Code	Last edited	Notes
2						
3						
4						
5						

i) Columns H to K:

- These are free-text fields.

- `Sequence order` (column H) is an integer value to specify the position in the order

- `Equation` (column I) and `Source code` (column K) specify addition c
- `Reference Link` (column J) is another external reference to details

ii) Columns L and M:

- `Last Edited` (column H) is a date field where you can enter the date
- `Notes` (column I) is for any extra comments or information.

Dataset template

1. **Columns A to H**

	A	B	C	D	E	F	G	H
1	Parent dataset ID	Dataset ID	Dataset creation date	Name	License	Description	Reference link	Language ID
2								
3								
4								

i) Columns A and B:

- These are identifier fields.
- `Dataset ID` (column B) is the unique identifier for this template, a
- For `Parent dataset ID` (column A), you can repeat the value between

ii) Column C

- `Dataset creation date` (column C) is a date field where you can ente

iii) Columns D, F, and G:

- These are free form fields in which you can enter various information related to th

- `Name` (column D) and `Summary` (column G) are optional field to report more detail

- `Reference Link` (column F) points to an external link for additional information,

iv) Columns E and H:

- These are categorical input fields for reporting additional metadata on the dataset

- `License` (column E) reports to usage rights of the dataset. For example, whether t
odm.org/sets.html#licSet).

- `Language ID` is the ISO-6393 code for the natural language in which the dataset wa
set and present in the [`languages` reference table](https://docs.phes-
odm.org/parts.html#languages).

2. **Columns I to O**

	I	J	K	L	M	N	O
1	Funder contact ID	Custody Contact ID	Funding agency ID	Data custodian ID	Original Data Format	Last edited	Notes
2							
3							
4							

i) Columns I to L:

- These are identifier fields.

- For information regarding funders, you can enter their `Funder Contact ID` (which is

- For information regarding Data Custodians, you can enter their `Custody Contact ID`

ii) Columns M, N and O:

- These are a categorical field (column M), date field (column N) and a

- `Original data format` (column M) is used to report the original stu
ODM to explain any structural odities resulting from the mapping process or c
odm.org/sets.html#ogFormSet).

- `Last edited` (column M) is the date when the entry was updated. This

- `Notes` (column O) is for any extra comments or information.

Instrument template

1. **Columns A to G**

	A	B	C	D	E	F	G	H
1	Instrument ID	Name	Model	Manufacturer	Description	Reference link	Instrument Type	Describe other instrument type, if applicable
2								
3								
4								

i) Columns A:

- This is the identifier field.

- `Instrument ID` (column A) is the unique identifier for this template

ii) Columns B to F:

- These are free-text fields where you can enter the `Name` (column B)

- A `Description` (coliumn E) and `Reference link` (column F) can also

iii) Columns G to H:

- `Instrument Type` (column G) is a categorical input to better describe the type of i
odm.org/sets.html#insTypeSet).

- `Describe other instrument type, if applcable` (column H) is a free text field to de

2. **Columns I to K**

	I	J	K
1	Index	Last edited	Notes
2			
3			
4			

i) Columns I to K:

- Most of these fields are free form in which you can enter relevant information regar

- You can use `Index` (column I) to differentiate two entries of data that are the sam

- `Last Edited` (column J) is a date field where you can indicate the date when the en

- `Notes` (column K) is for any extra comments or information.

`Organization` template

1. **Columns A to E**

	A	B	C	D	E	F	G	H	I
1	Organization ID	Name	Description	Address ID	Organization Type	Organization level	Organization sector	Last edited	Notes
2									
3									
4									

i) Columns A and D:

- These are identifier fields.

- `Organization ID` (column A) is the unique identifier for this templa

- For `Address ID` (column D), you can repeat the value between entrie

- You may have already created some of the identifiers in other templat

ii) Columns B and C:

- These columns are free form fields in which you can enter additional

iii) Columns E to G:

- These are fields with drop-down menus where you can select various c

- For the possible categorical values for `Organization type` (column
odm.org/sets.html#orgTypeSet).

- For the possible categorical values for `Organization level` (column
odm.org/sets.html#orgLevelSet).

- For the possible categorical values for `Organization sector` (colum
odm.org/sets.html#orgSectorSet).

iv) Columns H and I:

- These are a date field (column H) and a free form field (column I) where you can ent

- `Last edited` (column H) is the date when the entry was updated. This field is used

- `Notes` (column I) is for any extra comments or information.

Polygon template

1. **Columns A to I**

	A	B	C	D	E	F	G	H	I
1	Polygon ID	Dataset ID	Name	Description	Type of geography	European Petroleum Survey Group Coordinates	Well-known text	File location of polygon	Reference link
2									
3									
4									
5									

i) Columns A and B:

- These are identifier fields.

- `Polygon ID` (column A) is the unique identifier for this template, and cannot be re

- For `Dataset ID` (column B), you can repeat the value between entries (if needed). F

- You may have already created the `Dataset ID` in the `Dataset` template.

ii) Columns C to D, F to I:

- These are free form fields in which you can enter additional information regarding t

- `Name` (column C) is the name of the polygon, and `Description` (column D) offers a

- `European Petroleum Survey Group Coordinates` (or EPSG coordinates) (column F) is a
Known Text` (column G) provides wkt (the text markup language that can be used to represent

- `File location of the polygon` (column H) and `Reference link` (colu

iii) Columns F:

- For `Type of geography` (column E) of the polygon, you can select o
down menu.The possible values can be found in the [`Geographic set`](https:/
odm.org/sets.html#geoTypeSet).

2. **Columns J to N**

	J	K	L	M	N
1	Organization ID	Contact ID	Polygon License	Last edited	Notes
2					
3					
4					
5					

i) Columns J and K:

- These are identifier fields.

- `Organization ID` (column J) and `Contact ID` (column K) are for lin

ii) Column L:

- `Polygon license` (column L) is for specifying the usage rights of t

iii) Columns M and N:

- `Last edited` (column M) is a date field where you can enter the dat

- `Notes` (column N) is for any extra comments or information.

Polygon Relationships template

1. **Columns A to E**

	A	B	C	D	E	F
1	Polygon relationship ID	Polgygon ID Subject	Relationship between entities	Polygon ID Object	Last edited	Notes
2						
3						
4						
5						

i) Columns A, B, and D:

- These are identifier fields.

- `Polygon relationship ID` (column A) is a unique identifier for each row of this tab

- `Polygon ID subject` (column B) and `Polygon ID object` (column D) reference rows in

ii) Column C:

- `relationship between entities` (column C) describes the actual relationship between
odm.org/sets.html#polyRelSet).

iii) Columns E to F:

- `Last edited` (column E) is a date field where you can enter the date when the entry

- `Notes` (column F) is for any extra comments or information.

Public Helath Actions template

1. **Columns A to E**

	A	B	C	D	E	F
1	Public Health Action Group ID	Public Health Action ID	Measure Report ID	Measure set report set ID	Organization ID	Site ID
2						
3						
4						

i) Columns A to F:

- These are identifier fields.

- `Public health action ID` (column B) is the unique identifier for eac

- `Measure Report ID` (column C) and `Measure set report ID` (column D)

- `Organization ID` (column E) links to the organization orchestrating

2. **Columns G to N**

	G	H	I	J	K	L	M	N
1	Public health action type	Public health action	Public health threat targeted by action	Public health action datetime	relevance start date	relevance end date	Last edited	Notes
2								
3								
4								

i) Columns G to I:

- Thesee are categorical fields used to describe the nature and the tar

- `Public health acction type` (column G) describes the high-level nature of the action (action types are listed in [`Public Health Action odm.org/sets.html#actionTypeSet)), while `public health action` (column H) pr odm.org/sets.html#allActionsSet)).

- `Public health thrat targetted by action` is exactly as it describes, and it takes m
odm.org/sets.html#measurements)

ii) Columns J to L:

- These are all date fields.

- `Public health action datetime` (column J) specifies when the action was taken, whil

iii) Columns M to N:

- `Last edited` (column M) is a date field where you can enter the date when the entry

- `Notes` (column N) is for any extra comments or information.

Quality reports template

1. **Columns A to H**

	A	B	C	D	E	F	G	H
1	Quality report ID	Measure Report ID	Sample ID	Measure set report set ID	Quality flag	Severity indicator	Last edited	Notes
2								
3								
4								
5								

i) Columns A to D:

- These are identifier fields.

- `Quality report ID` (column A) is the unique identifier for this template, and canno

- For the rest of the columns, you can repeat the value between entries (if needed). F

- You may have already created some of the identifiers in other templates. For instanc

ii) Columns E and F:

- `Quality flag` (column E) is a drop-down menu field where you can sel
odm.org/sets.html#qualityIndicators).

- `Severity indicator` (column F) is is also a drop-
down menu field where you can indicate the severity of the quality flag. Poss
odm.org/sets.html#sevSet).

iii) Columns G and H:

- These are a free form field and a date field in which you can enter

- `Last edited` (column G) is a date field where you can enter the dat

- `Notes` (column H) is for any extra comments or information.

Sites template

1. **Columns A to J**

	A	B	C	D	E	F	G	H	I	J
1	Parent Site ID	Site ID	Dataset ID	Polygon ID	Site Type	Sample shed	Level of Aggregation of a Sampling Site	Address ID	Organization ID	Contact ID
2										
3										
4										
5										

i) Columns A to D, and H to J:

- These are identifier fields.

- `Site ID` (column B) is the unique identifier for this template, and

- For the rest of the columns, you can repeat the value between entries (if needed). F

- `Parent site ID` (column A) refers to the site that is parent to the site that is be

- `Address ID` (column H), `Organization ID` (column I), and `Contact ID` (column J) l

ii) Columns E to G:

- These are drop-down menu fields in which you can specify the `Site Type` (column E),

- A list of site types can be found in the [`Site Set`](https://docs.phes-odm.org/sets.html#siteTypeSet), and the sheds can be found in the [`Sampleshed Set`](https:/ odm.org/sets.html#shedSet).

- The `Level of Aggregation of a Sampling Site` (column G) is a field to specifie the

- Possible values for `Level of Aggregation of a Sampling Site` (column G) can be foun odm.org/sets.html#siteLevelSet).

2. **Columns K to T**

	K	L	M	N	O	P	Q	R	S	T
1	Name	Description	Primary reporting authority ID	Secondary reporting authority ID	Health Region for a Site	Latitude	Longitude	European Petroleum Survey Group Coordinates	Last edited	Notes
2										
3										
4										
5										

i) Columns K, L, and O:

- These are all free form fields in which you can enter in relevant information about

- `Name` (column K) and `Description` (column L) are for more internal details describ

- `Health Region for Site` (column O) reports the health region, and should match how

```
ii) Columns M and N:

    -   These are identifier fields that you can use to record additional in

    - These field differ from the `Organization ID` (column I) field in that

iii)  Columns P to R:

    -   These are free form fields where you can enter in additional informat

    -   `European Petroleum Survey Group Coordinates` (column Q) is a coordi

iv)  Columns S to T:

    -   `Last Edited` (column S) is a date field where you can enter the dat

    -   `Notes` (column T) is for any extra comments or information.
```

You have now entered in your metadata, congratulations!

Notes regarding templates

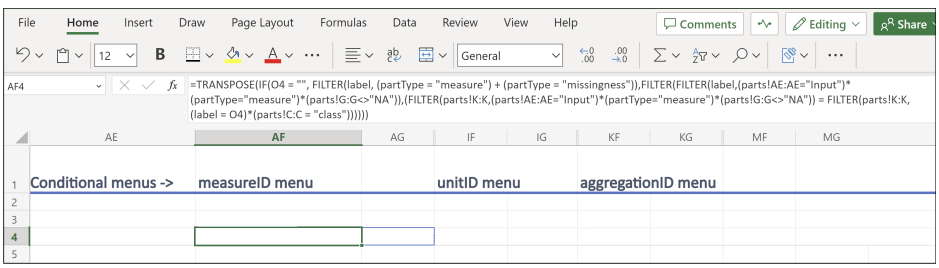
Templates with conditional menus (`Measure report` and `Protocol steps`)

Adding more conditional menus

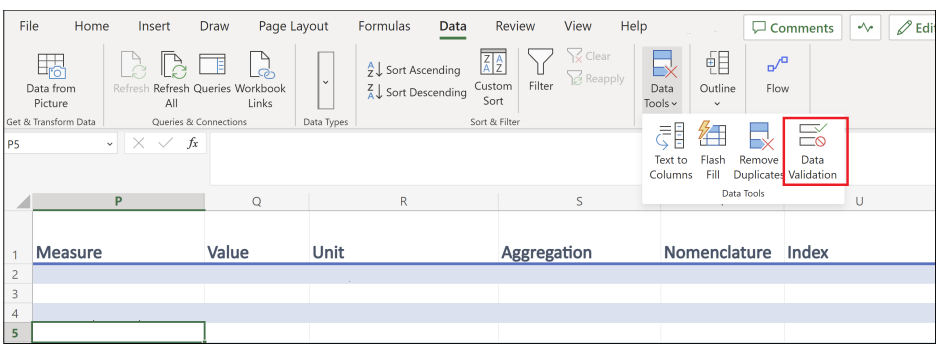
NOTE: The conditional drop-downs in the excel templates are very fragile. They have also been depreciated in version 3+ of the PHES-ODM. Drop-down menus are still available, but not with the conditional menus.

- The code to determine the entries for the conditional menus are found to the right of the main template. Unlike the main template, the rows containing the code will not be alternating in colour.

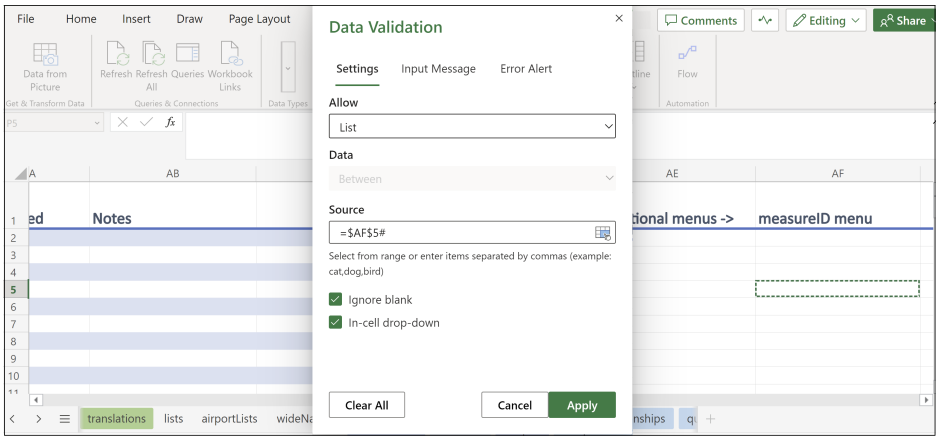
- The code is only present for the first three rows. If you want to use conditional menus for additional rows, you will need to copy the code to these rows as well as create the menus in the desired cells. As an example, pretend that you wanted to add a `Measure` field conditional menu to row 5 in the `Measure report` template. The first thing you would do is copy the code from AF4 to AF5 (see below, all images in this example are from Excel Online).



- Then, to create the new menu, you would go to P5 (which is where the new conditional menu will be located). You would select "Data validation", which is under "Data Tools" in the "Data" tab (it is outlined in red in the image below).



- Finally, you would select "List" from the "Allow" menu and then enter the following text "=AF5#" under "Source". The column and row indicators ("AF" and "5", in this example) match up with where you copied the new code ("AF5").



For additional menus, repeat the above steps. Adding conditional menus in an online environment (such as Excel Online) may slow down the templates considerably.

Troubleshooting conditional menus

- The conditional menus work by searching the `partLabels` column in the `parts` table that is included with the templates.

- If you obtained an error with these menus check if any changes were made to the `parts` table.

Templates with menus (all templates other than the `Measure sets`, `Protocols`, `Contact`, `Address` and `Dataset` templates)

Part IDs

- In the main parts of each of the templates, labels are used in the menus.
- If you wish to have the part IDs of these values, they are located to the right of the main template and, if applicable, the code for the conditional menus. Unlike the main template, the rows containing the part IDs will not be alternating in colour.
- The part IDs are present in the first 100 rows of each of the templates.

Troubleshooting menus (not including conditional menus)

- The menus are based on what is found in the `lists` tab that is included with the templates.
- If you obtained an error with these menus check if any changes were made to the `lists` tab.

Sample Relationships

Dictionary v3.0.1 Documentation v3.0.1

Context

To fully interpret the measures coming out of samples, it is sometimes helpful to know how they are related to each other. For example, two samples taken at the same site, at the same time, with the same method, can be used to characterize the variability inherent to the sampling strategy or sampling matrix. When samples are composited from several subsamples, it is useful to know which subsamples were used and where they came frame. Conversely, it is also helpful to know what pooled samples are related to a given subsample. Parts of samples can also be spiked with a viral target as part of a quality assurance protocol. Keeping a trace of the relationships linking various samples supports the retrieval of related samples inside the PHES-ODM database and thus improves the interpretability of the data.

Modelling sample relationships

There are several ways in which samples can be related.

Samples can be related via:

1. The splitting of an original sample

Sample Relationships

1. A subsample is related to its parent sample (`child`).
2. A sample split at the sampling location yields field replicates who are related to each other (`fieldReplicate`).
3. A field sample is related to a sample generated from it in the laboratory (`labDuplicate`).
4. Two samples collected at the same time and place are related to each other (`colocated`).
5. A field sample is related to a control sample processed alongside it (`control`).
6. A field sample is related to a subsample that has been modified as part of a general quality control procedure (`lcsd`), or as part of a recovery efficiency protocol (`msd`).

2. The combination of several samples

   1. Parent samples related to the final pooled sample (`pooled`).

Example of sample relationship webs are found in Figure A.

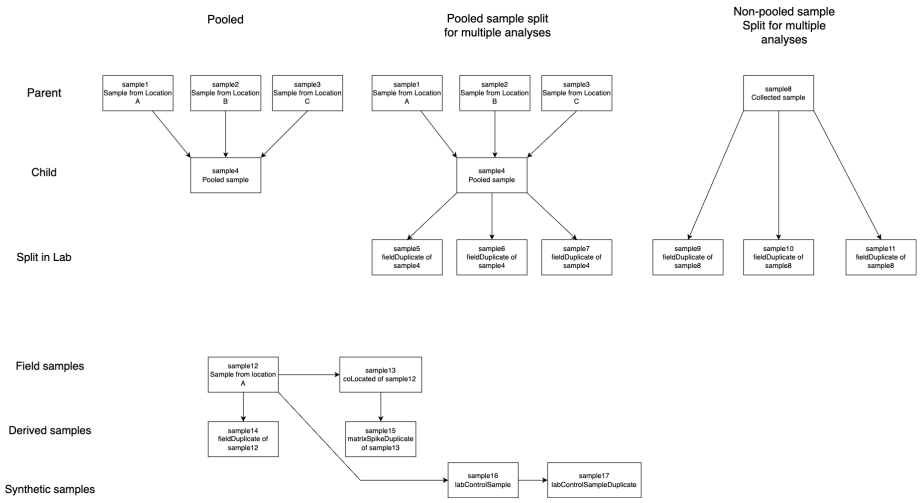


Figure 4.: **Figure A: Various possible sample relationships.**

Because a single sample can be related to many others, efficiently storing both the sample information (recorded in `samples`) and that sample's relationships to other samples in a single database table is impossible. This realization led to the creation of the separate `sampleRelationships` table in the PHES-ODM.

Implementation

The `SampleRelationships` table is responsible for linking samples with each other and for defining the nature of the relationships. Each row defines a relationship. A sample can have any number of relationships to other samples. The table implements four attributes:

1. `sampleRelationshipsID`
2. `sampleIDSubject`
3. `relationshipID`
4. `sampleIDObject`

Where `sampleRelationshipsID` exists as a primary key and unique reference for each row, while the remaining attributes of each row can be read as a sentence of the form:

```
[sampleIDSubject] is a [relationshipID] of [sampleIDObject]
```

The acceptable values for relationshipID are the following at the moment, though some more could be added to the dictionary of the need arises: (to request an new part to be added to the PHES-ODM, create a new issue on the GitHub repository, or fill out this Google Form)

```
    - child
    - colocated
    - fieldReplicate
```

```
    - msd
    - labDuplicate
    - lcsd
    - control
```

To complete the picture presented by the `sampleRelationships` table, one can read the attributes in the `samples` table that describe the sample's nature:

1. `repType` (replicate type) indicates what kind of replicate a sample is (field replicate, matrix spike replicate, lab control replicate, etc. - see replicateSet for the full list).
2. `pooled` indicates if the sample is the result of the combination of several samples. It is important to note that `pooled` is a transitive property: subsamples derived from a `pooled` sample are also `pooled`. This is a boolean variable, carrying either TRUE or FALSE as possible values.

Below are two examples of possible relationship webs between samples and the the resulting entries in a `sampleRelationships` table.

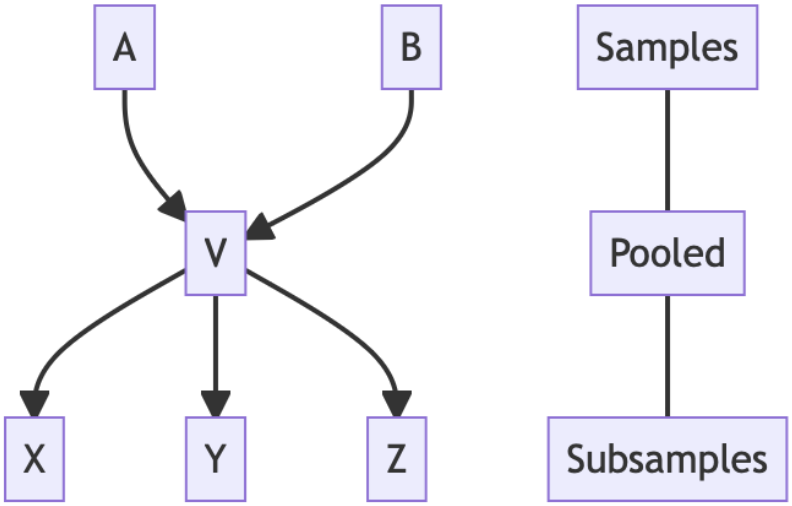


Figure 5.: Example A

sampleIsSubject	relationshipID	sampleIsObject
V	child	A
V	child	B
X	child	V
Y	child	V
Z	child	V

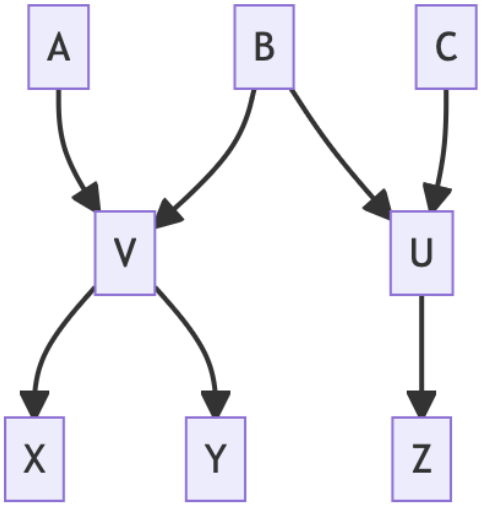


Figure 6.: Example B

sampleIsSubject	relationshipID	sampleIsObject
V	child	A
V	child	B
U	child	B
U	child	C
X	child	V
Y	child	V
Z	child	U

Long-format, wide-format, and wide-names

Dictionary v3.0.1 Documentation v3.0.1

Wide-format and long-format data

Wide- and long-formats are two broad categories for describing how to store or record data. For our purposes, long-format describes a situation with one row for each observation, measure, or data point. Wide-format describes a situation where all observations, measures, or data points of one day are recorded in one row.

For example, below is a long-format table for recording wastewater surveillance data:

date	measure	value	unit
dec 17	covid N1	32.1	gc/mL
dec 17	PMMoV	16.2	gc/mL
dec 17	pH	8.2	unitless
dec 20	covid N1	34.6	gc/mL
dec 20	PMMoV	19.6	gc/mL
dec 20	pH	7.9	unitless

The same table but in a wide-format is shown here:

date	covid N1 (gc/mL)	PMMoV (gc/mL)	pH
dec 17	32.1	16.2	8.2
dec 20	34.6	19.6	7.9

With each additional field for recording data points, the wide-format table becomes wider, and the long-format table become longer.

Issues with moving between formats

Data visualizations and analysis workflows commonly use wide-data, and it can be faster to input data in wide-format because there is less repetition. This is because date, sample ID, and other fields are not reentered across rows. Long-format is preferred for storage and aggregation.

The diversity in how wide-data is recorded can impact transparency and interoperability. Particularly, this creates problems when merging data from multiple sources. When data is merged between labs, wide-format tables can have hundreds of columns and missing data in many fields. When transforming data from one format to another, there may be differences in naming conventions. This can lead to mistakes in how the data is mapped, and create errors in the database where information is being stored.

PHES-ODM approach to wide- and long-formats

The PHES-ODM is designed as a series of long-format tables, but aims to provide robust infrastructure to support wide-formats. This support includes managing mapping between long- and wide-formats. To streamline mapping between formats, we have created a standardized approach to generating wide-format column names (or wide-names).

Long-format

compartment	specimen	fraction analysed	measure	unit	aggregation	index	value
water	sample	liquid	SARS-CoV-2-N1	gene copies per L	arithmetic mean	1	40

Wide-format

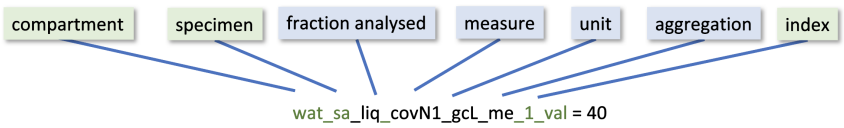


Figure 7.: **Figure 1 - Wide- and Long-names**

For long-formatted data in the ODM, names are all made using camel case (ex: `exampleName`). Each long format name is a 'part', which are the building blocks of the data model. All wide-format names are snake case (ex: `example_name`). Each section of the snake case wide name is an individual part that is combined to form the fully-specified wide-name. Using this approach, wide-names can be parsed automatically to move and transform data between formats without introducing errors.

Wide-names

The exact formula used to generate a wide-name in the ODM depends on the kind of data point you are recording. The three kinds of data and metadata for these column names are either attributes, measures, or protocol steps. An attribute column is metadata. These columns provide context about a measure, protocol, or sample. Measure columns report a specific measure, either from a site, sample, or population. Lastly, protocol columns report a specific protocol step or detail for a measure.

Attributes

The wide-name formula for attributes is

```
tableShortName_attribute
```

Wide-names

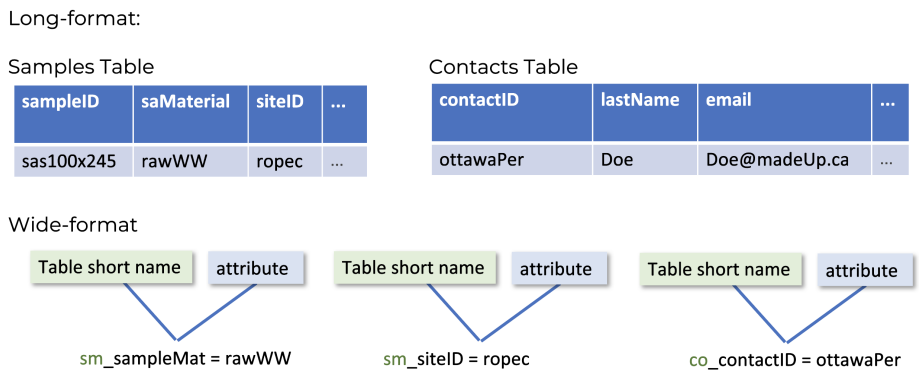


Figure 8.: **Figure 2 - Wide- to Long-format for Attributes**

For example, to record the sample material in long-format you would navigate to the `samples` table and populate the `saMaterial` column. In wide-format, all data are recorded in a single table. The table and attribute are combined for the wide-name, creating the name

```
sm_saMaterial
```

for this attribute. Here `sm` is the short name for the samples table, and `saMaterial` is the column name for the sample matrix or material.

Measures

The wide-name formula for a measure or measure-value is

```
compartment_specimen_fraction_measure_unit_aggregation_index_attribute
```

where the `attribute` at the end is always either `value`, `purpose`, or `qualityFlag`.

Long-format

compartment	specimen	fraction analysed	measure	unit	aggregation	index	value
water	sample	liquid	SARS-CoV-2-N1	gene copies per L	arithmetic mean	1	40

Wide-format

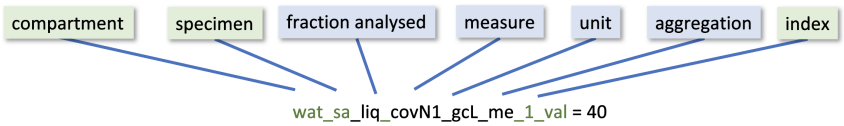


Figure 9.: **Figure 3 - Wide- to Long-format for Measures**

The ODM long-format specifies a `measure` column in the `measures` table, as well as a column for `units` and one for `aggregations`. The wide-format collapses all these columns into a single `value` column.

For example, the wide-name for mean chemical oxygen demand from a wastewater sampling site, recorded in milligrams per litre is

```
wat_si_NR_cod_mgL_m_NR_value
```

Here the measure is taken from wastewater/water (`wat`), it's a measure of the site (`si`), the fraction analyzed is not reported (`NR`), it is a measure of chemical oxygen demand (`cod`), the units are mg/L (`mgL`), it's a mean measure (`m`), the index is not reported (`NR`), and lastly this is the value for this measure (`value`).

Protocol steps

Like measures, protocol step wide-names record the `value` field. With protocols, the wide-name formula depends on whether the step uses a `measure` or a `method`. The formula if using a `method` is:

`tableShortName_partTypeShortName_method_attribute`

The formula if using a `measure` is:

`tableShortName_partTypeShortName_measure_unit_aggregation_index_attribute`

where in both instances, the table short name always specifies the `protocolSteps` table (`ps`), and the `partType` short name specifies whether this is a measure (`mes`) or a method (`met`). The attribute is always `value`.

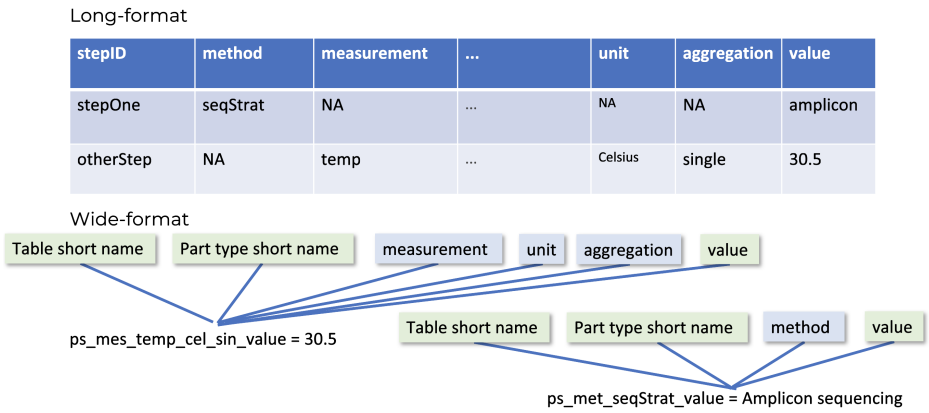


Figure 10.: **Figure 4 - Wide- to Long-format for protocol**

For example, the wide-name for the sequencing strategy protocol step (ie. a protocol step using a method) for a wastewater program would be

```
ps_met_seqStrat_value
```

The protocol steps table short name indicates the long-format table (`ps`), the protocol step uses a method part type (`met`), it reports the sequencing strategy (`seqStrat`), and the column records the value (`value`).

There are various pros and cons to each format, but generally it is ideal for data to be stored and analyzed in a long-format table, while it can be easier to record the data in a wide-format table. Differences in how naming conventions work across formats can lead to mistakes in how the data is mapped, stored and used.

Similarly, the wide-name for a storage temperature (i.e. a protocol step using a measure), would be

```
ps_mes_temp_cel_sin_NR_value
```

The protocol steps table short name indicates the long-format table (`ps`), the protocol step uses a measure part type (`mes`), it reports the temperature (`temp`) in degrees Celsius (`cel`), it is a single measure (`sin`, i.e. not aggregated), the index is not reported (`NR`), and the column records the value (`value`).

For combined long- and wide-formats

The PHES-ODM is designed as a series of long-format tables, but it is our aim to be as robust and easy to use as possible. To avoid issues of incongruity when moving between wide-format data recording templates and the final long-format data storage tables, we have designed a ~~specific series~~ of formulae to generate wide-format column names (or wide-names) using the part IDs from long-format tables, headers, and values. This may,

wide-names can be parsed automatically to reliably ~~move~~ translate data between formats ~~without introducing errors~~.

Many environmental surveillance and research programs use combined long- and wide-format tables. To account for this, wide-names can contain a "see header" part for each piece of their formulas. These reference the header they point to, promoting data readability for machines and humans.

Let's return to the first example tables from the start of this page:

date	compartment	specimen	fraction	measure	value	unit	aggregation
dec 17	water	sample	liquid	covid N1	32.1	gc/mL	single
dec 17	water	sample	liquid	PMMoV	16.2	gc/mL	single
dec 17	water	sample	liquid	pH	8.2	unitless	single
dec 20	water	sample	liquid	covid N1	34.6	gc/mL	single
dec 20	water	sample	liquid	PMMoV	19.6	gc/mL	single
dec 20	water	sample	liquid	pH	7.9	unitless	single

This is long-format data, and I've added some additional columns to record the fraction analyzed, the compartment, the specimen, etc. Now if we were to move to a wide-format, we could use the formulae described above and generate this kind of table:

date	wat_sa_ liq_covN1_ gcMl_sin_ NR	wat_sa_ liq_pmmov_ gcMl_sin_ NR	wat_sa_ liq_pH_ unitless_ sin_NR
dec 17	32.1	16.2	8.2
dec 20	34.6	19.6	7.9

Now let's look at an example of a mixed long- and wide-format table. Something like this might arise where the initial table was developed for ODM long-format, but ultimately it was decided that the program wanted to record multiple measures in a single row. For this, we have what looks like standard ODM long-format for the first eight columns, but then the wide-format for the last two.

date	compartment	specimen	fraction	measure	value	unit	aggregation	PMMoV (gc/ML)	pH (unitless)
dec 17	water	sample	liquid	covid N1	32.1	gc/mL	single	16.2	8.2
dec 20	water	sample	liquid	covid N1	34.6	gc/mL	single	19.6	7.9

In this example, you can see that compartment, specimen, and fraction analyzed are applied also to the PMMoV and pH columns, as well as the measure column. In these instances a measure of PMMoV where the fraction analyzed in specified in a different column would use the wide-name:

```
wat_sa_hFr_covN1_gcml_m_value
```

Here the `hFr` indicates by its placement and the letters used that the fraction analyzed is specified elsewhere.

Wide-names

Another example is for data is reported in long-format for one measure, but wide-format for all others. In this situation the fraction analyzed, the measure, the units, and the aggregation are all specified in other columns. Rather than simply reporting `value` as you would an attribute, you would use the wide name:

```
wat_sa_hFr_hMr_hUn_hAg_NR_value
```

to better link all the metadata pieces in other columns to this specific measurement. So to recreate the above mixed-format table with the ODM coded wide-names, we would get:

mr_ report Date	mr_ com- part- ment	mr_ speci- men	mr_ frac- tion	mr_ mea- sure	hCo_hSp_ hFr_hMr_ hUn_hAg NR_value	mr_ gre- unit	mr_ ag- ga- tion	hCo_hSp_ hFr_pm- mov _gcMl_sin NR_value	hCo_hSp_ hFr_pH_ unit- less_ sin_NR_ value
dec 17	wa- ter	sam- ple	liq- uid	covid N1	32.1	gc/mL	Sin- gle	16.2	8.2
dec 20	wa- ter	sam- ple	liq- uid	covid N1	34.6	gc/mL	Sin- gle	19.6	7.9

Wide-name exceptions

There is a diversity of wide-templates across labs. Sometimes these headers can combine two ODM attributes, or two or more methods or measures. This complicates mapping to the ODM, but unique wide-names can be generated for these as well.

Attribute naming exceptions

For combined attributes, the regular attribute formula (`tableShortName_attribute`) becomes

```
tableShortName_n_aggregation_attribute1_..._attributeN
```

Where `n` is an integer indicating the number of attributes being combined together, the `aggregation` is a boolean aggregation of either `OR` or `AND` to indicate whether the column records all of the attribute, or one or another. Finally, the attributes are listed in snake case. This wide-names is still machine readable.

For example, a wide-column name where sample collection period and collection number are reported together would be:

```
sm_2_AND_collPer_collNum
```

For `_AND_` style wide-names, the default separator must be a period (`.`). So for the is example, where we are recording the sample collection period and number together, a value of a 24-hour period with 12 collections would be `24.12`.

Measure and method naming exceptions

For combined measures or methods, the `..._n_...` approach is also used.

For measures, the formula is: `compartment_specimen_fraction_n_aggregation(bool)_mea` where all measures must share the same units and aggregation. For example, a column to measure the presence of "other" mutations, alleles, or variants uses the wide-name `wat_sa_liq_3_OR_otherM_otherA_otherV_gcMl_m_value`.

For Methods the use case is slightly more constrained. Protocol steps are rarely combined into a single field. Protocol steps using one or more measures which report a single value would be highly unlikely to exist. Protocol steps using methods combinations only work and make sense because the inputs are categorical and defined. The suggested structure for a protocol step using only methods (and no measures) would follow the formula `tableShortName_partTypeShortName_n_aggregation_method1_..._methodN_attribute`.

For example a column where one specifies the protocol step for either pcr or sequencing strategy in a wastewater program would be called `ps_met_wat_sa_liq_2_OR_pcrmeth_seqStrat_value`.

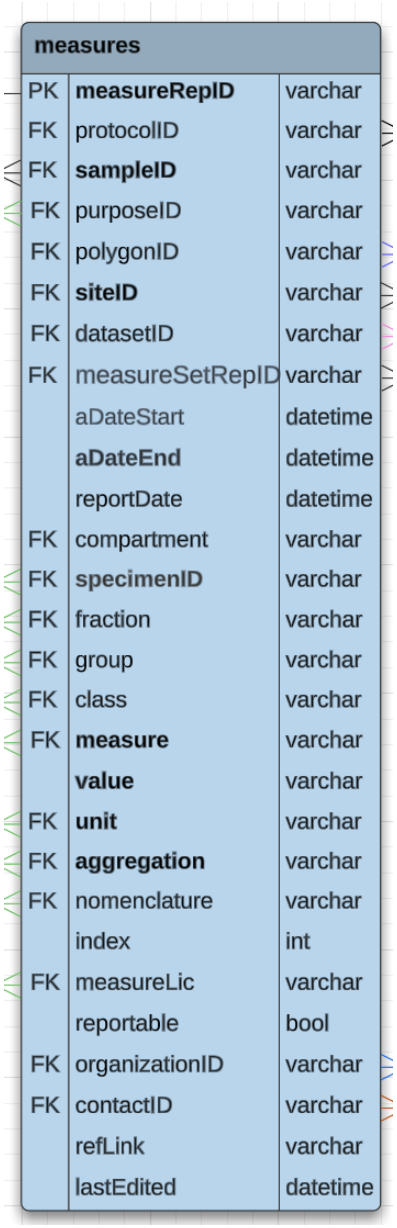
In instances of `OR` wide names, the values sets for the different measures or methods are distinct, and the `sets` information for the input can be used to determine which method or measure is being reported.

Tutorials

Here's an example to walk you through moving from long-format to wide-format. Try to go through slowly and see if you can determine the correct answer before you read it.

Building a wide-format ODM headers

We're going to transform an example long-format measure table to wide-format. In figure 5 we see the list of all the possible headers in the `measures` table. Not all of the headers are mandatory, so you may choose not to use them all. Our tutorial here is just to write out what the wide name would be for each of these headers.



measures		
PK	**measureRepID**	varchar
FK	protocolID	varchar
FK	**sampleID**	varchar
FK	purposeID	varchar
FK	polygonID	varchar
FK	**siteID**	varchar
FK	datasetID	varchar
FK	measureSetRepID	varchar
	aDateStart	datetime
	aDateEnd	datetime
	reportDate	datetime
FK	compartment	varchar
FK	**specimenID**	varchar
FK	fraction	varchar
FK	group	varchar
FK	class	varchar
FK	**measure**	varchar
	value	varchar
FK	**unit**	varchar
FK	**aggregation**	varchar
FK	nomenclature	varchar
	index	int
FK	measureLic	varchar
	reportable	bool
FK	organizationID	varchar
FK	contactID	varchar
	refLink	varchar
	lastEdited	datetime

Figure 11.: **Figure 5 - Headers in the Measures Table**

Everything in this table is an attribute, except for (eventually) the value field. We know that attributes use the structure:

```
tableShortName_attribute
```

So with that in mind, see if you can type up or write out what you think the ODM wide name would be for all of these headers - skipping the `value` header. Keep in mind that for **headers that are foreign keys (noted FK in figure 5), that the table short name used should be the table in which those attributes are a primary key**. You may want to consult the ERD and the parts list to double check which tables host the primary keys and what the short names are for those tables.

Once you have tried coming up with the wide names, check your answers against the equivalent wide names listed below:

- mr_measureRepID
- pr_protocolID
- sm_sampleID
- pa_purpose
- po_polygonID
- st_siteID
- ds_datasetID
- ms_meaureSetRepID
- mr_aDateStart
- mr_aDateEnd
- mr_reportDate
- pa_specimen
- pa_fraction
- pa_group
- pa_class
- pa_measure
- pa_unit
- pa_aggregation

- pa_nomenclature
- mr_index
- mr_mesureLic
- mr_reportable
- mr_organizationID
- mr_contactID
- mr_refLink
- mr_lastEdited
- mr_notes

Building a wide-format ODM table

Now lets try an example using a shortened version of the measures table, populated with some fake data.

date	compartment	specimen	fraction	measure	value	unit	aggregation	index
dec 17	water	sample	liquid	Mpox	32.1	gc/mL	single	1
dec 17	water	sample	mixed	PMMoV	16.2	gc/mL	single	2
dec 17	air	sample	NA	s2083i omicron-variant gene target	8.2	gc	single	NA
dec 20	water	site	liquid	Flow rate	34.6	ML/day	arith. mean	NA
dec 20	surface	sample	NA	Influenza virus A1	19.6	gc/mL	single	NA

date	compartment	specimen	fraction	measure	value	unit	aggregation	index
dec 20	water	sample	liquid	pH	7.9	unitless	single	2

Everything in this mini-table is part of a measurement-value wide-name, except for date. We know that measurements use the structure:

`compartment_specimen_fraction_measure_unit_aggregation_index_attribute`

So with that in mind, see if you can type up or write out what you think the ODM wide name would be for all of these headers - including `date` as an attribute. You may want to consult the ERD and the parts list to double check which tables host the primary keys and what the short names are for those tables.

The answer key for the wide version of this mini-table is here:

mr_reportDate	wat_sa_liq_mpox_gcml_sin_1_value	wat_sa_mix_pmmov_gcml_sin_2_value	air_sa_NA_s2083igc_sin_NA_value	wat_si_liq_floRate_mld_me_NA_value	surf_sa_NA_fluA1_gcml_sin_NA_value	wat_sa_liq_pH_unitless_sin_2_value
dec 17	32.1	16.2	8.2	NA	NA	NA
dec 20	NA	NA	NA	34.6	19.6	7.9

How-To Guides

The `wideNames` table has been added for the v2.3 release, and includes the wide-names that are in current use of which we are aware. The table has also been set up with drop down menus, similar to the data input templates. This way, users can fill out the information for a given header, and have the ODM-formatted wide name generated automatically.

Wide-name Templates

Please check out the wide names table and tamplate here [LINK TBA], and don't forget to let us know what wide names you are using, so that we can add them to the list.

Part I.

Reference guide

Dictionary v3.0.1 Documentation v3.0.1

The reference guide is a technical description of the ODM `parts`. There are three sections to the reference guide.

- `parts` – Parts are the smallest way of describing anything in the ODM. An analogy to parts of a car can be used to illustrate this point. If you own a car, your garage can access a parts list that contains every part of your car, right down to every nut and bolt. There are over 2200 parts, all listed in alphabetical order. Each part has up to 60 different attributes such as the part name and description.
- `tables` - The ODM database model has 26 tables in its full relational database. The full model is commonly referred to as "long" tables as it stores data with one measurement per row. The most important tables are the 'report' tables that are used for daily reporting of measures and samples.
- `sets` - Sets are lists or collections of parts. You can think of sets as the elements of drop down lists or categories.

Did you know that each part ID has its own URL?

Every part, table, and set has its own URL, that is created using the partID. partIDs are usually parentheses that follow a part, table, or set name.
For example, 'airport' is a sample shed category which would appear as: `Airport` (airport). The permanent link to the airport partID is, https://docs.phes-odm.org/parts.html#airport. Airport also is listed in the `Sampleshed category set` (shedCatSet).

Parts

Dictionary v3.0.1 Documentation v3.0.1

Parts are the smallest way of describing anything in the ODM. An analogy to parts of a car can be used to illustrate this point. If you own a car, your garage can access a parts list that contains every part of your car, right down to every nut and bolt. Similarly, the ODM has a `part ID` (partID) and `part description` (partDescription) for every measure, method, and attribute. There are also `part IDs` for `units`, `aggregations`, and other `parts`. The part list is presented below.

> Did you know you can identify part IDs by their specific naming format?
>
> Each part ID starts with a lowercase character and contains no special characters. Parts have less than 12 characters, while part types such as units and aggregations have a maximum of seven characters.
> The unique construction of part IDs serves several purposes in addition to generating valid URLs. Users can create wide table variable names (headers) using part IDs that are valid in all open software languages. ODM supports a standard method of generating wide variable names by concatenating partIDs with an underscore, `_`. For this reason, some part types have a limit of seven characters to ensure the total length of wide names remains less than 35 characters, which is the character limit length of some statistical language software. Details on wide variable naming and standards can be found in the Long-format, wide-format, and wide-names section.

16S Ribosomal Gene Sequencing

(16rgs). An amplicon sequencing assay in which the amplicon is derived from universal primers used to amplify the 16S ribosomal RNA gene from isolate bacterial genomic DNA or metagenomic DNA from a microbioal community. Resulting sequences are compared to reference 16S sequence databases to identify or classify bacteria present within a given sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

a1306s delta-variant gene target

(a1306s). a1306s delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

a1918v delta-variant gene target

(a1918v). a1918v delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

a2710t omicron-variant gene target

(a2710t). a2710t omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

a63t omicron-variant gene target

(a63t). a63t omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

a67v omicron-variant gene target

(a67v). a67v omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant a67v del69 and del70 mutations

(a67vDel69Del70). Omicron Variant a67v mutation mutation, and del 69 and del70 mutations co-occuring *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Atline Analyzer

(aas). Atline analyzer with sampler. An atline analyzer with sampler. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

ABRicate Software

(abricate). Software tool for screening bacterial genomes against multiple resistance databases. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/tseemann/abricate *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Absolute humidity

(absHum). A measure of the total mass of water vapour present in the air per volume of air. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* humid *Nomenclature:* humid *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* absHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Absolute humidity unit set

(absHumidUnitSet). Unit set for absolute humidity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compart-*

ment Set: anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* absHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ABySS

(abyss). A sequencing software that is a scalable de novo assembler for large genomes, designed for distributed computing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/bcgsc/abyss *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Accessions report table Shorthand

(ac). The abbreviated short name used to reference the report table for accessions and accessionIDs. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Academic institution

(academ). The category of organization type used for academic institutions or research groups. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Accel-NGS 2S Plus DNA Library Kit

(accelNGS2Splus). Accel-NGS 2S Plus DNA Library Kit by Swift Biosciences. A library prep kit designed for efficient library prep from fragmented or damaged DNA. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Accessions Index ID

(accessIndexID). Provisional ID to act as a primary key for each row of the accessions table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

accessions Table

(accessions). Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field. ac *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Accessions table column order

(accessionsOrder). Specifies the order of the columns in the accessions table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Accessions table required headers

(accessionsRequired). Required headers in the accessions table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Accession Number in Repository

(accessNum). The accession number for the data entry in the given data repository or hosting platform. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Acinetobacter

(acinetobacter). Acinetobacter *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* acinetobacterGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Acinetobacter Group

(acinetobacterGrp). A group of measures/methods related to acinebacter bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* acinetobacterGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases

(acti). Number of active cases. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Number of active cases by Onset date

(actiCaseOn). Number of active cases by onset date. Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by episode date

(actiEp). Number of active cases by episode date. Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Public health action

(action). The specific public health action or designation being taken or applied. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* allActionsSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health action datetime

(actionDT). The date and Time of the public health action. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public Health Action Group ID

(actionGrpID). ID used for linking multiple public health actions together for a single action. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health action type

(actionType). The type of public health action being taken. Sets out the category, with the detailed action being defined in ‘action‘ field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* actionTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public Health Action Type Value Set

(actionTypeSet). A set of valid categories for the public health action type field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* actionTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Number of active cases by Report date

(actiRep). Number of active cases by report date. Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by test date

(actiTest). Number of active cases by test date. Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units

Parts

Domain: bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Active

(active). Indicator that a part is in current use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Address table Shorthand

(ad). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

AdapterRemoval

(adapterRemoval). A sequencing data processing application that removes adapters and filters reads based on quality and length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://adapterremoval.readthedocs.io/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Analysis date

(aDate). Date the measurement was performed in the lab. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.1.0.

Analysis date end

(aDateEnd). Date the measurement or analysis was completed. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Analysis date start

(aDateStart). Date the measurement or analysis was started. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Address Line 1

(addL1). Line 1 (the street name, number and direction) for a given address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Address Line 2

(addL2). Line 2 (the unit number) for a given address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet

Aggregation Scale: naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Address table

(addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). The Sites, Organizations, and Contacts tables include a link to the addresses table through Address ID. The short name for the table (partID) can be found in the instructions field. ad *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Addresses table column order

(addressesOrder). Specifies the order of the columns in the Addresses table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Address table required headers

(addressesRequired). Specifies the columns required in a Addresses table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Address ID

(addressID). A unique identifier for an address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Adenovirus (F40/41)

(adenovirusF40). Adenovirus (F40/41) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* adenovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Adenovirus Group

(adenovirusGrp). A group of measures/methods related to Adenoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* adenovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Administrative regions

(admRegLevel). Administrative regions *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Adenovirus 40

(adv40). Adenovirus serotype 40. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* adenovirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation*

Scale: seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Adenovirus 41

(adv41). Adenovirus serotype 41. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* adenovirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Adenovirus F41 Fibre Gene Target

(advF41Fibre). Human Adenovirus Group F41 Fiber gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* adenovirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Aeration tank

(aerTank). A chamber in wastewater treatment where air is introduced to promote microbial breakdown of organic pollutants. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501469 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Academic Free License v3.0

(afl30). The licensing for the measure or data set is managed under the Academic Free License v3.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/afl-3.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Afternoon

(aft). Sample was collected in the afternoon, sometime after lunch. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

AfterQC

(afterQC). An automated QC pipeline tool for FASTQ data, combining quality assessment and error correction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/OpenGene/AfterQC *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Air filter

(afu). Air filter as part of filtration or circulating unit. Typically the unit would have a fan or blower. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation

(aggregation). Statistical measures used to report a measure. Each aggregation has a corresponding value. The default aggregation is ‘single‘, which corresponds to a single measurement. *Part Type:* attributes *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* aggregations *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation input (wide table)

(aggregationInput). The partID for the aggregation being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* aggregations *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Aggregation name (wide table)

(aggregationName). The aggregation referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* aggregations *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Aggregations

(aggregations). Statistical measures used to report a measure. Each measure reported as a number should be reported with an aggregation. The default aggregation is 'sin', which corresponds to a single measurement. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation scale

(aggregationScale). A scale used for an aggregation. Only applicable for measures and units. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* aggregationScales *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

Aggregation scales

(aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation set

(aggregationSet). The aggregation set for a unit. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* aggregationSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation sets

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

GNU Affero General Public License v3.0

(agpl30). The licensing for the measure or data set is managed under the GNU Affero General Public License v3.0. *Part Type:* categories *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/agpl-3.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Agricultural activity

(agri). Agricultural activity occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial gradient test

(agt). A gradient strip test is performed according to the manufacturer's instructions: a short plastic or paper strip impregnated with antibiotic is placed on inoculated agar. On the standardised 100 mm Petri dish, two strips may be placed, while on the larger 150 mm Petri dish, up to six antibiotics may be tested simultaneously. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* bactMisc *Class:* bactFung *Nomenclature:* bactFung *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Human Aichivirus (AiV) Group (Aichivirus A)

(aichivAGrp). A group of measures/methods related to human aichiviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* aichivAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Air compartment

(air). A measure or observation made from a substance in the air. *Part Type:* compartments *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* airCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Air compartment set

(airCompartmentSet). A compartment set for measures and methods in the air compartment. *Part Type:* compartmentSets *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* airCompartmentSet *Group:*

Parts

naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Airplane

(airpln). Airplane sample shed category type *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Airport

(airport). Airport sample shed category type *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Airport lists worksheet

(airportLists). Parts lists used to generate airport and airplane data entry templates. *Part Type:* dictionarySupport *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Airport Sheets Set

(airportSheetSet). Worksheets in the full airport surveillance template (list + template). 'ODM_template-planes_{version}.xlxs *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Airport Surveillance Template

(airportTemplate). The input template for airport and airplane surveillance in the EU. *Part Type:* dictionarySupport *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.1.0.

Air and surface compartment set

(airSurfaceCompartmentSet). A compartment set for measures and methods in the air or surface compartments. *Part Type:* compartmentSets *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* airSurfaceCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Environmental temperature

(airTemp). Environmental temperature. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Air and water compartment set

(airWaterCompartmentSet). A compartment set for measures and methods in the air or water compartments. *Part Type:* compartmentSets *Domain:*

allDo *Speciment ID:* anySpecimenSet *Compartment Set:* airWaterCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aichivirus A (formerly Aichi virus)

(aivA). Measures of Aichivirus A, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus B (Bovine kobuvirus)

(aivB). Measures of Aichivirus B, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called Bovine kobuvirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data*

Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus C (Porcine kobuviru)

(aivC). Measures of Aichivirus C, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called Porcine kobuvirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus D (kagovirus from black cattles)

(aivD). Measures of Aichivirus D, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called kagovirus from black cattle. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus E (Rabbit picornavirus)

(aivE). Measures of Aichivirus E, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called Rabbit picornavirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus F (Bat kobuvirus)

(aivF). Measures of Aichivirus F, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called bat kobuvirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus P1 protein gene

(aivP1). A gene target for aichivirus, it is the genomic segment that encodes the structural viral capsid proteins forming the outer shell of the Aichivirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* aichivAGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Alias depreciated

(aliasDep). ID of an assay that is the same or similar. A comma separated list. Deprecated as of version 2, please avoid use. Use notes instead. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Alias ID depreciated

(aliasIDDep). Alias id ID of an assay that is the same or similar. a comma separated list. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup

Class: naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

AliView

(aliView). Sequencing software that is a user-friendly alignment editor with consensus sequence options. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ormbunkar.se/aliview/ (common host) — I can verify with search if needed *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Alkalinity

(alkaline). Measure of alkalinity *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* alkalinitySet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Alkalinity unit set

(alkalinitySet). Unit set for alkalinity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* alkalinitySet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

All Public Health Actions Set

(allActionsSet). A set of all valid categories for public health action, regardless of action type. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* allActionsSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

All domains

(allDo). Domain that specifies that it could apply to al domains; biological, chemical, and physical. *Part Type:* domains *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Alleles class

(allele). Measures and methods related to alleles. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Allele unit set

(alleleUnitSet). Unit set for alleles. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* alleleUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Access to all org

(allOrgs). If this is 'no', this data will not be available to any partner organization. If missing, data will be available to the all organizations. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

AllPaths-LG

(allpathsLG). A sequencing software that was designed for high-quality assemblies using large, paired-end Illumina data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.broadinstitute.org/news/allpaths-lg-new-standard-assembling-billion-piece-genome-puzzle *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Data Adjustment Standard Value Set

(allStandardSet). Set of valid input values for the standard field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* allStandardSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Assay Limit of Detection (LOD)

(alod). The minimum level of a target consistently detectable (e.g., with 95% probability) using the assay considering only the amplification and quantification steps of RT-qPCR. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 3.0.0.

Aloh3 precipitation

(aloh3). Aloh3 precipitation *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

The number of ambiguous bases (Ns) normalized

(ambigNs). The number of ambiguous bases (Ns) normalized per 100 kilobasepairs (kbp). Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:*

measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Assay method id default depreciated

(amDefDep). Used as default when a new measurement is created for this lab. See ID in AssayMethod table. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (https://github.com/Big-Life-Lab/PHES-ODM/issues), or at phesd_odm@ohri.ca *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Amicon ultrafiltration

(amiconUf). Amicon ultrafiltration *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Amicon filter, extract with MP96

(amiMP96). Nucleaic acid extraction, usually used for the liquid fraction of a wastewater sample, using amicon filtration and using an MP96 for final extraction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Amplicon sequencing

(amp). Specifies the amplicon strategy for genetic sequencing *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Amplification Artifacts

(ampliArtifact). Sequence amplification artifacts detected. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Amplicon Size

(ampSize). The length of the amplicon generated by PCR amplification. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial resistance (AMR) classification

(amrClass). A public health action type wherein threat level classification has been done on a strain of antimicrobial resistant (AMR) microbes, and communicated to the public. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial Resistance (AMR) Classification Value Set

(amrClassSet). A set of valid categories for the public health action field, where the action type is 'antimicrobial resistance (AMR) classification'.

Part Type: mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* amrClassSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

AMRFinderPlus Software

(amrFinderPlus). Software tool that was developed by NCBI to detect AMR genes in bacterial genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/AMRFinder/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Anti-microbial resistance Group

(amrGrp). The group for measures and methods pertaining to anti-microbial resistant microbes (general). *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

AMR Analysis Software

(amrSoft). Software use to analyse bacterial genomes and genes for antimocrobial resistance (AMR). *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* amrSoftSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

AMR Software Set

(amrSoftSet). The valid set of AMR analysis software categories. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* amrSoftSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Anaplasma Group

(anaplasmaGrp). A group of measures/methods related to anaplasma bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* anaplasmaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

AND Boolean aggregation

(andBoo). "AND" aggreation. If all values in the aggregation is "TRUE" then the AND aggregation is also "TRUE". If all values in the aggregation is "FALSE" then the AND aggregation is also "TRUE". *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Andes virus (ANDV) hantavirus

(andv). Andes virus (ANDV) is the most common cause of hantavirus pulmonary syndrome (HPS) in South America. Andes virus is transmitted mainly by the long-tailed pygmy rice rat. Orthohantavirus andesense. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

annealing/extension

(anneal). Describes the annealing and/or extension cycle in a PCR process. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Any compartment set

(anyCompartmentSet). A compartment set for measures and methods in any compartment. *Part Type:* compartmentSets *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Any specimen set

(anySpecimenSet). A specimen set that inculdes any specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:*

NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Apache license 2.0

(apache20). The licensing for the measure or data set is managed under the Apache license 2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/apache-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Anaplasma phagocytophilum

(aPhagocytophilum). Anaplasma phagocytophilum *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* anaplasmaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Apollo PrepX Library Preparation Kits

(apolloPrepX). Apollo PrepX Library Preparation Kit by Takara Bio. An automated library preparation kit for Illumina sequencing on Apollo

systems. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ARACHNE

(arachne). A sequencing software that is an early assembler optimized for large, complex genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC155255/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Antibiotic Resistance Genes Database (ARDB)

(ardb). An archive for antibiotic resistance genes and associated information. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* ardb.cbcb.umd.edu *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Area proportional sample

(areaPr). An area proportional sample. Used for surface testing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

A-Tier Region-level Aggregation at Site

(aRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an "A-Tier" region and refers to large, dense urban areas made up of multiple overlapping cities/boroughs. This would be a greater metropolitan area. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ARG-ANNOT Annotation Tool

(argAnnotSoft). Software annotation tool for antimicrobial resistance genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

Link: https://pmc.ncbi.nlm.nih.gov/articles/PMC3910750/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ARIBA

(ariba). ARIBA. Focus: Genotyping, MLST, and serotyping from raw sequencing reads. Applications: Salmonella, Escherichia coli, Klebsiella pneumoniae, and more. Features: Works with custom databases for serotyping and resistance gene identification. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/sanger-pathogens/ariba Sanger page: https://www.sanger.ac.uk/tool/ariba/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Arrival temperature

(arTemp). The temperature of a sample upon arrival at the laboratory for analysis. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Artic V1 Primer Set

(articV1). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 1.0.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artic V2 Primer Set

(articV2). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 2.0.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Use of the articV3 primer

(articV3). Initial implementation of an ARTIC bioinformatics platform for nanopore sequencing of nCoV2019 novel coronavirus; Artic Foundation v3 primer. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Use of the articV4 primer

(articV4). Artic V4 sequencing primer for VOCs and VOIs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Artic V4.1 Primer Set

(articV41). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 4.1.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:*

https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5 Primer Set

(articV500). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.0.0 which produces amplicons approximately 400bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.1 Primer Set

(articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2with the attributes of version 5.1.0 which produces amplicons approximately 400bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.2 Primer Set, 1200bp

(articV520bp1200). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.2 Primer Set, 400bp

(articV520bp400). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 400bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.3.2 Primer Set

(articV532). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.3.2 which

produces amplicons approximately 400bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/artic-network/primer-schemes/tree/master/nCoV-2019 *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Artistic license 2.0

(artistic20). The licensing for the measure or data set is managed under the Artistic license 2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/artistic-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Assay ID

(asID). Links with the AssayMethod used to perform the analysis. Use instrument.ID for measures that are not viral measures. Deprecated as of version 2, please avoid use. Refer to methodID instead. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Astrovirus

(astrovirus). Astrovirus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* astrovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Astrovirus Group

(astrovirusGrp). A group of measures/methods related to astroviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* astrovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Amies Transport Medium

(atm). A buffer solution/medium that maintains viability of bacteria in wastewater and environmental samples during transport. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Atropos

(atropos). A QC pipeline tool for sequencing data that performs adapter trimming and quality filtering with built-in QC reporting. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://atropos.readthedocs.io/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Attribute input (wide table)

(attributeInput). The partID for the attribute being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* attributes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Attribute name (wide table)

(attributeName). The attribute referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* attributes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Attributes

(attributes). Attributes describe the who, where, when, and why of environmental surveillance. There are attributes for domain, specimen, compartment, or table. Attributes are one of the three main components or ways to report environment surviellence data. The other two components are measures and methods. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Automatic composite sampling

(autoComp). A composite sampler which is automated to collect and store multiple wastewater samples across multiple time points. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Autosamplers

(autoInst). Autosampler instruments, used to automatically collect flow- or time-proportional samples over a period (e.g., ISCO autosamplers). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Automatic sequential sampling

(autoSeq). A composite sampler which is automated to collect and combine multiple samples of equal volume taken at a set time interval. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Babesia

(babesia). Babesia *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* babesiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Babesia or Nuttallia Group

(babesiaGrp). A group of measures/methods related to babesia parasites. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* babesiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Bacterial culture

(bacCul). Growing a bacterial culture to test for bacterial presence. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* bactMisc *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BacMet Database

(bacMet). Database of antibacterial biocide and metal resistance genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* bacmet.biomedicine.gu.se *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bacteroides 16S forward primer (HF183) (ABI)

(bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* bacteroidesGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S probe (BacP234) (ABI)

(bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* bacteroidesGrp *Class:* pcr *Nomenclature:*

pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S reverse primer (BacR287) (ABI)

(bact16sABIRev). Bacteroides 16S reverse primer (BacR287) (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* bacteroidesGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Bacteria unit set

(bacteriaUnitSet). Unit set for bacteria-related measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Bacteroides Group

(bacteroidesGrp). A group of measures/methods related to bacteroides bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bacteroidesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Bacteria and Fungus Class

(bactFung). Measures and methods relating to bacteria. *Part Type:* classes *Domain:* bio *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* bactFung *Nomenclature:* bactFung *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Bacterial testing method

(bactMeth). Description of the bacterial testing/detection method. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bactMisc *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* bactMethSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bacterial testing method set

(bactMethSet). The set capturing containing all of the valid methods for the bacterial testing method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bactMisc *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* bactMethSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Miscellaneous bacteria group

(bactMisc). A group of measures/methods related to miscellaneous bacteria. The miscallenous bacteria are often have only one measure or method. When a bacteria has many measures, they will be given their own groupID in updated dictionary versions. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bactMisc *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Bag Mediated Filtration

(bagFilt). Sample was collected using bag-mediated filtration. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0102028 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BamQC (from Qualimap)

(bamQC). A QC pipeline tool for sequencing data that focuses on quality control for mapped data in BAM format, reporting alignment quality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://qualimap.bioinfo.cipf.es/ (QC for BAM files) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

bamUtil Dedup

(bamUtil). A deduplication method that removes duplicate reads directly from BAM files. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* https://genome.sph.umich.edu/wiki/BamUtil%3A_dedup *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bar screen

(barScreen). A bar screen is a mechanical device used to remove large solid debris from wastewater or sewage as it enters a treatment plant. It consists of a series of parallel bars or rods, spaced at specific intervals, that allow water to pass through while capturing larger objects. This process prevents damage to downstream equipment and ensures efficient treatment. Bar screens are typically installed at the inlet of wastewater treatment facilities and can be cleaned manually or mechanically, depending on the design and operational requirements. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501474 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Base-pair unit set

(basePairSet). Unit set for base-pair measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum*

Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BayesHammer (from SPAdes)

(bayesHammer). A sequencing data processing application that does error correction tool specifically for Illumina reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://bioinf.spbau.ru/en/spades/bayeshammer *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bayesian Smoothing applied

(bayesSmooth). This data treatment smooths the measurement value using bayesian smoothing techniques. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BBDuk (from BBTools)

(bbduk). A QC pipeline tool for sequencing data that is a part of the BBMap suite, performs filtering and trimming, and generates QC statistics.

Part Type: categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://jgi.doe.gov/data-and-tools/bbtools/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BBMap

(bbmap). BBMap. A general-purpose read mapper. High-sensitivity aligner for DNA and RNA reads. Best for: Error-prone reads from platforms like Nanopore or PacBio. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://jgi.doe.gov/data-and-tools/bbtools/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BBMap Reformat

(bbmapReform). A dehosting software that filters out host sequences by aligning to reference genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/BioInfoTools/BBMap (see BBMap suite) *Data Type:* varchar *Missingness Set:*

NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BBMap Suite

(bbmapSuite). A sequencing data processing application library that includes tools like BBDuk for quality trimming, adapter removal, and quality filtering. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/bbmap/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bead beating, extract with MP96

(bbMP96). Nucleaic acid extraction, usually used for solid fraction of a wastewater sample, using bead beating and using an MP96 for final extraction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Borrelia burgdorferi

(bBurgdorferi). Borrelia burgdorferi *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* borreliaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Bcftools

(bcfTools). Sequencing software that works with SAMtools to call variants and produce consensus sequences from alignments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/samtools/bcftools *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

bcov

(bcov). Measure of the amount of bovine coronavirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* betaCoronaGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet

Reference Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

bcov culture spike target

(bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

bcov spike target (unspecified)

(bcovGen). The bovine coronavirus (unspecified) is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

bcov vaccine spike target

(bcovVac). The bovine coronavirus vaccine is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Bayesian Evolutionary Analysis by Sampling Trees (BEAST) Software

(beast). A lineage or clade analysis software tool for estimating evolutionary relationships and divergence times in a Bayesian framework. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://www.beast2.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Beef extract flocculation

(beeExtractFloc). Beef extract flocculation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation*

Scale: naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Is Before

(before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Use only for protocolRelationships table relationshipID. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Below LOD

(beLOD). Measure is below the limit of detection (LOD) for a specific analyte. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measured levels below LOQ

(belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Beta

(beta). B.1.351 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Beta Coronavirus Group

(betaCoronaGrp). A group of measures/methods related to beta coronaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* betaCoronaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BIGSdb (Bacterial Isolate Genome Sequence Database)

(bigsdb). BIGSdb (Bacterial Isolate Genome Sequence Database). A flexible platform that supports serotyping alongside sequence typing and other typing schemes. Can be customized for various bacterial species, including Neisseria meningitidis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* CLI & docs: https://pubmlst.org/software/bigsdb Project: https://github.com/kjolley/BIGSdb *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Biologic

(bio). A living organism or biological substance. *Part Type:* domains *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Fragment analyzers or bioanalyzers

(bioanalys). Fragment analyzer or bioanalyzer instruments, used to assess fragment size distribution in libraries. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BioEdit

(bioEdit). Sequencing software that offers sequence alignment and visualization, used to manually generate consensus sequences. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://www.mbio.ncsu.edu/bioedit/bioedit.html (site may vary) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bioo Scientific NEXTflex Rapid DNA-Seq Kit

(biooSci). Bioo Scientific NEXTflex Rapid DNA-Seq Kit by PerkinElmer. A rapid and flexible library prep kit for DNA sequencing on Illumina platforms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Digital droplet emulsification PCR

(bioRadDdpcr). Describes a PCR analysis done using BioRad's digital droplet emulsification PCR technology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Biological replicate

(bioRep). A biological replicate not otherwise specified - these are parallel measurements of biologically distinct samples that capture random biological variation, which can be a subject of study or a source of noise itself. Biological replicates are important because they address how widely your experimental results can be generalized. They indicate if an experimental effect is sustainable under a different set of biological variables. Further examples of biological replucates are the more specific co-located samples and field sample replicate types for the repType field. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Beta-Lactamase Anti-microbial resistance Group

(bLacAMRGrp). The group for measures and methods pertaining to beta-lactamase-related anti-microbial resistance. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Cephamycin Beta-Lactamase-Resistance gene target

(blaCMY). Cephamycin Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

CTX-M Beta-Lactamase-Resistance gene target

(blaCTXM1). CTX-M Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpeci-

menSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Impenemase (IMP) Beta-Lactamase-Resistance gene target

(blaIMP). Impenemase (IMP) Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase-Resistance gene target

(blaKPC). Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

New-Delhi Metallo- (NDM) Beta-Lactamase-Resistance gene target

(blaNDM). New-Delhi Metallo- (NDM) Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

OXA-type Beta-Lactamase-Resistance gene target

(blaOXA48). OXA-type Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

SHV Beta-Lactamase-Resistance gene target

(blaSHV). SHV-type Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BLASR (Basic Local Alignment with Successive Refinement)

(blasr). BLASR (Basic Local Alignment with Successive Refinement). A long-read specific mapper. Optimized for PacBio data. Best for: High-quality long-read alignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/PacificBiosciences/blasr *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

TEM Beta-Lactamase-Resistance gene target

(blaTEM). TEM-type Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:*

geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase-Resistance-resistance gene target

(blaVIM). Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Binary Large Object (BLOB) data type

(blob). The data type for Binary Large Object (BLOB) data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

BMTagger

(bmtagger). A dehosting software developed by NCBI for identifying and removing host sequences based on local alignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Breadth of coverage (>=5x depth)

(boc). The percentage of the reference genome covered by the sequenced data, to a prescribed read depth greater or equal to 5. Report as percentage of positions. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Bocaparvovirus Group

(bocaparvGrp). A group of measures/methods related to bocaparvoviruses. Used to describe the organism information for general measures. *Part*

Type: groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bocaparvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Bocaparvovirus

(bocaparvo). Bocaparvovirus is a genus of viruses in the subfamily Parvovirinae of the virus family Parvoviridae. Humans, cattle, and dogs serve as natural hosts. There are 36 species in this genus. Diseases associated with this genus include, in humans, acute respiratory illness, and in cattle, diarrhea and mild respiratory symptoms. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bocaparvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

5-Day carbonaceous biochemical oxygen demand

(bod5c). The quantity of oxygen utilized for the biochemical degradation of organic matter under standard laboratory procedures in five (5) days in the presence of a nitrification inhibitor, expressed in milligrams per litre (mg/l). *Part Type:* measurements *Domain:* bio *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:*

NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* https://doi.org/10.1002/wer.1541 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

5-day total biochemical oxygen demand

(bod5t). 5 day total biochemical oxygen demand. *Part Type:* measurements *Domain:* bio *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* https://doi.org/10.1002/wer.1541 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Boolean data type

(boolean). The data type for boolean/binary data. Encoded as 'TRUE' or 'FALSE' *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Boolean aggregation set

(booleanAggrSet). Aggreagation set for boolean. *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Boolean value set

(booleanSet). Set that contains the valid possible values for a boolean measure (TRUE or FALSE). *Part Type:* mmaSets *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Border closure

(borderClos). A measure shutting entry points to limit cross-border movement and disease spread. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Borrelia burgdorferi or Lyme Disease Group

(borreliaGrp). A group of measures/methods related to Borrelia burgdorferi or Lyme Disease. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* borreliaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Body of water

(bow). An outdoor accumuation of water either on the surface or beneath the ground, no other additional details specified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bowtie2

(bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that

maps reads against a host reference genome to remove aligned reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://bowtie-bio.sourceforge.net/bowtie2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Host Subtraction with Bowtie2 & SAMtools

(bowtie2XSam). A combined workflow for dehosting where reads mapped to the host are removed from downstream analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* Bowtie2: https://bowtie-bio.sourceforge.net/bowtie2/ and Samtools: https://www.htslib.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Base-pairs

(bps). A base pair (bp) is a unit of measurement in molecular biology that represents a pair of complementary nucleotides in DNA or RNA. The length of DNA sequences is often measured in base pairs. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet

Aggregation Scale: quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Buffered Peptone Water

(bpw). A buffer solution/medium used for bacterial enrichment, can also serve as a temporary preservative. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bracken

(bracken). A QC pipeline tool for sequencing data and taxonomic profiling that can also be used to identify contamination and assess data quality in metagenomics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ccb.jhu.edu/software/bracken/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

B-Tier Region-level Aggregation at Site

(bRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an "B-Tier" region, and thus a region within a greater metropolitan area and larger than a single municipality, but smaller than the entire metropolitan area. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bovine respiratory syncytial virus group

(brsv). Bovine respiratory syncytial virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

brsv culture spike target

(brsvCul). Cultured bovine respiratory syncytial virus (BRSV) is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

BRSV-N

(brsvN). bovine respiratory syncytial virus capsid protein gene region *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

brsv vaccine spike target

(brsvVac). The bovine respiratory syncytial virus (BRSV) vaccine is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Brucella

(brucella). Brucella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* brucellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Brucella Group

(brucellaGrp). A group of measures/methods related to brucella bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* brucellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BSD Zero-Clause license

(bsd0). The licensing for the measure or data set is managed under the BSD Zero-Clause license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/0bsd/

Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BSD 2-clause "Simplified" license

(bsd2Clause). The licensing for the measure or data set is managed under the BSD 2-clause "Simplified" license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/bsd-2-clause/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BSD 3-clause "New" or "Revised" license

(bsd3Clause). The licensing for the measure or data set is managed under the BSD 3-clause "New" or "Revised" license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/bsd-3-clause/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BSD 3-clause Clear license

(bsd3ClauseClear). The licensing for the measure or data set is managed under the BSD 3-clause Clear license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/bsd-3-clause-clear/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

BSD 4-clause "Original" or "Old" license

(bsd4Clause). The licensing for the measure or data set is managed under the BSD 4-clause "Original" or "Old" license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/bsd-4-clause/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Boost Software License 1.0

(bsl10). The licensing for the measure or data set is managed under the Boost Software License 1.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/bsl-1.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Branch sewer pipleline

(bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municpal sewer lines, allowing drainage into the main sewer. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Building cleanout

(buildCO). Specifies a site type that is a capped pipe that connects to a building's main sewer line. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Building-level Surveillance

(builLev). Surveillance is done only at the level of a single building. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Bundibugyo virus, Orthoebolavirus bundibugyoense

(bundibugyoV). The species Bundibugyo ebolavirus is the taxonomic home of one virus, Bundibugyo virus (BDBV), that forms filamentous virions and is closely related to the Zaire ebolaviruses (EBOV). The virus is one of several that can cause Ebola disease in humans, taking the form of viral hemorrhagic fever. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ebolaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Bus

(bus). A large motor vehicle carrying passengers by road, typically one serving the public on a fixed route and for a fare. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Bus Station

(busStat). A terminal where buses arrive and depart. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

BWA (Burrows-Wheeler Aligner)

(bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/lh3/bwa *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BWA for Host Filtering

(bwaHost). A dehosting software that maps reads to a host genome, filtering mapped reads from analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/lh3/bwa *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

BWA-MEM with Duplicate Marking

(bwaMEM). A deduplication method that is used with SAMtools or Picard to mark duplicates during read mapping. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.htslib.org/algorithms/duplicate.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

C28311T Omicron N1 Point Mutation

(c2811t). A measure of the C to T point mutation at position 28311 (C28311T) of the N1 probe, present in all Omicron sub-linages. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Cacipacore virus (Orthoflavivirus cacipacoreense)

(cacipacore). Orthoflavivirus cacipacoreense, causitive agent of the rare Cacipacore virus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirus-Grp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Caffeine

(caff). Caffeine (usually measured as a human fecal chemical indicator) *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Calculation Type

(calcType). A field to explain the purpose/nature of a single calculation/data treatment. Possible inputs are: normalization, standardization, smoothing, and predictiveModelling. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* calcTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Calculation type set

(calcTypeSet). The set of valid inputs for the calculation type field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* calcTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Calculation ID

(calculationID). A unique identifier and primary key for every row of the calculations table. Typically generated as a composite key of container ID and step ID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Calculations Table

(calculations). Table for recording data on data treatments and calculations applied to measurements and reported values. cl *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Calculations table column order

(calculationsOrder). Specifies the order of the columns in the calculations table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Calculations table required headers

(calculationsRequired). Required headers in the calculations table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Calibration purpose

(cali). Purpose of calibrating a machine, method, or other. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Calprotectin

(Calprotectin). Calprotectin is a calcium- and zinc-binding protein of the S-100 protein family which is mainly found within neutrophils and throughout the human body. The presence of calprotectin in faeces is a consequence of neutrophil migration into the gastrointestinal tissue due to an inflammatory process. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* metaboliteGrp *Class:* protein *Nomenclature:* protein *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation*

Scale: seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 3.0.0.

Campylobacter

(camp). Campylobacter. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* campGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Campylobacter Group

(campGrp). A group of measures/methods related to campylobacter bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* campGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Canal

(canal). Artificial watercourse with no flow or a controlled flow used for navigation, drainage or irrigation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Canu

(canu). A sequencing software that is a de novo assembler specifically optimized for long-read data from PacBio and Oxford Nanopore. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/marbl/canu *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Capacity class

(capacity). Measures and methods relating to capacity. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* capacity *Nomenclature:* capacity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* capacityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA

Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Capacity unit set

(capacityUnitSet). Unit set for capacity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* capacityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

CapsuleFinder

(capFin). CapsuleFinder Used for typing capsular polysaccharides in a variety of bacteria, especially Escherichia coli and Klebsiella species. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Capital city endonym

(capitalEndonym). The name locals use for their country's capital. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Capital city exonym

(capitalExonym). The English name foreigners use for the country's capital. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Comprehensive Antibiotic Resistance Database (CARD)

(cardDtbase). Database that provides high-quality reference sequences for resistance genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://card.mcmaster.ca *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

CARD Resistance Gene Identifier (RGI)

(cardRGI). Software tool that is a part of the Comprehensive Antibiotic Resistance Database (CARD) used for annotation and prediction of AMR. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://card.mcmaster.ca/analyze *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Case report date

(caRepDate). Date that the numbers were reported publicly. Typically, reported data and this measure is most commonly reported and used. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Episode date of confirmed cases

(caseEpDate). Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Onset date of confirmed cases

(caseOnDate). Earliest that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Report date of confirmed cases

(caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and this measure is most commonly reported and used. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Test date of confirmed cases

(caseTestDate). Date that the covid-19 test was performed for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Central average smoothing applied

(caSmooth). This data treatment smooths the measurement value using central average smoothing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Categorical data type

(categorical). The data type for categorical data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Categories

(categories). A discrete list of values that can be reported for a measure, method or attribute. A use-case example of categories would be how they are used to record the site where a measure is taken (partID = geoType). For the geoType attribute there are different type of sites where samples can be taken: a wastwater treatment plant, airplane holding tank, wastwater pumping station, etc. Each of these site types is recorded as a category that can be identified in categorySetID = sTypeCatSets *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Candida auris

(cAuris). The yeast species Candida auris, or C. auris. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cAurisGrp *Class:* bactFung *Nomenclature:* bactFung *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Candida auris Group

(cAurisGrp). A group of measures/methods related to Candida auris. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cAurisGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Carbonaceous Biochemical Oxygen Demand

(cbod). A measure of the amount of oxygen required by microorganisms to break down organic carbon-based compounds in water over a specified period, typically five days at 20°C (CBOD). Unlike BOD (Biochemical Oxygen Demand), CBOD excludes oxygen demand from the oxidation of nitrogenous compounds (such as ammonia). It is used to assess organic pollution in wastewater and natural waters. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Carbapenemase-encoding genes

(cbp). Carbapenemase-encoding genes. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Cary-Blair Transport Medium

(cbtm). A buffer solution/medium commonly used for bacterial preservation in stool and wastewater samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Creative Commons Zero v1.0 Universal

(cc010). The licensing for the measure or data set is managed under the Creative Commons Zero v1.0 Universal. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/cc0-1.0/ *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Creative Commons Attribution 4.0

(ccby40). The licensing for the measure or data set is managed under the Creative Commons Attribution 4.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/cc-by-4.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

CC BY-NC 4.0 license

(ccbync40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial international license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://creativecommons.org/licenses/by-nc/4.0/deed.en *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

CC BY-NC-SA 4.0 license

(ccbyncsa40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial, and sharealike international license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://creativecommons.org/licenses/by-nc-sa/4.0/deed.en *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Creative Commons Attribution ShareAlike 4.0

(ccbysa40). The licensing for the measure or data set is managed under the Creative Commons Attribution ShareAlike 4.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/cc-by-sa-4.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Long-term acute care hospital

(ccc). Acute care hospitals, or complex contuing care, that provide care for patients with average length of stay longer than 25 days. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Child day care

(cdc). Child day care facility. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sarbeco_E forward primer (IDT)

(cdcCovEIDTFor). Sarbeco_E forward primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E probe (IDT)

(cdcCovEIDTProbe). Sarbeco_E probe (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* na-

CompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E reverse primer (IDT)

(cdcCovEIDTRev). Sarbeco_E reverse primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 forward primer (IDT)

(cdcCovN1IDTFor). 2019-nCoV_N1 forward primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 probe (IDT)

(cdcCovN1IDTProbe). 2019-nCoV_N1 probe (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 reverse primer (IDT)

(cdcCovN1IDTRev). 2019-nCoV_N1 reverse primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 forward primer (IDT)

(cdcCovN2IDTFor). 2019-nCoV_N2 forward primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 probe (IDT)

(cdcCovN2IDTProbe). 2019-nCoV_N2 probe (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 reverse primer (IDT)

(cdcCovN2IDTRev). 2019-nCoV_N2 reverse primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 forward primer (IDT)

(cdcCovN3IDTFor). 2019-nCoV_N3 forward primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 probe (IDT)

(cdcCovN3IDTProbe). 2019-nCoV_N3 probe (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 reverse primer (IDT)

(cdcCovN3IDTRev). 2019-nCoV_N3 reverse primer (IDT) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

CD-HIT

(cdHIT). A sequencing data processing application that clusters and removes duplicate sequences, useful for dereplication. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sites.google.com/view/cd-hit/home (main page) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA

Minimum Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Clostridium difficile

(cDiff). Clostridium difficile *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* clostridiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Corynebacterium diphtheriae

(cDip). Corynebacterium diphtheriae *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* diptheriaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

CeCILL Free Software License Agreement v2.1

(cecill21). The licensing for the measure or data set is managed under the CeCILL Free Software License Agreement v2.1. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/cecill-2.1/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Degrees Celcius

(cel). Degrees Celsius. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* -60 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Celera Assembler

(celera). A sequencing software that was initially developed for the Human Genome Project, still used in some workflows for large genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/wgs-assembler/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population census

(census). Government or other agency census for determining site/polygon population. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Centrifugation

(cent). Describes solid separation from a wastewater sample via centrifugation. Likely connected to other method steps prior to analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Centricon ultrafiltration

(centriconUf). Centricon ultrafiltration. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Centrifuges

(centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Ultracentrifuge are a separate instrument type option. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Centrifugation speed

(centSpeed). Centrifugation speed *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* speed *Nomenclature:* speed *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* speedUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ceres nanotrap

(ceres). Ceres nanotrap. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Cesspit

(cesspit). Cesspit, cesspool and soak pit in some contexts are terms with various meanings: they are used to describe either an underground holding tank (sealed at the bottom) or a soak pit (not sealed at the bottom). A cesspit can be used for the temporary collection and storage of feces, excreta, or fecal sludge as part of an on-site sanitation system and has some similarities with septic tanks or with soak pits. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Colony Forming Units

(cfu). Colony forming units *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

CFU per 100 ml

(cfu100). Colony forming units per 100 ml of filtered sample. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Colony forming units per grams total solids

(cfugTS). colony forming units per grams total solids (CFU/gTS) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Colony forming units per milliliter

(cfumL). colony forming units per milliliter (CFU/mL) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Changes column

(changes). A column for recording the changes from a previous version. Use this column as a short-hand change log for dictionary development. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

character length

(charLength). The number of characters used for the wide names. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* 50 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Chemical

(che). A chemical compound. *Part Type:* domains *Domain:* che *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Chemical contaminant surveillance

(chemSurv). Purpose of sampling/measure is to test for the presence of certain chemicals or chemical contaminants. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Chemagic viral dna/rna 300 kit

(chemVir). Nucleic acid extraction performed using the chemagic viral dna/rna 300 kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ChewBBACA

(chewBBACA). ChewBBACA. Focus: Core genome MLST (cgMLST) with optional serotyping analysis. Applications: Broad-spectrum bacterial pathogens. Features: Efficient with large datasets and highly customizable.

Parts

Part Type: categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/B-UMMI/chewBBACA Docs: https://chewbbaca.readthedocs.io/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Chikungunya Group

(chikungunyaGrp). A group of measures/methods related to chikungunya virus. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* chikungunyaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Chikungunya virus (CHIKV)

(chikv). Chikungunya virus (CHIKV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* chikungunyaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Child relationship

(child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Chlamydia

(chlamydia). Chlamydia *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* chlamydiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Chlamydia Group

(chlamydiaGrp). A group of measures/methods related to chlamydia bacteria. Used to describe the organism information for general measures.

Parts

Part Type: groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* chlamydiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Circovirus Group

(circoGrp). A group of measures/methods related to circoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* circoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

City

(city). The city where a site or organization is located; part of the address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Campylobacter jejuni bacteria

(cJejuni). Campylobacter jejuni gene target/measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* campGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0882401017303728?via%3Dihub *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Composite Key

(cK). Composite key for a table. All report tables have a primary key - the composite key acts as a primary key, but it prouced as a combination of other fields. Each row in a report table has unique identifier recorded in the primary key/composite key. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Calculations Table Short Name

(cl). The abbreviated short name used to reference the table for recording data on data treatments and calculations applied to measurements and

reported values. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Lineage- or Clade-analysis Software

(cladeAn). Software tool or pipeline for determining the clade or lineage of an organism. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* cladeAnSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Lineage- or Clade-analysis Software Set

(cladeAnSet). Valid category set for lineage or clade analysis software types. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* cladeAnSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Clarified sample

(clari). Clarified sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

CLARK

(clark). A dehosting software that classifies reads taxonomically, which helps filter out host reads in metagenomic data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://clark.cs.ucr.edu/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Class

(class). A unique identifier for a class, which is akin to a sub-group; it's a way of grouping parts within a given group. A group can have one or more classes to describe different parts of the class. Currently, class is only used for biologics. For example, SARS-CoV-2 is a group of measures with the following classes of allele, variant, mutation, sequence, and protein. *Part Type:* attributes *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* classes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Classes

(classes). A class is a collection of one or more related measures or methods within a group. A group can have one more more classes to describe different parts or the class. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

CleanPlex DNA Library Prep Kit

(cleanPlex). CleanPlex DNA Library Prep Kit by Paragon Genomics. A library target enrichment kit optimized for high sensitivity and low input. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ClermonTyping

(clermonTyp). ClermonTyping. Focus: MLST and phylogenetic typing for Escherichia coli. Applications: Ideal for epidemiological studies. Features: Combines MLST and phylogroup-specific information. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/A-BN/ClermonTyping *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Clinic

(clinic). A medical clinic, may be used to provide treatment, remedial work, and/or instruction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ClonalFrameML Software

(clonalFrameML). A lineage or clade analysis software tool for reconstructing phylogenetic relationships considering recombination, used in bacterial lineage analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp

Parts

Class: software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/xavierdidelot/ClonalFrameML *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Clostridium Group

(clostridiumGrp). A group of measures/methods related to clostridium bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* clostridiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Cloudy

(cloudy). Qualitative category for the weather measure, specifying an overcast day with no rain. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

BBMap's Clumpify

(clumpify). A deduplication method that groups identical sequences, often used to deduplicate reads efficiently. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/BioInfoTools/BBMap/blob/master/sh/clumpify.sh *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Clustal Omega

(clustalO). Sequencing software that is widely used for multiple sequence alignment and producing consensus sequences. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://www.clustal.org/omega/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Centimetres

(cm). Unit part for the SI unit of centimetres. *Part Type:* units *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Contact table Shorthand

(co). The abbreviated short name used to reference the The table that contains information about a contact; a person who is the contact of a site or laboratory. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Carbon Dioxide

(co2). A measure of an amount or concentraion of carbon dioxide. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* gas *Nomenclature:* gas *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* dissGasUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Chemical Oxygen Demand

(cod). Chemical oxygen demand. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Time from collection to storage

(col2Frdg). The amount of time between sample collection and the samples placement in stable storage/refrigeration. *Part Type:* measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Colistin Anti-microbial resistance group

(colAMRGrp). The group for measures and methods pertaining to colistin-related anti-microbial resistance. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* colAMRGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:*

NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Collection group

(colGrp). A group of measurement-like attributes related to sample collection. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Colistin resistance

(colis). Colistin-resistant bacteria. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Collection Approximate Time Period Set

(collAppxSet). The category set of valid inputs for the collGenT attribute field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpeci-

menSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* collAppxSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Collection Approximate Time Period

(collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection. used when exact time in unknown. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* collAppxSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Collection Date (time not included)

(collDate). Sample collection date, where time is reported in a separate field. Only for use in combination with the collection approximate time period field. Otherwise report date and time together. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* date *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Collection date time

(collDT). For grab samples this is the date, time and timezone the sample was taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Collection date time end

(collDTEnd). For integrated time average samples this is the date, time and timezone the sample was finished being taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Collection date time start

(collDTStart). For integrated time averaged samples this is the date, time and timezone the sample was started being taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sample collection set

(collectSet). Methods for collection samples. Sample collection methods include water, air, and surface. See the attribute 'Compartment set' of the sample collection method. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* collectSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Collection number

(collNum). The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Collection period and number

(collNumPer). Composite collection number.period. This a composite measure that combines ‘collection period‘ (collPer) and ‘collection number‘ (collNum). Collection number and period can be used to reduce the number of table headings during data collection. In data storage, ‘collNum‘ and ‘collPeriod‘ should be transformed to ‘collPer‘ and ‘collNum‘. For Grab sample, Surface swab, or Area proportional sample just enter 1

In case of Composite, Flow-proportional collection, the number of subsamples followed by a dot, followed by the period of the sampling, in hours. For example, for 4 composite subsamples covering a 8 hours period, the entry would be 4.2 For time-proportional 24 subsamples collected every hour, the entry would be 24.1 For volume-proportional, the entry for 24 subsamples collected over 24 hours should be 24.24, in this case the period part of the entry should be understood as the total collection time instead of the periodicity of the collection.

For a COSCA ball or Moore swab collecting for 24 hours, the entry would be 1.24 *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 6 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 3.0.0.

Collection period

(collPer). Collection period. The time period over which the sample was collected, in hours. Alternatively, use collectionStart and collectionEnd. Examples: 1 hour, 6 hours, 24 hours *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample collection type

(collType). The type of collection. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* collectSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Co-located relationship

(colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Column name depreciiated

(columnNameDep). Name for the column Depreciated in ODM version 2. Look-up tables are now incoprated into parts and sets. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Commercial facility - not specified

(commFacOth). Specifies a site type which is a commercial facility/worksite that is not otherwise captured or described in the geotype set. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Community-level Surveillance

(communitLev). Surveillance is done at the level of an entire community. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* popGrp *Class:* popClass

Nomenclature: popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Communitor

(communitor). A mechanical device that grinds large solid waste in wastewater into smaller particles to prevent clogging. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501472 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Composite sample - archival

(comp). A composite sample, usually generated by an autosampler. This is intended for use in updating and mapping archival data into the newest version of the ODM. Generally, autosamplers do time or flow-proportional sampling, and so those collection methods should be used instead. This is only for composite/autosampler samples where these additional details have not yet been specified. Use collectionPeriod to describe how many hours the sample was taken, and collectionNum to record the number of samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness*

Set: NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Composite grab sample of 3

(comp3). A grab-composite sample composed of 3 separate grab samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite grab sample of 3 depreciate

(comp3dep). A grab-composite sample composed of 3 separate grab samples. Deprecated in version 2, please do not use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite 3hr grab sample

(comp3h). A 3-hour composite with 3 grab samples each taken once per hour, generally manually performed. *Part Type:* categories *Domain:* naDo-

main *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite 3hr grab sample depreciate

(comp3hdep). A 3-hour composite with 3 grab samples each taken once per hour, generally manually performed. Deprecated in version 2, please do not use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite 8hr grab sample depreciated

(comp8h). An 8-hour composite with 8 grab samples each taken once per hour, generally manually performed. Deprecated in version 2, please do not use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite 8hr grab sample deprecated

(comp8hDep). A 8-hour composite with 8 grab samples each taken once per hour, generally manually performed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Compartment

(compartment). The attribute identifying the substance from which where a sample was taken. For more information, see partID = compartment. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* compartments *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Compartment input (wide table)

(compartmentInput). The partID for the compartment being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* compartments *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Compartment name (wide table)

(compartmentName). The compartment referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* compartments *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Compartments

(compartments). The substance from which a sample was taken. For example, wastewater has component of "water". Compartments are attributes of measures, methods, units, and aggregations. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Compartment Set Header

(compartmentSet). An idenfication of a set of compartments that can be applied for a measure or method. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* compartmentSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Compartment sets

(compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured in people (humans), water, surface, or air. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Composting toilet

(compToi). A self-contained toilet system wherein human waste is designed to be composted. Usually with the addition of secondary materials, like sawdust. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:*

naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Concentration measure

(conc). Measurement of concentration (generalized) - designed for describing protocols. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Is concurrent to

(concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Use only for protocolRelationships table relationshipID. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample volume after concentration

(concVol). The total volume of a sample after the concentration step. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Water conductivity

(cond). Measurement of conductivity of sample or site. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* conductivity *Nomenclature:* conductivity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* conductivityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Conductivity class

(conductivity). Measures and methods related to conductivity. *Part Type:* classes *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* naGroup *Class:* conductivity *Nomenclature:* conductivity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* conductivityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:*

NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Conductivity unit set

(conductivityUnitSet). Unit set related to conductivity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* conductivityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Cone-shaped sampling

(cone). Intrument type is a grab sample that has a controlled valve that opens to take a sample from a specific depth, then closes to bring the sample out. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Number of confirmed cases

(conf). Number of confirmed cases. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Number of confirmed cases by episode date

(confEp). Number of confirmed cases of a given disease, totaled by episode date. Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed Cases Onset date

(confOn). Number of confirmed cases of a given disease, totaled by onset date. Onset date is the earliest date that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA

Reference Link: NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed cases by report date

(confRep). Number of confirmed cases of a given disease, totaled by report date. Report date is the date that the numbers were reported publicly for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed cases test date

(confTest). Number of confirmed cases of a given disease, totaled by test date. Test date is the date that the covid-19 test was performed for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.2.0.

consensus genome length

(conGenLen). The length of the genome defined by the most common nucleotides at each position. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Consensus Sequence Software

(conSeqSoft). Software use to run consensus sequence on sequencing analyses. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* conSeqSoftSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Consensus Sequence Software Set

(conSeqSoftSet). The valid set of consensus sequencing software categories. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* conSeqSoftSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Contact ID

(contactID). A unique identifier for a given contact person. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Contact name

(contactName). Contact person or group, for the lab. Depreciated in ODM version 2. see 'name' *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Contact table

(contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table

(partID) can be found in the instructions field. co *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Contacts table column order

(contactsOrder). Specifies the order of the columns in a Contacts table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Contact table required headers

(contactsRequired). Specifies the columns required in a Contacts table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Contact table set

(contactTableSet). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Contamination

(contam). The presence of a constituent, impurity, or some other undesirable element that spoils, corrupts, infects, makes unfit, or makes inferior a material, physical body, natural environment, place of human occupancy, or other material entity. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Control measure implementation

(contMeasImp). A public health action type wherein authorities have begun implementing infection control measures. *Part Type:* categories *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Control Measure Implementation Value Set

(contMeasImpSet). A set of valid categories for the public health action field, where the action type is 'control measure implementation'. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* contMeasImpSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Control sample

(control). Denotes a relationship to a primary sample where the object sample serves as a control to the subject sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Contact phone

(coPhone). Contact phone number, for the lab. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 10 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Core sampling

(core). Intrument type is a grab sampler that captures a vertical section of the substrate matrix of fecal sludge. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Correctional facility

(corFcil). Correctional facility *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Cosavirus (CosaV)

(cosaV). Cosavirus is a genus of viruses in the order Picornavirales, in the family Picornaviridae. Human serve as natural hosts. There are 5 species od enteric viruses in this genus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cosaVGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Cosavirus Group

(cosaVGrp). A group of measures/methods related to cosaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cosaVGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

COSCa ball

(cosca). COSCa passive sampling device. Use collectionPeriod to describe how many hours the ball was used to collect the sample *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://pubs.rsc.org/en/content/articlelanding/2021/ew/d1ew00207d *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Population count

(count). A count of residents for determining site/polygon population. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Country-level Aggregation at Site

(countLevel). Specifies that a sewershed/site represents an entire nation or country. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:*

genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Countries look-up tables

(countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. cu *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Countries table column order

(countriesOrder). Specifies the order of the columns in the countries table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Counries table required headers

(countriesRequired). Required headers in the countries table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomen-*

clature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Country

(country). The country where a site or organization is located; part of the address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* geoRefMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 3.0.1.

Country endonym

(countryEndonym). The name locals use for their country. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Country exonym

(countryExonym). The English name foreigners use for the country. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Countries or sovereign states

(countryLevel). Countries or sovereign states *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Districts, counties, regions

(countyLevel). Districts, counties, regions *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Covid-19

(cov). Covid-19 infection. Any form of Covid-19 human infetion - including testing for Covid-19, symptomatic Covid-19, asymptomatic Covid-19, hospitalized Covid-19, long-Covid-19, etc. If needed, define the specific form Covid-19 with units. See populationUnits. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* sarsCov2 *Class:* disease *Nomenclature:* disease *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 measure

(cov2Me). Measure the amount of SARS-CoV-2 virus. This measure should only be used if there is no other SARS-CoV-2 measure. See groupID = sarsCov2. Use a note to describe the specific measure used. *Part Type:* measurements *Domain:* bio *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Covaris truXTRAC FFPE DNA Library Kit

(covarisTruXTRAC). Covaris truXTRAC FFPE DNA Library Kit. A specialized library prep kit for extracting and preparing DNA from FFPE tissue. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2-B.1.1.7

(covB117). Variant B.1.1.7 of the SARS-CoV-2 virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

SARS-CoV-2-B.1.351

(covB135). Variant B.1.351 of the SARS-CoV-2 virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

SARS-CoV-2-E

(covE). SARS-CoV-2 E gene. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENEPIO:0100151 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2 M Gene target

(covM). SARS-CoV-2 M gene (orf5) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100152 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2-N1

(covN1). SARS-CoV-2 nucleocapsid gene, allele 1. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2-N2

(covN2). SARS-CoV-2 nucleocapsid gene, allele 2. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2-N200

(covN200). SARS-CoV-2 nucleocapsid gene, amino acids 199-202. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2-N3

(covN3). SARS-CoV-2 nucleocapsid gene, allele 3. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2-P.1

(covP1). Variant P.1 of the SARS-CoV-2 virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

SARS-CoV-2-RdRp

(covRdrp). SARS-CoV-2 RdRp gene. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENEPIO:0100168 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2 S Gene Target

(covS). S sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-COV-2 5' UTR Gene target

(covUTR5). SARS-COV-2 5' UTR Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100183 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Clostridium perfringens

(cPerfrigens). Clostridium perfringens *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* clostridiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Covid-19 population measurement date

(cphDate). date of reporting for covid-19 measure. Depreciated in ODM version 2. The measure identication is now measureReportID with report dates as for any measure report. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Cphd ID

(cphid). Unique identifier for the table. Depreciated in ODM version 2. The measure identication is now measureReportID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Critical priority pathogen

(cpp). A microorganism with resistance to multiple drugs and a high threat to human health. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gene copies per well

(cpWell). Gene or variant copies per well. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum*

Length: NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

crAssphage-N

(cra). crAssphage virus capsid protein gene region *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Crassphage Standarized

(crassStand). This data treatment standardizes the measurement value to concentration levels of crassphage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Creatinine

(crea). Creatinine (usually measured as a human fecal chemical indicator) *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet

Compartment Set: waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Crosswalk table set

(crosswalkTableSet). Tables used to translate to and from other environmental dictionaries and models. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Cryptosporidium

(cryptosporidium). Cryptosporidium *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cryptosporidiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Cryptosporidium Group

(cryptosporidiumGrp). A group of measures/methods related to cryptosporidium parasites. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cryptosporidiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Cycle threshold or quantification cycle (Ct or Cq)

(ct). Cycle thresholds in a PCR assay. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Cycle threshold per quantification cycle

(ctcq). cycle threshold (Ct) / quantification cycle (Cq) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA

Minimum Length: NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

CTFinder

(ctFinder). CTFinder. Designed for Clostridioides difficile serotyping and subtyping. Identifies capsular polysaccharide synthesis gene clusters to assign serogroups. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Countries look-up tables Shorthand

(cu). The abbreviated short name used to reference the Look up table for the possible country inputs. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Cumulative count

(cuCo). The cumulative count of cases of a given disease. Aggregation for a population or disease measure to explain population-level clinical effects.

Part Type: aggregations *Domain:* naDomain *Speciment ID:* poSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Cufflinks (with TopHat integration)

(cufflinks). Cufflinks (with TopHat integration). A specialized read mapper. Combines mapping with transcriptome assembly and quantification. Best for: RNA-seq studies with integrated analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://cole-trapnell-lab.github.io/cufflinks/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Custody Contact ID

(custodyCont). A unique identifier for data custodians. Use Contact ID to populate this field, and the organizations table to describe contact information and other details for the data custodian. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Data custodian ID

(custodyID). The data custodian of a database. Use Organization ID to populate this field, and the organizations table to describe contact information and other details for the data custodian. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Cutadapt

(cutadapt). A sequencing data processing application that does adapter removal and trimming tool for high-throughput sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://cutadapt.readthedocs.io/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Circulating vaccine-derived poliovirus type 2

(cVDPV2). Circulating vaccine-derived poliovirus type 2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polioGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Number of cycles

(cyNum). The number of cycles of a PCR machine, or any other cycling process. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

D339H Mutation

(d339h). The FLiRT/SLip variant mutation D339H. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

d377y delta-variant gene target

(d377y). d377y delta-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-CompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

d3g omicron-variant gene target

(d3g). d3g omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-CompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

d63g delta-variant gene target

(d63g). d63g delta-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

d796y omicron-variant gene target

(d796y). d796y omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

d950n delta-variant gene target

(d950n). d950n delta-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

DADA2

(dada2). A sequencing data processing application that is primarily used in amplicon sequencing for error correction and generating amplicon sequence variants. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://benjjneb.github.io/dada2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Daily count

(daiCo). The daily count of cases of a given disease. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* poSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Database and Data Repository Class

(database). Measures and methods related to databases and data repositories. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Data collection sector or organization

(dataColl). Describes organization who collect compile, analyze, and or manage data as their central focus. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Host Data Repository or Bank

(dataHost). The external repository or database/bank in which a sequence (or other external data) is stored. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* dataRepoSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:*

categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Data Repository Set

(dataRepoSet). The mma set for all valid input categories for the dataRepo field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* dataRepoSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dataset creation date

(datasetDate). Specifies the date a given dataset was created. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dataset ID

(datasetID). The name of the dataset that stores information for MeasureReport, SampleReport and other reporting tables. Where possible,

datasetID name should correspond the orignial data custodian responsible for generating environmental data. (suggestion for a default name convention.) *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Dataset table

(datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. ds *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Datasets table column order

(datasetsOrder). Specifies the order of the columns in a Datasets table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1

Maximum Value: NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dataset table required headers

(datasetsRequired). Specifies the columns required in a Datasets table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Data Type column (Reported)

(dataType). The recorded data type for every part in the part table. This is the attribute in the parts table, not to be confused with dataTypes, the part type. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* dataTypes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Data types part type

(dataTypes). The data type for a part. Data types used in the ODM include: varchar, booleen, float, category, date, time, datetime, url, email. dataType corresponds the the entry or cell within a data table, most commonly within

a report table. If the data entry has a unit, then the dataType corresponds to the unit and the dataType refers to 'unit'. If the data entry is a category, then the dataType refers to 'category'. All categories are varchar. Otherwise the dataType is identifed within the part entry. TBA: dataType for dictionary. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

Date data type

(date). The data type for date data (does not include time). Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Date

(dateDep). Date date on which the assayMethod was created or updated (for version update). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 3.0.0.

Datetime data type

(datetime). The data type for date and time data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

7-day smoothing of values

(day7Smooth). This data treatment smooths the measurement value across 7-days. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Days

(days). A unit for indicating a length of time in days. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* na-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

DNA Data Bank of Japan (DDBJ)

(ddbj). DNA Data Bank of Japan (DDBJ) archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ddbj.nig.ac.jp/index-e.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ddcov_e sars-cov-2 gene target

(ddcovE). ddcov_e sars-cov-2 mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ddcov_n sars-cov-2 gene target

(ddcovN). ddcov_n sars-cov-2 mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Digital Droplet PCR (ddPCR)

(ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Deaths

(death). Units for describing a population measure of patients who have died from a given cause. Unit for a population or disease measure to explain population-level clinical effects. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

DeconSeq

(deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://deconseq.sourceforge.net/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

DecontaMiner

(decontaMiner). A QC pipeline tool for sequencing data for contamination detection and removal in NGS datasets, especially useful in clinical samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/decontaminer/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Decreased surveillance

(decSurv). Scaling back of monitoring activities, often due to reduced risk. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Deduplication Method

(dedup). Sequencing and PCR deduplication method. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* dedupSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Deduplication Method Set

(dedupSet). The valid set of deduplication method categorical inputs. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* dedupSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:*

NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

DeepARG Software

(deepARG). Software tool that predicts AMR genes using deep learning on metagenomic data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/gaarangoa/deeparg *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dehosting Method

(dehost). Sequencing and PCR dehosting method. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* dehostSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dehosting Method Set

(dehostSet). The valid set of dehosting method categorical inputs. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:*

sequence *Ontology Reference:* NA *Category Set ID:* dehostSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Omicron Variant 142-144 Deletion

(del142144). Omicron Variant 142-144 Deletion mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

del143/145

(del143). 143 or 145 deletion omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Delta Variant 156-157 Deletion

(del156157). Delta Variant 156-157 Deletion mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

del 157/158

(del157). 157 or 158 deletion delta-variant gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

del2084/2084

(del2084). 2084 or 2084 deletion omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

del212/212

(del212). 212 or 212 deletion omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant 142-14431-33 Deletion

(del3133). Omicron Variant 142-14431-33 Deletion mutation. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

del3674/3676

(del3674). 3674 or 3676 deletion omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

del69/70

(del6970). 69 or 70 deletion omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Delayed Arrival or Prolonged Transit

(delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Delta

(delta). B.1.617.2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 Delta Variant Group

(deltaGrp). A group of measures/methods related to the SARS-CoV-2 Delta Variant. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NCIT:C169076 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Deltaretrovirus

(deltaretro). Deltaretrovirus is a genus of the Retroviridae family. It consists of exogenous horizontally transmitted viruses found in several groups of mammals. This genus of viruses is known for its propensity to target

immune cells and oncogenicity. Infection is usually asymptomatic, but inflammation and cancer can develop over time. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaretroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Deltaretrovirus Group

(deltaretroGrp). A group of measures/methods related to deltaretroviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaretroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Dengue Virus Type 1

(den1). Dengue virus, Type 1, general measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum*

Length: NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus Type 2

(den2). Dengue virus, Type 2, general measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus Type 3

(den3). Dengue virus, Type 3, general measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus Type 4

(den4). Dengue virus, Type 4, general measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:*

anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

denaturation

(denat). Describes the denaturation cycle in a PCR process. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Dengue

(dengue). Dengue virus, general measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

depth of coverage threshold

(depCovThresh). The threshold used as a cut-off for the depth of coverage. Provide the threshold fold coverage. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Depreciated

(depreciated). Indicator to say that a part is no longer in current use in the model. See partID = status *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Derived data

(derived). Derived data, data that has undergone agregation, standardization, adjustment, or any cleaning prior to reporting. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Derived sample

(derivedSamp). A sample that is derived or made from another sample or material. A derived sample is a type of sample created by mixing material obtained from a field sample (e.g., wastewater, soil, or air) with additional additives in a laboratory setting. This process can involve diluting the original field sample with clean water or other solutions, as needed. Derived samples are typically used to adjust the concentration of the target substance or organism, making it more suitable for analysis or to test the efficiency and sensitivity of detection methods. In the example given, a derived sample might be a sub-sample of wastewater that is diluted with clean water to achieve a specific concentration, allowing for more accurate and reliable analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Description

(descr). A detailed description of a measure, method, or attribute. A description of the part that serves a clear presentation of the part to a wide audience including techinical and not techincal staff. A description should allow any person who generates environment surveillance data to know how to identify how to record their data elements in the ODM. partReference

can be used to further describe a part. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Description of change

(descrChange). A description of change in a part from the previous version. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Desk or counter

(desk). Desk, table, countertop or other flat working surface. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dewatered solids

(deso). Dewatered solids. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Detected

(det). Substance detected or not detected. TRUE = detected, FALSE = not detected *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 1 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Access to details deprecated

(detailsDep). More details on the existing confidentiality requirements of this measurement. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Detected Lineage or Clade Name

(detLinClade). The measurement for reporting detected lineage or clade information - used as an "other" for measurements not already captured in the ODM structure. Most useful if bundled into a measurement set with other relevant measures. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* othAgg *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

De-escalated variant

(dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Development

(development). Indicator that a part is under development use. See partID = status *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dictionary reference table set

(dictionaryRefTableSet). Reference or look-up tables. For example, the parts table describe all elements of the ODM, including tables, table headers, measures, methods, categories, and units. sets are collections of parts. For example, units can be grouped together in a unitSet. languages and translations support translations. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Additional dictionary sheets

(dictionarySupport). Additional sheets for the Excel version of the ODM dictionary. Sheets or tabs for the ODM Excel dictionary include: all ERD tables (look-up tables and data entry tables) and additional supportig tables.

Parts

Part Type: partTypes *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dictionary set type

(dictSets). Sets used to describe and group dictionary tables. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dilution factor

(dilFact). Specifies the extent to which a sample or aliquot was diluted prioir to analysis. Dilution factor is reported as a unitless measure, where a value of 10 indicates a 10:1 dilution. *Part Type:* measurements *Domain:* che *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* dilution *Nomenclature:* dilution *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Point dillutions

(dillute). Exact concentration or dillutions for generating a standard curve. *Part Type:* measurements *Domain:* che *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* dilution *Nomenclature:* dilution *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dilution Class

(dilution). Measures and methods relating to dilutions. *Part Type:* classes *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* dilution *Nomenclature:* dilution *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Diphtheria Group

(diptheriaGrp). A group of measures/methods related to the diptheria bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* diptheriaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

DISCOVAR de novo

(discovar). A sequencing software that is an assembler optimized for Illumina data in whole-genome sequencing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://software.broadinstitute.org/software/discovar/blog/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Diseases (human) class

(disease). Measure and methods related to disease or infection in humans. *Part Type:* classes *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* disease *Nomenclature:* disease *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dissolved gas concentration unit set

(dissGasUnitSet). Unit set for carbon dioxide concentrations measurements in water or air. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* dissGasUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Dissolved oxygen

(dissOxy). Measure of dissolved oxygen in liquid medium *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

DNA Template

(dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

DNA Fragment Length

(dnaFragLen). The length of the DNA fragment generated by mechanical shearing or enzymatic digestion for the purposes of library preparation. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nextera DNA Flex/DNA Prep Library Prep Kit

(dnaPrep). Nextera DNA Flex Library Prep Kit, now called DNA Prep, by Illumina. A flexible, transposase-based library prep kit for a wide range of DNA input amounts, suitable for microbial and human DNA. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

DNA/RNA Shield

(dnaRNAshield). A stabilizing solution for nucleic acids in samples, including wastewater, protecting against degradation at room temperature. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Data Not Collected

(dnc). A missingness value for when when data was not measured or collected; an analysis not run, etc. Missing value indicator when the value was never collected and should be missing. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus E Gene

(dnvE). Dengue Type 2-specific gene taget. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus NS5 Gene

(dnvNS5). Dengue Type 1-specific gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus prM Gene

(dnvprM). Dengue Type 3 and 4-specific gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dobrava-Belgrade virus (DOBV) hantavirus

(dobv). Dobrava-Belgrade virus (DOBV) is the main cause of hemorrhagic fever with renal syndrome (HFRS) in southern Europe. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet

Reference Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Depth of coverage

(doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Used to interpret the confidence in a presence or amount of a varient. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Domain

(domain). Domain is the highest level of describing of a measure. The domain ID that corresponds to a given part. Mostly applicable for measures, methods, units, and aggregations. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* domains *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Domains

(domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature). *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Domestic travel hub surveillance

(domSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to domestic travel. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Higher education domitory or residential building

(dorm). Higher education domitory or residential building *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Digital PCR (dPCR)

(dpcr). Describes a PCR analysis done using digital PCR technology (general). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Digital PCR (dPCR) intruments

(dPCRinst). Digital PCR instruments, enables absolute quantification without the need for standard curves (e.g., Bio-Rad QX200). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

DDBJ sequence Read Archive (DRA)

(dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ddbj.nig.ac.jp/dra/index-e.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sewer (drain)

(drain). A pipe that carries water or sewage away from a place, or an opening in a surface that leads to said pipe. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Drug surveillance

(drugSurv). Purpose of sampling/measure is to surveil drug use in a population. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dataset table Shorthand

(ds). The abbreviated short name used to reference the report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Duration time of a method

(duration). The duration of time for a given method as described in protocols. *Part Type:* measurements *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

e156g delta-variant gene target

(e156g). e156g delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA

Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

e484a omicron-variant gene target

(e484a). e484a omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Enteroaggregative Escherichia coli (EAEC)

(eaec). Enteroaggregative Escherichia coli (EAEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

EAGER

(eager). A QC pipeline tool for sequencing data for ancient DNA, providing quality filtering, contamination estimates, and other QC metrics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/ComputationalGenomicsBeijing/EAGER *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

EasySeq NGS Targeted Capture Kit

(easySeqNGS). EasySeq NGS Targeted Capture Kit by Nimagen. A library preparation kit and targeted capture in one, ideal for small panels. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Orthoebolavirus Group

(ebolaGrp). A group of measures/methods related to Orthoebolaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ebolaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet

Aggregation Scale: seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Ebola virus, Orthoebolavirus zairense

(ebolaV). Orthoebolavirus zairense or Zaire ebolavirus, more commonly known as Ebola virus, is one of six known species within the genus Ebolavirus. Four of the six known ebolaviruses, including EBOV, cause a severe and often fatal hemorrhagic fever in humans and other mammals, known as Ebola virus disease (EVD). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ebolaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Epstein–Barr virus (EBV)

(ebv). Epstein–Barr virus (EBV), formerly known as Human gammaherpesvirus 4 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* herpesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Educational Community License v2.0

(ecl20). The licensing for the measure or data set is managed under the Educational Community License v2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/ecl-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Escherichia coli

(ecoli). Concentration of bacteria that are passed through the faecal excrement of humans, livestock and wildlife *Part Type:* measurements *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* surfaceWaterCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Escherichia coli group

(ecoliGrp). A group of measures/methods related to Escherichia coli bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:*

organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Eden V1 Primer Set

(edenV1). An amplicon strategy which was developed by John-Sebastian Eden with primers for SARS-CoV-2 and attributes of version 1.0.0 which produces amplicons approximately 2500bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Educational facility

(edFac). A school or other educational facility not otherwise specified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Education

(education). A measure or sample taken for education or training. Use this purpose, for example, when teaching how to use the PHES-ODM. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Eastern equine encephalitis virus (EEEV)

(eeev). Eastern equine encephalitis virus (EEEV) is defined as a neurotropic alphavirus that causes severe disease in horses, characterized by high mortality rates and pathological lesions in the central nervous system, including inflammation and infiltration of immune cells. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* eeevGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Eastern equine encephalitis virus group

(eeevGrp). A group of measures/methods related to eastern equine encephalitis viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet

Parts

Compartment Set: anyCompartmentSet *Group:* eeevGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Efficiency

(efficient). The efficiency reported for a standard curve. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater Effluent - non-specified

(effluNS). Sample material is wastewater effluent - whether primary, secondary or other is unspecified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Enterohemorrhagic Escherichia coli (EHEC)

(ehec). Enterohemorrhagic Escherichia coli (EHEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Enteroinvasive Escherichia coli (EIEC)

(eiec). Enteroinvasive Escherichia coli (EIEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Electrical potential unit set

(electricPotentSet). Unit set for measurements of electrical potential. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* electricPotentSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Eluate/Resuspended filter material retained

(eluate). The eluate fraction, or material resuspended from filtration, is retained after solid separation/centrifugation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Elution buffer

(elutionBuff). Elution buffer is used to resuspend material. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Contact email

(email). Contact e-mail address, for the lab. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Emboss Cons

(embossCons). Sequencing software that is part of the EMBOSS suite, generates consensus sequences from multiple alignments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.bioinformatics.nl/cgi-bin/emboss/help/cons *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Emergency targetted surveillance program

(emergSurv). A targeted surveillance strategy which is considered important and/or urgent. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

European Nucleotide Archive (ENA)

(ena). European Nucleotide Archive (ENA). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ebi.ac.uk/ena/browser/home *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ENA Format

(enaForm). Dataset was originally recorded and/or stored in ENA format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ebi.ac.uk/ena/browser/checklists *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

European Nucleotide Association Mapping Column

(enaMap). ENA header *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

European Nucleotide Association (ENA) - notes

(enaNotes). ENA notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Enterobase archives

(enterobase). Enterobase archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://enterobase.warwick.ac.uk *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Enterovirus

(enterovirus). Enterovirus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* enterovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA

Parts

Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Enterovirus Group

(enterovirusGrp). A group of measures/methods related to enteroviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* enterovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Enumeration for set values

(enumeration). The numeric value that corresponds to a given value in a set, defined in the sets table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Temperature and pH probes

(enviroInst). Local probe insturments for temperature or pH; allow monitoring of environmental conditions at sites, for example. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Rainfall

(envRnF). Rainfall, i.e. amount of precipitation in the form of rain. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* precipitation *Nomenclature:* precipitation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Ground snow depth

(envSnwD). Total depth of snow on the ground. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* precipitation *Nomenclature:* precipitation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet

Reference Link: NA *Data Type:* float *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Snowfall

(envSnwF). Snowfall, i.e. amount of precipitation in the form of snow. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* precipitation *Nomenclature:* precipitation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Enteropathogenic Escherichia coli (EPEC)

(epec). Enteropathogenic Escherichia coli (EPEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Episode date

(epiDate). Episode date is the earliest of onset, test or reported date. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

EpiWeek Mean

(epiMean). The mean of all measures taken in one epiweek. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

EpiWeek Number

(epiWeek). The number of the epi week in which a sample what collected, or to which a measure would apply. Used in conjunction with the epiYear field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum*

Value: 1 *Maximum Value:* 52 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

EpiWeek Start Date

(epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start dat resolves the possible ambiguity. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* date *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Year of the EpiWeek

(epiYear). The year in which the epi week is occuring. Used in conjunction with the epiWeek field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 1900 *Maximum Value:* 3000 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Eclipse Public License 1.0

(epl10). The licensing for the measure or data set is managed under the Eclipse Public License 1.0. *Part Type:* categories *Domain:* naDomain *Spec-*

iment ID: naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/epl-1.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Eclipse Public License 2.0

(epl20). The licensing for the measure or data set is managed under the Eclipse Public License 2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/epl-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Equation

(equation). The equation used in the calculation/data treatment. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 300 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ERD table set

(erdTableSet). All tables listed in the Entity Relationship Diagram. The full ODM model is commonly referred to as "long" tables as it stores data with one measurement per row. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Erythroparvovirus

(erythroparvo). Erythroparvovirus is defined as a small DNA virus that belongs to the Parvoviridae family, known for causing various illnesses, including fifth disease, arthritis, and anemia, particularly in immunocompromised individuals. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* erythroparvoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Erythroparvovirus Group

(erythroparvoGrp). A group of measures/methods related to erythroparvoviruses. Used to describe the organism information for general measures.

Part Type: groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* erythroparvoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Sarbecovirus-specific E sars-cov-2 gene target

(eSarbec). Sarbecovirus-specific E sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ESBL-encoding genes

(esbl). Extended-spectrum beta-lactamase-encoding genes. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

exclusions based sample preparation (ESP)

(esp). exclusions based sample preparation (ESP) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Estimated frequency of reads

(estFreqReads). Estimated frequency of reads in a sequencing assay *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Estimated data

(estimate). Estimated data, data that should be understood to be an estimation, possiblynot taken directly from sample measures. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Estuary, natural water body

(estuary). Estuary, natural water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Enterotoxigenic Escherichia coli (ETEC)

(etec). Enterotoxigenic Escherichia coli (ETEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

European Union Public License 1.1

(eupl11). The licensing for the measure or data set is managed under the European Union Public License 1.1. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/eupl-1.1/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

European Union Public License 1.2

(eupl12). The licensing for the measure or data set is managed under the European Union Public License 1.2. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/eupl-1.2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ebola Virus Disease (EVD)

(EVD). Ebola, also known as Ebola virus disease (EVD) and Ebola hemorrhagic fever (EHF), is a zoonotic viral hemorrhagic fever in humans and other primates, caused by four of the six known ebolaviruses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ebolaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:*

seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Evening

(eve). Sample was collected in the evening, late in the day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Exceptions Part Type

(exceptions). An exception part type for use in creating wide names that do not follow the general structure. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 exoN gene (nsp14)

(exoNnsp14). SARS-CoV-2 exoN gene (nsp14) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100170 *Category Set ID:* NA *Unit Set:* geneticUnitSet

Aggregation Scale: seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Extraintestinal pathogenic Escherichia coli (ExPEC)

(expec). Extraintestinal pathogenic Escherichia coli (ExPEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* genetic-UnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Experiment Failed

(expFail). PCR experiment failed. No value reported. Value should be blank for a measure with this qualityFlag value. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Extraction Blank - Control

(extBlank). Binary Y/N indicator for if extraction blank was used as a control for the nucleic acid extraction process. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

4s method

(extract4s). Nucleic acid extraction performed using the 4s method. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.protocols.io/view/v-4-direct-wastewater-rna-capture-and-purification-bpdfmi3n *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Nucleic acid extraction method

(extraction). Description of the nucleic acid extraction method. Description of the method used to extract the sample *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* extractSet *Unit Set:* unitlessUnitSet *Aggregation Scale:*

qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Extraction Recovery Percent

(extractRecov). The percentage of spiked in or endogenous compound used to assess extraction recovery of nucleic acids. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nucleic Acid Extraction set

(extractSet). set used for storing all the valid category values for the nucleic acid extraction method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* extractSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Extraction volume of sample

(exvol). Extraction volume of sample. Size of the sample that is analyzed. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

F456L Mutation

(f456l). The FLiRT/SLip variant mutation F456L. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Fecal matter

(faeces). Fecal matter. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Fast-flowing

(faFlow). A quality of a body of water wherein there is a fast flow. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Degree Fahrenheit

(fah). Unit for temperature, degrees Fahrenheit. *Part Type:* units *Domain:* phy *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FALSE

(FALSE). Boolean data type = FALSE Use these values and their set for any boolean measure or attribute. Use only "FALSE" (case sensitive) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 5 *Maximum Length:* 5 *Part Status:* active. First released: 1.0.0. Last updated: 2.3.0.

Farm

(farm). An aggricultural area, builing, or tract of land. Used for the cultivation of crops or grazing of livestock, including any buildings. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FastMLST

(fastMLST). FastMLST. Focus: Lightweight MLST and serotyping from assembled genomes or raw reads. Applications: Broad bacterial species. Features: Quick and simple, designed for routine use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/EnzoAndree/FastMLST *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FASTP

(fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/OpenGene/fastp *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FastQC

(fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.bioinformatics.babraham.ac.uk/projects/fastqc/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FASTQ Screen

(fastqScreen). A dehosting software that checks reads against multiple reference genomes, including host genomes, to remove contamination. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software

Nomenclature: software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.bioinformatics.babraham.ac.uk/projects/fastq_screen/ (official page) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FastUniq

(fastUniq). A deduplication method that is specifically designed to remove duplicates in paired-end sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/fastuniq/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

FASTX Toolkit

(fastXTools). A sequencing data processing application that provides various functions for FASTQ processing, including quality filtering. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://hannonlab.cshl.edu/fastx_toolkit/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Male-specific (F+) coliphage - general

(fColiphage). Male-specific (F+) coliphage - general *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

F+ DNA coliphage

(fDNA). F+ DNA coliphage *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Fecal coliform count

(fecalCol). Measure of prevalence of fecal coliform bacteria *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Fecal-contamination

(fecContam). A contamination quality in which fecal matter is a key component of the contamination. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Field sample

(field). Specifies a sample taken from the field; directly collected from an area for testing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Field sample replicate

(fieldReplicate). A sample divided into two or more homogeneous parts. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

File location of polygon

(fileLocation). The location of the file containing the geometry of the polygon. File path specified, or a URL *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 65535 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Filtration

(filt). Describes solid separation from a wastewater sample via filtration. Proceeds further concentration or analysis of the liquid filtrate. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Filtration units

(filtInst). Filtration instruments; remove large particulates or concentrate targets (e.g., tangential flow filtration). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

First Nation

(fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Likely for internal use only, Indigenous data can and should not be shared without explicit consent of the nation in quesiton. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Final volume

(finVol). The final volume of a testing solution or sample. *Part Type:* measurements *Domain:* che *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality*

Set: genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

First name of contact

(firstName). Specifies the first name of a given contact. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

First released version

(firstReleased). The version in which a part was first released *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Foreign key

(fK). Foreign key for a table. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Foreign Key Alias ID

(fKAliasID). The primary key that is being referenced by another name in another table as a foreign key. For example, in the relationships tables, like sampleRelationships, "sampleIDObj" takes the value of a sampleID. It is sampleID as a foreign key, but under a different name. This column says what value is actually linked. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

AI - Inhibition present but addressed

(flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

B - Trace levels of contamination

(flagB). Analytical result may be subject to "trace" levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

FI - Inhibition present and unaddressed

(flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

J - Weak signal extrapolation

(flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ND - Non-detect

(flagND). No amplification occurred in the reaction; non-detect. For the value of a non-detected measure, report the actual value even if it is below the limit of detection. The flag here ensures that it's recorded as a non-detect regardless. In instances where the original data doesn't record a value, but only has the flag, please populate the value field with either a 0 if dealing with variant percentages, and a 1 for all other purposes to further indicate a null result. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

UJ - Trace signal extrapolation

(flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., "trace" signal observed); the reported value is based on the extrapolation of the standard curve in the non-linear region. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

UQ - Unquantifiable

(flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Flavivirus (West Nile, Dengue, Zika) Group

(flavivirusGrp). A group of measures/methods related to flaviviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

anyCompartmentSet *Group:* flavivirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

FLiRT/SLip Variant Group

(flirtSLipGrp). The group for measures and methods pertaining to the FLiRT and SLip variants of SARS-CoV-2. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

FLiRT Variants

(flirtV). FLiRT is the name given to an entire family of COVID-19 subvariants that are gaining dominance. They've evolved from the JN.1 subvariant. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Float data type

(float). The data type for float data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Flocculation

(floc). The process of aggregating suspended particles into larger clusters (flocs) using coagulants to aid in sedimentation or filtration. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Flow-normalized mean

(floMean). Mean measure normalized to wastewater flow. Mostly used for reporting specific alleles (N1, N2, E, etc.) *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal

Maximum Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Floor

(floor). Floor of a building or room. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Flow rate

(floRate). Wastewater volumetric flow rate at the sample collection location over the 24-hr period during which the sample was collected. If only an instantaneous flow measurement is available, it may be reported in units of million gallons per day. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* flowClass *Nomenclature:* flowClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* flowUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Flow proportional 24hr sample depreciated

(flow24hDep). A flow proportional 24-hour composite sample generally collected by an autosampler. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Flow class

(flowClass). Measures and methods related to flow. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* naGroup *Class:* flowClass *Nomenclature:* flowClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* flowUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Flow meters

(flowInst). Flow meter instruements; used to measure wastewater flow rates to enable standardization of sample data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Flow proportional sample

(flowPr). A flow proportional composite sample generally collected by an autosampler. Use collectionPeriod to describe how many hours the sample was taken. The volume of wastewater taken is proportional to the flow rate flowing at each instant of sampling. This is also called constant time, variable volume (CTVV). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Flow Standarized

(flowStand). This data treatment standardizes the measurement value to flow rates. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Volume flow rate unit set

(flowUnitSet). Unit set for volume flow measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* flowUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Flow volume

(flowVol). Volume of influent. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* flowClass *Nomenclature:* flowClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* flowUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Influenza virus measure

(flu). General influenza virus measure This measure should only be used if there is no other influenza virus measure. See groupID = virusMisc. Use a note to describe the specific measure used. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* MONDO:0005812 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet

Reference Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Influenza A virus

(fluA). Influenza A virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Influenza virus A1

(fluA1). Influenza virus A1 type *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Influenza virus A1 and A2 combined

(fluA1A2c). Measure of influenza virus A1 and A2 combined, usually due to single fluorescence channel. *Part Type:* measurements *Domain:*

bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

influenza virus A2

(fluA2). influenza virus A2 type *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Influenza A Virus Group

(fluAGrp). A group of measures/methods related to Influenza A viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Influenza virus B

(fluB). Influenza virus B type *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluBGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Influenza B Virus Group

(fluBGrp). A group of measures/methods related to Influenza B viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluBGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Influenza Virus General Group

(fluGrp). A group of measures/methods related to general influenza viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA

Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Influenza A H5 hemagglutinin gene

(fluH5hema). Measure of the H5 hemagglutinin gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Influenza A M gene

(fluIAVm). A measure of the M gene found in Influenza A viruses (IAV). The virus has segmented RNA genome and 7th segment, M gene, encodes 2 proteins. M1 is a matrix protein and M2 is a membrane protein. The M gene may be involved in determining host tropism. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* https://virologyj.biomedcentral.com/articles/10.1186/1743-422X-6-67#:~:text=The%20M%20gene%20of%20all%20known%20human%20influenza%20A%20virus *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Fluidigm digital PCR

(fluiDpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Influenza A N1 neuraminidase gene

(fluN1neur). Measure of the N1 neuraminidase gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Flye

(flye). A sequencing software that is an assembler for long-read data, particularly effective on nanopore sequencing data. *Part Type:* cate-

gories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/fenderglass/Flye *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

First Nation Territory/Métis Settlement-level Aggregation at Site

(fnmiLevel). Specifies that a sewershed/site represents the entirety of a First Nations territory or reservation, or a Métis settlement. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Formazin nephelometric unit

(fnu). formazin nephelometric unit (FNU) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Foggy

(foggy). Qualitative category for the weather measure, specifying a foggy or hazy day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Feet

(foot). foot (ft) *Part Type:* units *Domain:* phy *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Fqtrim

(fqtrim). A sequencing data processing fast tool for adapter removal, quality trimming, and quality control. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ccb.jhu.edu/software/fqtrim/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:*

NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Fraction analyzed

(fraction). Fraction of the sample that is analyzed. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* fractionSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Fraction input (wide table)

(fractionInput). The partID for the fraction being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* fractionSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Fraction name (wide table)

(fractionName). The fraction analyzed referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* fractionSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sample fraction set

(fractionSet). set for the fraction of the sample (solid, liquid, etc.). *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* fractionSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

FRCbam

(frcBam). A QC pipeline tool for sequencing data that assesses read quality and genome assembly quality metrics for high-throughput data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/vezzi/FRC_align *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Freyja Script

(freyja). Freyja Script for sequencing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/andersen-lab/Freyja *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

F-Specific RNA bacteriophages

(fRNABact). A measure for amount of F-Specific RNA bacteriophages. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

F+ RNA coliphage

(fRNAColi). F+ RNA coliphage *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:*

seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

F-Specific RNA bacteriophages, G2

(frnaG2). A measure for amount of G2 F-Specific RNA bacteriophages. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample frozen

(frozen). Sample was frozen before analysis or processing *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Field sample temperature

(fst). Temperature that the sample is stored at while it is being sampled. This field is mainly relevant for composite samples which are either kept at ambient temperature or refrigerated while being sampled. *Part Type:*

measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Francisella tularensis

(fTularensis). Francisella tularensis *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tularemiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Full dictionary sheets set

(fullDictionarySheetSet). Worksheets in the full Excel dictionary. The full dictionary is 'ODM_full-dictionary.xlxs *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Funder contact ID

(funderCont). A unique identifier for a funder. Use Contact ID to populate this field, and the organizations table to describe contact information and other details for the data custodian. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Funding agency ID

(funderID). The funding agency of the dataset. Use Organization ID to populate this field, and the organizations table to describe contact information and other details for the funding agency. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Giardia 18S rRNA

(g18s). The 18S ribosomal RNA (18S rRNA) gene in Giardia is a primary genetic target used for detecting, identifying, and classifying the microscopic intestinal parasite responsible for giardiasis. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

anyCompartmentSet *Group:* giardiaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

g215c delta-variant gene target

(g215c). g215c delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-CompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

g339d omicron-variant gene target

(g339d). g339d omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-CompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

g496s omicron-variant gene target

(g496s). g496s omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

g662s delta-variant gene target

(g662s). g662s delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Gamma

(gam). P.1 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:*

seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Gammaretrovirus

(gammaretro). Gammaretrovirus is a genus in the Retroviridae family. Example species are the murine leukemia virus and the feline leukemia virus. They cause various sarcomas, leukemias and immune deficiencies in mammals, reptiles and birds. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* gammaretroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Gammaretrovirus Group

(gammaretroGrp). A group of measures/methods related to gammaretroviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* gammaretroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Gas class

(gas). Measures and methods relating to gas and gases. *Part Type:* classes *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* gas *Nomenclature:* gas *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* dissGasUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Gaussian distribution stanrdized/Normalized

(gauss). Standardize the data to a gaussian/normal distribution, such that the data have a mean of zero and a standard deviation of one. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gene copies

(gc). Gene or variant copies *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per copy of crAssphage

(gcCrA). Gene or variant copies per copy of crAssphage. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per day

(gcDay). Unit of measurement of the number of gene copies per day. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

gene copies per day per 100,000 people

(gcDay100k). The unit for measures reflecting the gene copies per day per 100,000 people in the population. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies per gram solids

(gCGS). Gene or variant copies per gram solids. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per L

(gcL). Gene or variant copies per litre. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per mL

(gcMl). Gene or variant copies per millilitre of solution. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per millilitre per 100,000 people

(gcMl100k). Unit of measurement of the number of gene copies per millilitre per 100,000 people. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gene copies per PMMoV copy

(gcPpmov). Gene or variant copies per copy of PMMoV. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per Reaction

(gcRx). Gene or variant copies per reaction in PCR *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Giardia duodenalis

(gDuodenalis). A protozoan parasite that causes anthroponotic or zoonotic diarrheal disease which can be opportunistic or affect healthy, immunocompetent individuals. Giardia duodenalis is the one commonly described type of Giardia, that is found in mammals including humans. This species complex comprise eight assemblages *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* giardiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

GEM Mapper

(gemMapper). GEM Mapper. A specialized read mapper. High-speed and accurate alignment tool for short reads. Best for: Genomic applications with short reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* Bio.tools: https://bio.tools/gem3 BioinformaticsHome: https://bioinformaticshome.com/tools/rna-seq/descriptions/GEMMapper.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

GenBank Archives

(genBank). GenBank Archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ncbi.nlm.nih.gov/genbank/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

genome completeness

(genComplete). The percentage of expected genes identified in the genome being sequenced. Missing genes indicate missing genomic regions (incompleteness) in the data. Provide the genome completeness as a percent (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum*

Value: 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Geneious

(geneious). Sequencing software that is popular for sequence assembly, alignment, and consensus sequence generation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.geneious.com/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Genetics unit set

(geneticUnitSet). Unit set for genetic-related measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

General missingness set

(genMissingnessSet). The general set for missingness values. *Part Type:* missingnessSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:*

naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

GenoTyphi

(genoTyphi). GenoTyphi. Focus: Specific MLST and serotyping for Salmonella Typhi. Applications: Outbreak investigations and epidemiology. Features: Highly specialized for typhoidal Salmonella. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/typhoidgenomics/genotyphi *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Generic quality flag set

(genQualitySet). A quality set to specify any generic quality concerns about a measure or sample. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

European Petroleum Survey Group Coordinates

(geoEPSG). The unique EPSG code specifying a given geospatial area. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Latitude

(geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721) *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* -90 *Maximum Value:* 90 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Longitude

(geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000) *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* -180 *Maximum Value:* 180 *Minimum Length:*

NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Geographical Reference Missingness Set

(geoRefMissingnessSet). A missingness set for field populated by the geographical reference tables (countries, zones) Used for fields populated by geographical reference tables to avoid confusion of NA and nr as missingness indicators, vs. legitimate ISO country codes. *Part Type:* missingnessSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Type of geography

(geoType). Type of geography that is represented by the polygon. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* geoTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Geographic set

(geoTypeSet). set for different type of geographic components. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* geoTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Well-known text

(geoWKT). Well-known text of the polygon *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 3.0.1.

GNU Free Documentation License v1.3

(gfdl13). The licensing for the measure or data set is managed under the GNU Free Documentation License v1.3. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/gfdl-1.3/ *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Giardia Group

(giardiaGrp). A group of measures/methods related to Giardia. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* giardiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Global Initiative on Sharing All Influenza Data (GISAID) archives

(gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://gisaid.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

GitHub

(github). GitHub external data storage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gram per kilogram

(gkg). gram per kilogram (g/kg) *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gram per liter

(gL). gram per liter (g/L) *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

10% Glycerol Solution

(glycerol10). 10% Glycerol Solution - Common cryoprotectant for bacterial and viral storage in environmental samples. *Part Type:* categories *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gram per cubic metre

(gm3). Density unit. Used for absolute humidity and other measures. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

GMAP

(gmap). GMAP. A specialized read mapper. A long-read aligner for genomic mapping. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://research-pub.gene.com/gmap/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Geometric mean

(gmn). Geometric mean. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Nitrogen per total solids

(gNgTS). nitrogen per total solids (gN/gTS) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gonococcus Group

(gonococcusGrp). A group of measures/methods related to gonococcus bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* gonococcusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Government agency

(govt). The category of organization type used for government agencies, programs, or crown-owned bodies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Grams per total solids

(gPergTS). Grams per total solids (g/gTS) *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

GNU General Public License v2.0

(gpl20). The licensing for the measure or data set is managed under the GNU General Public License v2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/gpl-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

GNU General Public License v3.0

(gpl30). The licensing for the measure or data set is managed under the GNU General Public License v3.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/gpl-3.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Orthophosphate per total solids

(gPO43gTS). orthophosphate per total solids (gPO43–/gTS) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Orthophosphate as phosphorus per total solids

(gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Grab samplers

(grabInst). Grab sampler instruments; manually collect a single sample at a point in time. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Grams

(grams). A unit of mass or weight. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Gram stain

(gramSt). After the sample is taken, the Gram stain is colored purple. Then, a solvent is added to the stain. When the solvent combines with bacteria in a sample, the bacteria will either stay purple or turn pink or red. If the bacteria remain purple, they are Gram-positive. If the bacteria turn pink or red, they are Gram-negative. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* bactMisc *Class:* bactFung *Nomenclature:* bactFung *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

GraphMap

(graphmap). GraphMap. A long-read specific mapper. Long-read aligner optimized for highly error-prone reads. Best for: De novo assemblies using long-read data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/isovic/graphmap *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gravity settling

(graSet). Describes solid separation from a wastewater sample where the sample material is allowed to settle by gravity, and then separated. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Grab sample

(grb). A single large representative grab sample. If the sample was collected over a series of hours or is a composite sammple, please use partID = comp *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Grit chamber

(gritCham). A sedimentation basin in wastewater treatment that removes heavy, inorganic particles (e.g., sand, gravel) before biological treatment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501467 *Category*

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Gromstole 1.0 Script

(gromstole). Gromstole 1.0 Script for sequencing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/PoonLab/gromstole *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Group

(group). Unique identifier for a group of measures. Mostly applicable for measures, methods, units, and aggregations. A collection of related measures. For example, SARS-CoV-2 is a group. Within the SARS-CoV-2 group, there are measure classes tht include RNA alleles (N1, N2, E, etc.), mutations, (E484K0), an entire sequence, viral proteins, etc. Currently groups are used for measures only. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* groups *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Groups

(groups). A collection of related measures. Used primary to group measurements and methods, this helps pare down the drop down list for a given measurement or methods. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Growth in enrichment broth

(growBroth). The selective cultivation of microorganisms in a nutrient-rich liquid medium to increase their concentration before analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* bactFung *Nomenclature:* bactFung *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Ground water

(grWa). Underground water which is located in pore spaces found in rock or unconsolidated deposits such as soil, clay, or gravel. *Part Type:*

categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Genome Sequence Archive (GSA)

(gsa). Genome Sequence Archive (GSA). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ngdc.cncb.ac.cn/gsa/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

GSNAP

(gsnap). GSNAP. A specialized read mapper. A splice-aware aligner for RNA-seq reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://research-pub.gene.com/gmap/ (GSNAP suite) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Guanidine Thiocyanate

(gt). A buffer solution/medium that serves as a strong preservative for viral RNA, commonly used in molecular biology for RNA preservation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Genomic Target Enrichment

(gte). The molecular technique used to selectively capture and amplify specific regions of interest from a genome. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* gteSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Genomic Target Enrichment Methods Set

(gteSet). The set for valid inputs for the Genomic Target Enrichment method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* gteSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

H5N1 avian influenza A virus (IAV)

(h5n1). General measurement for the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human mastadenoviruses (HAdVs)

(hadv). Human mastadenoviruses (HAdVs) are non-enveloped, double-stranded icosahedral DNA viruses, approximately 90–100 nm in diameter, with fibre projections on each of the 12 vertices. The genome is approximately 30–35 kilobases in length and encodes more than 30 structural and non-structural proteins. HAdV belongs to the genus Mastadenovirus, one of five genera within the Adenoviridae family. Within Mastadenovirus, seven known groups have been identified (A-G), which can be further classified into 54 serotypes. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:*

seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group A

(hadvA). Group A of the human mastadenovirus genus (HAdV-A). Includes serotypes 12, 18, and 31. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group B

(hadvB). Group B of the human mastadenovirus genus (HAdV-B). Includes serotypes 3, and 16. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group C

(hadvC). Group C of the human mastadenovirus genus (HAdV-C). Includes serotypes 1, 2, 5, and 6. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group D

(hadvD). Group D of the human mastadenovirus genus (HAdV-D). Includes serotypes 8, 17, 19, 23, 36, 51, and 58. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group E

(hadvE). Group E of the human mastadenovirus genus (HAdV-E). Includes serotype 4. *Part Type:* measurements *Domain:* bio *Speciment*

ID: saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group F

(hadvF). Group F of the human mastadenovirus genus (HAdV-F). Includes serotypes 40 and 41. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Haemophilus Group

(haemophilusGrp). A group of measures/methods related to haemophilus bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* haemophilusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

See Header for Aggregation

(hAg). An indicator to show in a wide-name that aggregation information is located in a different column. Not a valid value for aggregation in the standard long-format. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human Aichi virus (AiV)

(hAiV). Viral strain of Aichivirus A known to infect humans, typically of three known genotypes: A, B, or C. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* aichivAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) Genotype A

(hAiVGA). Viral strain of Aichivirus A known to infect humans of genotypes A. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* aichivAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) Genotype B

(hAiVGB). Viral strain of Aichivirus A known to infect humans of genotypes B. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* aichivAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) Genotype C

(hAiVGC). Viral strain of Aichivirus A known to infect humans of genotypes C. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* aichivAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:*

NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Hand hygiene advisory

(handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Orthohantavirus Group

(hantaGrp). A group of measures/methods related to Orthohantaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human bocavirus (HBoV)

(hbov). Human bocavirus (HBoV) is the name given to all viruses in the genus Bocaparvovirus of virus family Parvoviridae that are known to infect humans. Some of these viruses cause human disease. HBoV1 is strongly implicated in causing some cases of lower respiratory tract infection, especially in young children, and several of the viruses have been linked to gastroenteritis, although the full clinical role of this emerging infectious disease remains to be elucidated. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bocaparvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Hank's Balanced Salt Solution (HBSS)

(hbss). Hank's Balanced Salt Solution (HBSS) - Nutrient-rich buffer that maintains cell and microbial integrity in samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Healthcare activity

(hcAct). Healthcare activity occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Healthcare facility

(hcf). A building for the provision of healthcare, not otherwise specified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Compartment

(hCo). A indicator for wide-names that the compartment information is stored in a separate column. Not a valid value for compartment in the standard long-format. *Part Type:* compartments *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* wideCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Haemophilus ducreyi

(hDucreyi). Haemophilus ducreyi *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* haemophilusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Header

(header). Header for a table. Also known as a table variable or entiy relationship 'attribute'. Header is the top row or the variable name in a table. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Health administration or planning agency

(healthAdm). Health adminstrative or planning organization. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Health Region for a Site

(healthRegion). A free-text variable for listing the health region for a given site. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Heat inactivated sars-cov-2 virus spike target

(heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 hel gene (nsp13)

(hel). SARS-CoV-2 hel gene (nsp13) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100169 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Hepatitis A

(hepA). Hepatitis A *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis B

(hepB). Hepatitis B *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum*

Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis C

(hepC). Hepatitis C *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis E

(hepE). Hepatitis E *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

hep g armored rna

(hepGRna). Measure of the amount Hepatitis G Armored RNA. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

hep g armored rna spike target

(hepGRnaMat). Hepatitis G armored RNA is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Hepatitis Group

(hepGrp). A group of measures/methods related to hepatitis viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Herpes Virus Group

(herpesGrp). A group of measures/methods related to herpes viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* herpesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

HF183 Bacteriodes 16S

(hf183). Human-Specific HF183 Bacteriodes 16S rRNA *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bacteroidesGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

See Header for Fraction Analyzed

(hFr). An indicator in wide-names to show that information on the fraction analyzed in found under a separate header. Not a valid value for fraction analyzed in the standard long-format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Hantavirus hemorrhagic fever with renal syndrome (HFRS)

(hfrs). Hantavirus hemorrhagic fever with renal syndrome (HFRS) is a hemorrhagic fever caused by hantavirus infection. Symptoms usually occur 2 weeks after exposure to the hantavirus and come in five distinct clinical stages: febrile (toxic), hypotensive, low urine production (oliguric), high urine production (diuretic), and recovery. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Roseolovirus (Human Herpesvirus-6)

(hhv6). Roseolovirus refers to a group of viruses, including HHV-6A and HHV-6B, that are characterized by their ability to cause various diseases, persist in latency within different cell types, and integrate into the human genome. Their detection does not necessarily indicate causation of disease, highlighting the need for careful interpretation of diagnostic results within clinical contexts. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hhvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale

Quality Set: pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Herpesvirus-6A (HHV-6A)

(hhv6A). HHV-6A is a roseolovirus that has been described as more neurovirulent, and as such is more frequently found in patients with neuroinflammatory diseases such as multiple sclerosis. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hhvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Herpesvirus-6B (HHV-6B)

(hhv6B). HHV-6B is a roseolovirus and the cause of the common childhood illness exanthema subitum (also known as roseola infantum or sixth disease). It is passed on from child to child. It is uncommon for adults to contract this disease as most people have had it by kindergarten, and once contracted, immunity arises and prevents future reinfection. Additionally, HHV-6B reactivation is common in transplant recipients, which can cause several clinical manifestations such as encephalitis, bone marrow suppression, and pneumonitis. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hhvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale

Quality Set: pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Roseolovirus (Human Herpesvirus-6) Group

(hhvGrp). A group of measures/methods related to roseoloviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hhvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

5-hydroxyindoleacetic acid (5-HIAA)

(hiaa5). A serotonin metaboliteused for normalizing wastewater surveillance signal. Analysis of 5-HIAA is done in clinical settings to assess the possibility of carcinoid syndorme in patients, and used in wastewater analysis to estimate human population numbers. Studies have shown that 5-HIAA can be quanitified in samples from WWTPs, and that measured quantities of this molecule have a positive correlation with the population calculated using hydrochemical parameters, and are also correlated well with the census population measures. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness*

Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

High severity

(high). Indicates a very sever quality issue, likely meaning the data should not be reported. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Haemophilus influenzae

(hInfluenzae). Haemophilus influenzae *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* haemophilusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

HISAT2

(hisat2). HISAT2. A general-purpose read mapper. Successor to TopHat, optimized for RNA-seq data with splicing awareness. Best for: Large-scale

RNA-seq experiments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://daehwankimlab.github.io/hisat2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Human Immunodeficiency Virus (HIV)

(hiv). Human Immunodeficiency Virus (HIV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hivGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

HIV Group

(hivGrp). A group of measures/methods related to Human Immunodeficiency Virus (HIV). Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hivGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sewer Network Health Region

(hlthReg). Health region served by the sewer network *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Hand Measurement

(hma). Handheld measurement analyzer. A handheld measurement analyzer. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

See Header for Measure

(hMe). An indicator to show in a wide-name that measure information is located in a different column. Not a valid value for measure in the standard long-format. *Part Type:* measurements *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human Metapneumovirus (HMPV)

(hmpv). Human Metapneumovirus (HMPV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Hollow fiber dead end ultrafiltration

(hollowFiberUF). Hollow fiber dead end ultrafiltration *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Stay-at-home order

(homeOrder). A directive requiring people to remain at home except for essential activities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Horizontal grab sampling

(horGrb). Intrument type is a grab sampler in which the container for the sample is mounted on the end of a rod, which is suitable for collecting discharge from a pipe or truck. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

General Hospital Admissions

(hosa). Hospital admissions or patients newly admitted to hospital. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Hospital Census

(hosc). Hospital census or the number of people admitted with an ailment. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Hospital

(hosptl). Hospital *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Version of Data Hosting Platform/Repository

(hostVersion). The version of the data repository or hosting platform being used. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Holding tank wastewater depreciated

(hoTaWa). Wastewater from a holding tank, such as from an airplane or ship Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Hotel or motel

(hotel). A building which 1) contains multiple dwellings of pre-furnished accomodation and 2) is rented for lodging on a short term and/or longer-term basis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501347 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Hours

(hours). A unit for indicating a length of time in hours. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

human parvovirus B19 (B19V)

(hParvB19V). Human parvovirus B19 is defined as a nonenveloped, single-stranded DNA virus belonging to the Erythrovirus genus of the Parvoviridae family, which primarily infects humans and can cause a variety of syndromes, including erythema infectiosum, arthropathy, and complications such as aplastic anemia and fetal hydrops. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* erythroparvoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Parechovirus (PeV)

(hpev). Human parechovirus (HPeV; family Picornaviridae, genus Parechovirus) is a nonenveloped virus with a positive-sense single-stranded RNA genome that infects humans. HPeV strains are currently subdivided

into 16 genotypes (i.e., HPeV1 to HPeV16), and HPeV1 and HPeV3 are the genotypes mostly causing gastroenteritis, respiratory syndrome, and febrile illness mainly in young children. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* parechoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Parechovirus-1 (HPeV1)

(hpev1). Human parechovirus (HPeV) of the genotype 1 (HPeV1), capable of causing gastroenteritis, respiratory syndrome, and febrile illness in humans. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* parechoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Parechovirus-3 (HPeV3)

(hpev3). Human parechovirus (HPeV) of the genotype 3 (HPeV3), capable of causing gastroenteritis, respiratory syndrome, and febrile illness in humans. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* parechoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set*

Parts

ID: NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Parainfluenza Virus (HPIV)

(hpiv). Human Parainfluenza Virus (HPIV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* parafluGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

High priority pathogen

(hpp). A resistant organism of serious concern, requiring urgent attention. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Hantavirus pulmonary syndrome (HPS)

(hps). Hantavirus pulmonary syndrome (HPS), also called hantavirus cardiopulmonary syndrome (HCPS), is a severe respiratory disease caused by hantavirus infection. The main features of illness are microvascular leakage and acute respiratory distress syndrome. Symptoms occur anywhere from one to eight weeks after exposure to the virus and come in three distinct phases. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Human Papiloma Virus (HPV)

(hpv). Human Papiloma Virus (HPV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* papilomavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV)

(hrv). Human Rhinovirus (HRV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

Group: hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) A

(hrvA). Human Rhinovirus (HRV) A *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) B

(hrvB). Human Rhinovirus (HRV) B *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) C

(hrvC). Human Rhinovirus (HRV) C *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Rhinovirus Group

(hrvGrp). A group of measures/methods related to rhinoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

See Header for Specimen

(hSp). An indicator to show in a wide-name that specimen information is located in a different column. Not a valid value for specimen in the standard long-format. *Part Type:* specimens *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Herpes Simplex Virus

(hsv). Herpes Simplex Virus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* herpesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Hantaan virus (HTNV) hantavirus

(htnv). Hantaan virus (HTNV) is the main cause of hemorrhagic fever with renal syndrome (HFRS) in East Asia. Hantaan virus is transmitted by the striped field mouse (Apodemus agrarius). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Holding tank wastewater

(htSam). Wastewater sampled from a holding tank, such as from an airplane or ship *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Holding tank

(htSite). Holding tank *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Human compartment

(hum). A measure or observation made about a human. *Part Type:* compartments *Domain:* bio *Speciment ID:* anySpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Human compartment set

(humanCompartmentSet). A compartment set for measures and methods in the human compartment. *Part Type:* compartmentSets *Domain:* bio *Speciment ID:* anySpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Humidity class

(humid). Measures and methods related to humidity. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* airCompartmentSet *Group:* naGroup *Class:* humid *Nomenclature:* humid *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* humidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

General Humidity Unit Set

(humidUnitSet). A unit set for all types of humidity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:*

humidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

See Header for Unit

(hUn). An indicator to show in a wide-name that unit information is located in a different column. Not a valid value for unit in the standard long-format. *Part Type:* units *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 3.0.1.

Animal husbandry

(husb). Animal husbandry occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Hybrid Selection Method

(hySel). Selection by hybridization in array or solution for genomic target enrichment. *Part Type:* categories *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

i1566v omicron-variant gene target

(i1566v). i1566v omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

i3758v omicron-variant gene target

(i3758v). i3758v omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

i82t delta-variant gene target

(i82t). i82t delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Ibuprofen

(ibu). Ibuprofen (usually measured as a human fecal chemical indicator) *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

International Classification of Diseases

(icd). Classification system for diseases in humans. *Part Type:* nomenclatures *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* disease *Nomenclature:* disease *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Intensive care unit patients

(icu). Units for describing a population measure of patients who are in intensive care due to a given cause. Unit for a population or disease measure to explain population-level clinical effects. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

IDBA-UD

(idbaUD). A sequencing software that is an iIterative assembler optimized for metagenomics and complex genomic datasets. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/loneknightpy/idba *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Illumina DNA Prep with Enrichment

(illuminaDNAprep). Illumina DNA Prep with Enrichment by Illumina. A library prep kit that integrates DNA library prep with enrichment for target regions, ideal for targeted sequencing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Instrument table Shorthand

(in). The abbreviated short name used to reference the The table that contains information about instruments. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Inch

(inch). inch (in) *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum*

Parts

Value: 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Increased surveillance

(incSurv). Intensified efforts to monitor disease trends or case counts. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Index

(index). Index number in case the measurement was taken multiple times. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Industrial plant

(indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occaisonally services, and making them into products. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Industrial activity

(indus). Industrial activity occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Industrial input

(indusIn). Percentage of total wastewater input coming from industrial sources. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Influent equilibration

(influEqui). Binary indicator for whether a site stores influent wastewater prior to treatment to equilibrate flow rates. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Influent pump station

(infPump). A facility that ransports raw wastewater from collection systems to treatment plants. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501465 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Inhibition set

(inhibitionSet). Category set for inhibition methods. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* inhibitionSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical

Missingness Set: NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Inhibition measure

(inhibMe). Parameter to report whether or not inhibition was detected in the sample. Detected = TRUE, not detected = FALSE. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Inhibition method

(inhibMeth). Description of the method used to evaluate molecular inhibition. Description of the inhibition parameters. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* inhibitionSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Innovaprep ultrafiltration

(innovaprepUF). Innovaprep ultrafiltration *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Input

(input). Input for a table. Indicates if a part can be used in a table. "Input" is used to indicate if a part can be used as an entry in a table (something with partType = table). For example, covN1 is a specific measure that can be entered in the measureID field of the measures table. Therefore, covN1 is has a value "input" in the measures column in the parts list. ODM users can generate their own custom template by modifying using the value "input" for only the parts that are applicable for their program. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant ins214epe Insertion

(ins214epe). Omicron Variant ins214epe Insertion mutation. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment*

Set: anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

International Nucleotide Sequence Database Collaboration (INSDC) Archives

(insdc). International Nucleotide Sequence Database Collaboration (INSDC) Archives - often includes ENA, NCBI, or DDBJ inputs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.insdc.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Institution-level Surveillance

(instituLev). Surveillance is done at the level of an entire insitution. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Instrument ID

(instrumentID). A unique identifier for an instrument. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Instrument table

(instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. in *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Instruments table column order

(instrumentsOrder). Specifies the order of the columns in the Instruments table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum*

Value: 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Instrutment table required headers

(instrumentsRequired). Specifies the columns required in the Instruments table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Other instrument

(instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. An other type of measurement instrument. Add description to notes. See documentation for how to request new instruments added to the dictionary. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Instrument Type

(insType). Type of instrument used to perform the measurement. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Com-*

partment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* insTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Describe other instrument type, if applicable

(insTypeOth). Description of the instrument in case it is not listed in instrumentType. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Instrument set

(insTypeSet). List of instruments that are used for measures and methods *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* insTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Integrase Anti-microbial resistance Group

(intAMRGrp). The group for measures and methods pertaining to integrase-related anti-microbial resistance. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* intAMRGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Integer data type

(integer). The data type for integers. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Integrase Class I gene target

(integraseCl1). Integrase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* intAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal

Minimum Length: NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Intercept

(inter). Intercept value of the calibration curve. Used for storing calibration curve information, potentially also applicable for other curve types. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Internal reference

(internalRef). Reference an internal (i.e. private) database within the user's own organization. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

International travel hub surveillance

(internatSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to international

travel. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Combined ip2 and ip4 sars-cov-2 gene target

(ip2ip4). Combined ip2 and ip4 sars-cov-2 gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

IQ-TREE Software

(iqTree). A lineage or clade analysis software tool for constructing phylogenetic trees with clade support. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://iqtree.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ISC

(isc). The licensing for the measure or data set is managed under the ISC license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/isc/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

ISO639-1

(iso6391). The first part of the ISO 639 series of international standards for language codes. Part 1 covers the registration of two-letter codes. There are 183 two-letter codes registered as of June 2021. The registered codes cover the world's major languages. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

ISO639-2B

(iso6392B). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter

(ISO 639-1) codes where they exist. The 'B' specifies the bibliographic code (B code). Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 3.0.0.

ISO639-2T

(iso6392T). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'T' specifies the terminological code (T code). Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

ISO639-3

(iso6393). A set of international standards that lists short codes for language names. ISO 639-3 extends the ISO 639-2 alpha-3 codes with an aim to cover all known natural languages. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup

Class: naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 3.0.0.

ISO639-6

(iso6396). A set of international standards that lists short codes for language names. ISO 639-6 builds off ISO639-3 with the use of four-letter codes, and allowing users to differenciate between variants of languages and language families, such as histroical vs. revived versions of languages. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 3.0.0.

ISO 3166-1 alpha-2 country code

(isoCode). The ISO 3166-1 alpha-2 code, a two-letter country code which is also used to create the ISO 3166-2 country subdivision code and the Internet country code top-level domain. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:*

genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 2 *Maximum Length:* 2 *Part Status:* active. First released: 2.1.0. Last updated: 3.0.0.

ISO 3166-1 alpha-3 country code

(isoCodeX). The ISO 3166-1 alpha-3 code, a three-letter country code which may allow a better visual association between the code and the country names than the 3166-1 alpha-2 code. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 3 *Maximum Length:* 3 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

ISO 3166-2 code for country sub-domain

(isoZone). The ISO 3166-2 codes for the names of the principal subdivisions (e.g., provinces, states, departments, regions) of all countries coded in ISO 3166-1. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 4 *Maximum Length:* 6 *Part Status:* active. First released: 2.1.0. Last updated: 3.0.0.

iVar

(iVar). A sequencing data processing application that is designed for viral amplicon data, removes primers and can trim low-quality bases. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/andersen-lab/ivar *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

JN.1.7 Variant

(jn17V). The JN.1.7 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

JN.1 Variant

(jn1V). The JN.1 variant is a subvariant of Omicron variant BA.2.86, and contains several mutations that are associated with escape from vaccine-mediated immune protection. The source of the FLiRT variants of SARS-CoV-2. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:*

variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

k856r omicron-variant gene target

(k856r). k856r omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

KAPA HyperPrep Kit

(kapaHyperPrep). KAPA HyperPrep Kit by Roche. An optimized library prep kit for high-quality libraries from low-input or degraded DNA, commonly used for Illumina platforms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Kaptive

(kaptive). Kaptive. Identifies capsular (K) serotypes in Klebsiella pneumoniae and related species using whole-genome sequence data. Useful for studying capsule diversity and epidemiology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* CLI: https://github.com/klebgenomics/Kaptive Web: https://kaptive-web.erc.monash.edu/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Kilogram per cubic meter

(kgm3). Kilogram per cubic meter (kg/m^3) *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Kilogram per second

(kgS). Kilograms per second. *Part Type:* units *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA

Minimum Value: 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Kilolitres

(kl). Kilolitres of volume *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Klebsiella Group

(klebsiellaGrp). A group of measures/methods related to klbsiella bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* klebsiellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Klebsiella pneumoniae

(klebsiellaPneu). Klebsiella pneumoniae *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* klebsiellaGrp *Class:* organism *Nomenclature:* organism *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

KneadData

(kneadData). A sequencing data processing pipeline for quality control, including trimming and host decontamination (uses Trimmomatic and Bowtie2). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://huttenhower.sph.harvard.edu/kneaddata/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Kobuvirus Group

(kobuGrp). A group of measures/methods related to kobuviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* kobuGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

KP.1.1 Variant

(kp11V). The KP.1.1 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

KP.1 Variant

(kp1V). The KP.1 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

KP.2 Variant

(kp2V). The KP.2 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness*

Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

KP.3.1.1 Variant

(kp311V). The KP.3.1.1 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

KP.3 Variant

(kp3V). The KP.3 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Kraken2

(kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. *Part Type:* categories *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ccb.jhu.edu/software/kraken2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Litres

(l). Litres of volume *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant l24s mutation

(l24s). Omicron Variant l24s mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

l452r delta-variant gene target

(l452r). l452r delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

L455S Mutation

(l455s). The FLiRT/SLip variant mutation L455S. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

l981f omicron-variant gene target

(l981f). l981f omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Language Look-up table Shorthand

(la). The abbreviated short name used to reference the Look up table for all languages, used to give structure to the translation table. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Laboratory

(lab). Laboratory for environmental testing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Lab ID default depricated

(labDefDep). Used as default when a new sample is created by this reporter. See ID in Lab table. Deprecated as of version 2, no defaults please specify. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Laboratory duplicate

(labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Label

(label). A human readable label of a part. Typically, a part label has no acrynomns (every word is spelled out). Equivalent to a LOINC common name. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Lab ID

(labID). Unique identifier for a laboratory. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.1.0.

Lachnospiraceae (Lachno3)

(lachno3). Human-associated bacteria in the family Lachnospiraceae (Lachno3), often used as microbial source tracking markers for human fecal pollution tracking in environmental waters. *Part Type:* measurements *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Low Average Genome Coverage

(lAGC). Average coverage of the genome is low/poor. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Lagoon system

(lagoon). Lagoon system for extensive wastewater treatment *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Lake, natural water body

(lake). Lake, natural water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Lambda

(lamba). C.37 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale

Quality Set: seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Land-based Transit Hub

(landTH). A transport hub is a place where passengers and cargo are exchanged between land-based vehicles and/or between land-based transport modes. Used when not greater detail can be provided *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Language ID

(lang). Language code for translation purposes. Specifies the langage for each translation, other than the default English. Uses the ISO-6393 code. Follow the ISO639-3 codes for now. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Language family

(langFam). Specifies the language family of a given language for translation and language tracking purposes. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Language name

(langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

National language script

(langScript). The language(s) and script(s) used for the country's capital endonyms. The scripts are listed in parenthesis, in the order of their appearance. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Language Look-up table

(languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. la *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Language table column order

(languagesOrder). Specifies the order of the columns in the Languages table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Language table required headers

(languagesRequired). Required headers in the Languages table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

LAST (Large-Scale Alignment and Search Tool)

(last). LAST (Large-Scale Alignment and Search Tool). A long-read specific mapper. Flexible tool for aligning long and error-prone reads. Best for: Comparative genomics with long reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://last.cbrc.jp/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Last edited

(lastEdited). The date the entry was last updated. Use lastEdited if an entry is updated. Leave lastEdited blank or 'NA' for the first entry. Updates can include additions or revisions of the entry for any reason. For example, a wastewater measure was repeated later with an improved method. You can revise the entry by updating the value and then adding the date the new measure was performed to 'lastEdited'. To ensure data

provenance, the best practice in this example is to generate a new entry with the same measureID as the original measureID. The original and new measures are kept in the database with a date in the 'lastEdited' field for the new entry but not the original one. Some databases may choose a delete-and-replace approach where the original entry is deleted and replaced by a new entry. In this approach, the 'lastEdited' field indicates the delete and replace occurred. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Last name of contact

(lastName). Specifies the last name of a given contact. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Last updated version

(lastUpdated). The version in which the part was last updated. Any change to the part of list will result in a change in the lastUpdated field to the dictionary version where the update occurred. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

LaTeX expression

(latExp). LaTeX expression used to generate formulas, symbols, etc. Mainly relevant for units. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Latrine

(latrine). A toilet or outhouse, especially a communal one in a camp or barracks. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

LB.1 Variant

(lb1V). The LB.1 variant of SARS-CoV-2,similar to other FLiRT variants but with an additional mutation. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Low breadth of coverage

(lBC). The percentage of the genome covered by reads (the breadth) is low. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory control sample duplicate

(lcsd). Known amounts of an analyte or representative compounds are added to a second “clean” matrix (lab water or clean sand) in laboratory. Duplicate of LCS *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Parts

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Litres per day

(lday). Unit of litres per day, usually for measuring flow. *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Low depth of coverage

(lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Leaked sample

(leaked). Sample leaked, some volume and material was lost. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Legionella

(legionella). Legionella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* legionellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Legionella Group

(legionellaGrp). A group of measures/methods related to legionella bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* legionellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum*

Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Lentivirus Group

(lentiGrp). A group of measures/methods related to lentiviruses, including viral vectors such as the Puro virus vector. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* lentiGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

<10 people

(less10). Fewer than 10 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

10 - 100 people

(less100). Between 10 and 100 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

10,000 - 100,000 people

(less100k). Between 10,000 and 100,000 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

1,000 - 10,000 people

(less10k). Between 1,000 and 10,000 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

100 - 1,000 people

(less1k). Between 100 and 1,000 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

100,000 - 1,000,000 people

(less1mil). Between 100,000 and 1,000,000 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

GNU Lesser General Public License v2.1

(lgpl21). The licensing for the measure or data set is managed under the GNU Lesser General Public License v2.1. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/lgpl-2.1/ *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

GNU Lesser General Public License v3.0

(lgpl30). The licensing for the measure or data set is managed under the GNU Lesser General Public License v3.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/lgpl-3.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Liter per hour

(lhour). liter per hour (L/h) *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Link

(li). Link to an external reference that describes the geometry of the polygon. Deprecated as of version 2, please avoid use. Use referenceLink

instead. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Library preparation instruments

(libPrepInst). Instruments for the preparation of sequencing libraries, e.g., automation platforms like the Illumina NeoPrep. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Library Preparation Kit

(libraryKit). The name of the DNA/RNA library preparation kit used to generate the library being sequenced. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* libraryKitSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Library Preparation Kit Set

(libraryKitSet). The valid set of categorical values for sequencing library preparation kits. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* libraryKitSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

License

(license). The license of a dataset. Specify the dataset's license name or provide a description of the license. Individual measures may possess their own licenses, which take precedence over the overall database license. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* licSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Data license set

(licSet). The set to describe valid categorical values for the licensing fields for measures or datasets. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: licSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ligase-Dependent Library Prep Kits

(ligaseDep). Ligase-Dependent Library Prep Kits by Lucigen/Epicentre. A library prep kit suitable for long-read applications and used with Illumina platforms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

LINEAGE Software

(lineage). LINEAGE - Tool for bacterial lineage analysis, often applied to genome sequences in epidemiology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Linear scale aggregation set

(linearAggrSet). The aggregation set that contains all aggregations that exist on the linear scale. *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Liquid fraction

(liq). Liquid fraction of a sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Liquid/Supernatant retained

(liquid). The liquid or supernatant is retained after solid separation/centrifugation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Liquid

(liquidMat). Material is liquid, ie. is a state of matter with a definite volume but no fixed shape, adapting to the shape of their container. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Listeria

(listeria). Listeria *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* listeriaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Listeria Group

(listeriaGrp). A group of measures/methods related to listeria bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* listeriaGrp *Class:* organism *Nomenclature:*

organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

List worksheet

(lists). Parts lists for template dropdowns and other documentation. Sheets or tabs for the ODM Excel dictionary include: all ERD tables (look-up tables and data entry tables) and additional supportig tables. *Part Type:* dictionarySupport *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

List set

(listSet). PartTypes that contain categories, sets, or lists. Used to generate documentation. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* airCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Liter per minute

(lmin). liter per minute (L/min) *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Limit of Blank (LOB)

(lob). The highest concentration of a target analyte (DNA or RNA) that can be expected in a blank sample (a sample with no target DNA/RNA) while still considering the sample as negative. Defines the upper limit of "noise" or background signal that should not be confused with a true positive. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Access to local ha

(localHA). If this is 'no', the, data will not be available to local health authorities. If missing, data will be available to local health authorities. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Lockdown

(lockdown). Broad restrictions on movement and activities within a region to control disease spread. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Limit of detection (LOD)

(lod). Limit of detection, ie. the minimum level of a genetic target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 3.0.0.

Limit of detection (LOD) - sewage

(lodSewa). Limit of detection, ie. the minimum level of a genetic target, for sewage samples. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

log10 gene copies per g

(log10cpG). Unit for log10 copies per gram *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

log10 gene copies per L

(log10cpL). Unit for log10 copies per litre *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum*

Length: NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

log10 gene copies per mL

(log10cpml). Unit for log10 copies per mililitre *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Log10 gene copies per 100 milliliter

(log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Log10 gene copies per nanogram total DNA

(log10gcngDNA). log10 gene copies per nanogram total DNA *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

log10 micrograms per g

(log10ugG). Unit for log10 micrograms per gram *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

log10 micrograms per L

(log10ugL). Unit for log10 micrograms per litre *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Logarithmic scale aggregation set

(logAggrSet). The aggregation set that contains all aggregations that exist on the logarithmic scale (rather than linear or qualitative). *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Longitudinal, repeat sampling surveillance program

(longSurv). A surveillance strategy in which an individual or site is selected to undergo repeat sampling over a defined period of time. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Dictionary tables

(lookup). Tables to describe and support the ODM dictionary. These tables hold information on sets, all parts, and support multiple languages and translations. The tables are updated by the ODM development team when a new ODM version is created. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Limit of quantification (LOQ)

(loq). Sample limit of quantification (LOQ) is defined as "the concentration of a target that can be quantified with an acceptable level of precision when present in a sample" (Ahmed et al., 2021). Limit of quantification (LOQ) for this method if one exists. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 3.0.0.

Low severity

(low). A marker for low severity *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Low Coverage of Characteristic Mutations

(lowCovMut). Low coverage of characteristic mutations. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Lower limit of a 95% confidence interval

(lowerCI95). Specifies the the lower limit of a 95% confidence interval. Should typically be linked to an upper limit, and some indication of data spread (ie. standard deviation), and a mean/median measure. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Low-quality Sequence

(lowQualSeq). Low-quality sequence. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Low Signal-to-Noise Ratio

(lowSNRatio). Low signal-to-noise ratio. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Low-volume sample

(lowVol). Sample is low-volume, but was run regardless. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

LP.8.1 Variant

(lp81V). The LP.8.1 variant of SARS-CoV-2, a Omicron subvariant of JN.1, and FLiRT variant. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Low Percent of Genome Captured

(lPGC). Only captured a small/low percentage of the genome. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Omicron Variant LPPA24S mutation

(lppa24s). Omicron Variant LPPA24S mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

LaTeX Project Public License v1.3c

(lppl13c). The licensing for the measure or data set is managed under the LaTeX Project Public License v1.3c. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://chooseallicense.com/licenses/lppl-1.3c/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Lactated Ringer's Solution

(lrs). A buffer solution/medium sometimes used in combination with other preservatives to stabilize microbial samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Liter per second

(lsec). liter per second (L/s) *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Long-term care facility

(ltcf). A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Long-term care - assisted living or retirement home

(ltcfAl). A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Other long-term care

(ltcfO). Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or assisted living facilities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Life technologies digital PCR

(ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

luminultra wastewater extraction kit

(luminWWExtract). luminultra wastewater extraction kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Lymphocryptovirus

(lymphocrypto). Lymphocryptovirus is a genus of viruses in the order Herpesvirales, in the family Orthoherpesviridae, in the subfamily Gamma-

herpesvirinae. This genus includes the human-infecting Epstein–Barr virus, as well as viruses that infect both Old World monkeys and New World monkeys. Also called gamma-1 herpesviruses, there are nine species in this genus. Diseases associated with this genus include: mononucleosis, Burkitt's lymphoma, and nasopharyngeal carcinoma. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* lymphocryptoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Lymphocryptovirus Group

(lymphocryptoGrp). A group of measures/methods related to lymphocryptoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* lymphocryptoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Lysis buffer

(lysi). Lysis buffer. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Cubic metres per day

(m3D). Cubic metres per day. *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Cubic metres per hour

(m3H). Cubic metres per hour. *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Cubic meter per minute

(m3min). cubic meter per minute (m^3/min) *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Cubic metres per second

(m3S). Cubic metre per second. *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

MAFFT

(mafft). Sequencing software that performs multiple sequence alignment, commonly used in consensus sequence generation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://mafft.cbrc.jp/alignment/software/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Magnetic nanobead binding

(magBead). The use of tiny, magnetized beads to selectively capture and isolate biological molecules (e.g., DNA, proteins) in a magnetic field. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Magnetic separation racks

(magInst). Magnetic separation rack instrument; may be used with magnetic beads for nucleic acid extraction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Plasmodium or Malaria Group

(malariaGrp). A group of measures/methods related to plasmodium parasites or malaria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* malariaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA

Reference Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Shopping mall

(mall). A large commercial complex with multiple retail stores, services, and restaurants. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501207 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Manual Composite Sample

(manComp). Specifies a composite sample where the sub-samples were collected manually. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Manufacturer

(manufacturer). Manufacturer of an instrument. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* na-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

MapSplice

(mapSplice). MapSplice. A specialized read mapper. Designed specifically for spliced alignment of RNA-seq reads. Best for: Transcriptomics with a focus on detecting splice junctions. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.netlab.uky.edu/p/bioinfo/MapSplice/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

mash Software

(mash). A lineage or clade analysis software tool for the clustering-based method of lineage and clade analysis, comparing large genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/marbl/Mash *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mask mandate

(maskMand). A legal requirement for individuals to wear masks in specified settings. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mask recommendation

(maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Human mastadenovirus Group

(mastadenoGrp). A group of measures/methods related to human mastadenoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet

Compartment Set: anyCompartmentSet *Group:* mastadenoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* https://www.sciencedirect.com/science/article/pii/S0048969719316912#s0075 *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Maryland Super Read Celera Assembler (MaSuRCA)

(masurca). A sequencing software that is a hybrid assembler that can integrate both short and long reads for high-quality assemblies, and large, complex genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/alekseyzimin/masurca *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample Material Characteristics

(matChar). A site measurement for describing the qualitative characteristics of the sample material in situ (ie. The material from which the sample is collected. *Part Type:* measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* matCharSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample Material Characteristics Set

(matCharSet). The set for recording the possible valid values for describing the sample material characteristics. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* matCharSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mate pair layout

(mateLay). Specifies the mate pair layout for a sequencing method. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Maximum length

(maxLength). The maximum length of the value of a part or measure. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Maximum value

(maxVal). Highest value in a range of values for a measure. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Maximum value part support

(maxValue). The maximum value of a part. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Concentration Factor

(mCF). Concentration Factor (CF) is the degree to which the concentration observed in the final qPCR assay volume has been magnified compared to concentration of the analyte in the original sample (see Box 2.1 Protocol).

Part Type: measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

MCR-1.1 Colistin-resistence gene target

(mcr11). The MCR-1.1 colistin anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* colAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Arithmetic mean

(me). Arithmetic mean. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Measurement group

(measGrp). A group of measures that cannot be otherwise categorized. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measles

(measles). Measles *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measlesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Measles Group

(measlesGrp). A group of measures/methods related to the measles virus. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measlesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum*

Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Other Measure

(measOth). Other measure, not otherwise specified in measures. Add description to categoryOther. *Part Type:* measurements *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* othAgg *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Measures quality set

(measQualitySet). A quality set for any measure, includes all the quality flag options for any measure. Used as an "any quality set" for measures, but excludes the sample quality flags to avoid confusion and data entry errors. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure

(measure). A measurement or observation of any substance including a biological, physical or chemical substance. An measurement is recorded from a specimen (i.e. a site, sample, person or population). Measures are organized into groups and classes (sub-groups). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* measurements *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Measure input (wide table)

(measureInput). The partID for the measure being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* measurements *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Measure license

(measureLic). Specifies the access and use licensing for a given single measurement. Populated by partID = licenseID *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass

Ontology Reference: NA *Category Set ID:* licSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measures

(measurements). The attribute to describe a part type of measures. All measures have 'partType' = "measure". mes *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 60 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure name (wide table)

(measureName). The measure referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* measurements *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 60 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Measure Report ID

(measureRepID). Unique identifier for a measurement. Report IDs cannot be repeated. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Measure report table

(measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. mr *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Measure set report set ID

(measureSetRepID). Unique identifier that links together a group of related measures. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure set report table

(measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or varients that are identified in a single sample. The short name for the table (partID) can be found in the instructions field. ms *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure sets table column order

(measureSetsOrder). Specifies the order of the columns in a Measure Sets table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure Set table required headers

(measureSetsRequired). Specifies the columns required in a Measure Sets table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measures table column order

(measuresOrder). Specifies the order of the columns in a Measures table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measures table required headers

(measuresRequired). Specifies the columns required in a Measures table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Meat processing plant

(meatPl). A processing plant for slaughtering, processing, packaging, labelling, handling, and storing of food animal carcasses, parts of carcasses, and meat products. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Median

(med). Median. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Molecular Evolutionary Genetics Analysis (MEGA)

(mega). Sequencing software that provides tools for sequence alignment and consensus sequence extraction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

naAggrScale *Quality Set:* NA *Reference Link:* https://www.megasoftware.net/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mega-bases or Mega-base-pairs

(megaB). A mega-base (Mb) or mega-base-pair (Mbp) is equal to one million base pairs (1,000,000 bp). It is commonly used to describe the size of genomes or large DNA sequences. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

MEGAHIT

(megahit). A sequencing software that is a fast and memory-efficient assembler for large metagenomic datasets. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/voutcn/megahit *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

MEGARes database

(megares). A comprehensive database of antimicrobial resistance genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* megares.meglab.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

membrane filtration with addition of mgcl3

(memMgCl3). membrane filtration with addition of mgcl3 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Normalized arithmetic mean

(menr). Arithmetic mean, normalized. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

Missingness Set: NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Other Measure Description

(meOthDe). Description of other measure (measOtherDesc). *Part Type:* measurements *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* othAgg *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 60 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Milliequivalent per liter

(meqL). Unit for alkalinity, miliequivalents per litre. *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Measures Part-type Shorthand

(mes). The abbreviated short name used to reference the The attribute to describe a part type of measures. All measures have ‘partType‘ = “measurements”. part type *Part Type:* shortName *Domain:* naDomain *Speciment*

ID: naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Effective Sample Size/Volume

(mESV). Effective Sample Size/Volume (ESV) is the amount of the original sample size/volume that was actually analyzed in a qPCR reaction (see Box 2.1 Protocol) *Part Type:* measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Methods part-type Shorthand

(met). The abbreviated short name used to reference the Procedures or steps for collecting samples or performing measures. part type *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Metabolite Group

(metaboliteGrp). A group of measures/methods related to metabolites. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* metaboliteGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

MetAMOS

(metAMOS). A sequencing software that is an automated pipeline for metagenomic assembly and annotation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/marbl/metAMOS *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

MetaPhlAn Software

(metaPhIAn). Software tool that profiles microbial communities and can provide resistance gene insights. Also used for deduplication. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

Link: https://huttenhower.sph.harvard.edu/metaphlan/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Meter

(meter). meter (m) *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Method

(method). A procedure for collecting a sample or performing a measure. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* methods *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Concentration method

(methodConc). Description of the method to concentrate a wastewater sample. Description of the method used to concentrate the sample *Part Type:* methods *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment*

Set: anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* methodConcSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Concentration method set

(methodConcSet). A set a concentration methods. *Part Type:* mmaSets *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* methodConcSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Method input (wide table)

(methodInput). The partID for the method being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* methods *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Method name (wide table)

(methodName). The method referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* methods *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Methods

(methods). Procedures or steps for collecting samples or performing measures. For example, 'methodExtract' is a method that describes the how a sample was extracted. met *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with acidification and mgcl2

(mfAcidmgcl2). Membrane filtration with acidification and mgcl2 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with acidification and mgcl2, membrane recombined with separated solids

(mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with addition of mgcl2

(mfMgcl2). Membrane filtration with addition of mgcl2 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with mgcl2 and separated solids

(mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated solids *Part Type:* categories *Domain:* naDo-

main *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with no amendment

(mfNoAmend). Membrane filtration with no amendment *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with no amendment, membrane recombined with separated solids

(mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with sample acidification

(mfSampleAcid). Membrane filtration with sample acidification *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with sample acidification, membrane recombined with separated solids

(mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Millions of gallons per day (MG/D)

(mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of gallons per day. Also can be used to measure flow. *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:*

NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Mycoplasma genitalus

(mGenitalus). Mycoplasma genitalus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mycoplasmaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

MGIEasy DNA Library Prep Kit

(mgiEasy). MGIEasy DNA Library Prep Kit by MGI/BGI. A library prep kit designed for MGI sequencing platforms, offering flexibility in sample input. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams per litre

(mgL). Milligrams per litre. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Milligram per liter of calcium carbonate

(mgLCaCO3). Unit for alkalinity, miligram per litre of calcium carbonate. *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams orthophosphate per liter

(mgPO43L). milligrams orthophosphate per liter (mg PO43–/L) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams orthophosphate as phosphorus per liter

(mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Murine Hepatitis Virus

(mhv). A measure for amount of murine hepatitis viurs. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hepGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

murine hepatitis virus (MHV) spike target

(mhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Multiple issues

(mI). Multiple issues have arisen in the sequencing process. When using the 'multiple issues' quality flag, please specify the issues and details in the notes section. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Mid-level severity

(mid). A marker for med-level severity, where there are some concerns. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Midnight and BC-CDC V1 Primer Set

(midnightBCCDCv1). An amplicon strategy which is for SARS-CoV-2 and based on the original Midnight scheme developed by Oxford Nanopore

Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V2 Primer Set

(midnightBCCDCv2). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V3 Primer Set

(midnightBCCDCv3). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 3.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V4 Primer Set

(midnightBCCDCv4). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 4.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V1 Primer Set

(midnightV1). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V2 Primer Set

(midnightV2). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V3 Primer Set

(midnightV3). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Miniasm

(miniasm). A sequencing software that is a lightweight assembler for long reads, typically followed by polishing steps. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/lh3/miniasm *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Minimap2

(minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/lh3/minimap2 *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Minimum length

(minLength). The maximum value of measure. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* na-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

minimum post-trimming read length

(minPTLength). The threshold used as a cut-off for the minimum length of a read after trimming. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Minutes

(minutes). A unit for indicating a length of time in minutes. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Minimum value

(minVal). Lowest value in a range of values for a measure. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Minimum value part support

(minValue). The minimum value of part. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Miscellaneous attribute group

(miscAttr). A group of miscellaneous measurement-like attributes. Examples of these would be longitude and latitude, or EPSG coordinates. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum*

Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Miscellaneous measure group

(miscMeas). A group of measures that cannot be otherwise categorized. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Missing data

(miss). A general missingness value for missing data, used when data is not included for an unknown reason. Missing value indicator when the value is unavailable for an unknown reason. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Missingness

(missingness). The part type for missingness values. Only used for the dictionary entries of parts. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:*

naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Missingness Set

(missingnessSet). Missingness sets for measures, methods or attributes. Inputted data into an ODM field may have missing data. The missingness set lists valid missing categories for the measure, method, or attribute. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* missingnessSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Missingness sets

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

MIT

(mit). The licensing for the measure or data set is managed under the MIT license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/mit/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

MIT No Attribution

(mit0). The licensing for the measure or data set is managed under the MIT no attribution license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/mit-0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

MitoZ Deduplication

(mitoZ). A deduplication method that is used primarily for mitochondrial genomes but can handle deduplication by read clustering. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/linzhi2013/MitoZ/releases *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mixed/homogenized sample

(mix). Mixed or homogenized sample or fraction analyzed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Millilitres

(ml). Millilitres of volume *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Megalitres per day (ML/d)

(mld). Megalitres per day. *Part Type:* units *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Method Limit of Detection (LOD)

(mlod). The minimum level of a target necessary for its consistent detection considering all sample processing steps as in the definition of SLOD), but considering biases attributable to method losses. The MLOD is experimentally determined using a rigorous and iterative testing approach and it is sensitive to the recovery surrogate used and the sample matrix encountered. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 3.0.0.

MLST (Center for Genomic Epidemiology)

(mlst). MLST (Center for Genomic Epidemiology). Focus: Classical MLST and optional serotype determination. Applications: Compatible with curated schemes for various pathogens. Features: Web-based and

command-line versions available. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.genomicepidemiology.org/services/ (includes MLST service) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Millimetres

(mm). Unit part for the SI unit of millimetres. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Measure, Method, or Attribute Set Header

(mmaSet). The set for a measure, method, or attribute. Only applicable for categorical fields, and the categories that populate them. The use has meean extended to include 'partType' values as well, to codify instances where a catgeorical variable takes any part of a certain part type. Examples of the part type use case insclude using the 'measurements' partType in this column to illustrate that the part 'measure' takes any part of that part type as a valid entry. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Set ID: mmaSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure, method, or attribute sets

(mmaSets). A set of categories. For example, site type has a list of different sites, such as a wastewater treatment plant, a septic tank, or a pumping station. Only used for the dictionary entries of parts. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Millimho per centimeter

(mmhocm). Millimho per centimeter (mmho/cm) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Model

(model). Model number or version of the instrument. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo)

(monarchRNA). monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Months

(months). A unit for indicating a length of time in months. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum*

Value: NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Moore swab passive sample

(moorSw). Moore swab passive sample. Use collectionPeriod to describe how many hours the Moore swab was used to collect the sample *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

1,000,000+ people

(more1mil). More than 1,000,000 people. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Morning

(morn). Sample was collected at some point in the morning, early in the day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA

Unit Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mozilla Public License 2.0

(mpl20). The licensing for the measure or data set is managed under the Mozilla Public License 2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/mpl-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Most probable number per 100 milliliters

(mpn100mL). most probable number per 100 milliliter (MPN/100 mL) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Most probable number per milliliter

(mpnmL). most probable number per milliliter (MPN/mL) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompart-

mentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mpox

(mpox). The virus known as Mpox, previously also known as Monkey Pox. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

MPox Clade I Group

(mpoxCldIGrp). A group of measures/methods related to Mpox Clade I (formerly "Monkey Pox"). Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

MPox Clade II Group

(mpoxCldIIGrp). A group of measures/methods related to Mpox Clade II (formerly "Monkey Pox"). Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIIGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

MPox Group

(mpoxGrp). A group of measures/methods related to Mpox (formerly "Monkey Pox"). Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Medium priority pathogen

(mpp). A resistant organism of moderate concern, needing ongoing monitoring. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA

Reference Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Metres per second

(mps). metres per second. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Metapneumovirus Group

(mpvGrp). A group of measures/methods related to metapneumoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mpox B6R Gene Target

(mpxB6R). Human MPox Virus (hMPXV) gene target. Envelope protien gene CDC Assay; selective for MPXV. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompart-

mentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://doi.org/10.1016/j.jcv.2006.03.012 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Clade I Mpox C3L Gene Target

(mpxC3L). Human MPox Virus (hMPXV) Clade I gene target. hMPXV C3L primers and probe detect Clade I viruses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://doi:10.1016/j.jviromet.2010.07.012 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mpox Clade I

(mpxClI). The virus known as Mpox, previously also known as Monkey Pox, Clade I virus type. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mpox Clade II

(mpxClII). The virus known as Mpox, previously also known as Monkey Pox, Clade II virus type. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIIGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mpox & Orthopox E9L-NVAR Gene Target

(mpxe9lNVAR). Human MPox Virus (hMPXV) gene target for Orthopoxvirus DNA polymerase. CDC Assay detects all hMPXV clades and non-variola Orthopox viruses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://doi.org/10.1016/j.jcv.2006.03.012 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mpox & Orthopox E9L-OPX3 Gene Target

(mpxe9lOPX3). Human MPox Virus (hMPXV) gene target using the generic orthopox virus OPX3. Lower sensitivity for MPox. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://doi.org/10.4269/ajtmh.2010.09-0716 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mpox Clade I F3L Gene Target

(mpxF3L). Human MPox Virus (hMPXV) Clade I gene target, F3L *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Mpox G2R-G Gene Target

(mpxG2RG). Human MPox Virus (hMPXV) gene target using the G2R_G primers and probe which detects all MPox Virus strains . *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet

Aggregation Scale: seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://doi.org/10.1016/j.jviromet.2010.07.012 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mpox G2R-NML Gene Target

(mpxG2RNML). Human MPox Virus (hMPXV) gene target using the G2R_NML primers and probe which detects all MPox Virus strains. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIIGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Clade II Mpox G2R-WA Gene Target

(mpxG2RWA). Human MPox Virus (hMPXV) Clade II gene target, measured with G2R_WA primers and probe to detects Clade II viruses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIIGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://doi:10.1016/j.jviromet.2010.07.012 *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mpox GT Molecular Gene Target

(mpxGTmol). Human MPox Virus (hMPXV) gene target - this specific measure and gene target are proprietary to GT Molecular *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Measure report table Shorthand

(mr). The abbreviated short name used to reference the The table that contains information and details about a given measure table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

MrBayes Software

(mrBayes). A lineage or clade analysis software tool for bayesian inference of phylogeny, used for inferring clade relationships with high accuracy. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA

Unit Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://nbisweden.github.io/MrBayes/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Methicillin-resistant Staphylococcus aureus (MRSA)

(mrsa). Methicillin-resistant Staphylococcus aureus (MRSA) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* staphGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Measure set report table Shorthand

(ms). The abbreviated short name used to reference the The table that identifies sets of measures. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

ms2 coliphage

(ms2Col). Measure of the amount of ms2 coliphage. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ms2 coliphage spike target

(ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

MilliSiemen per centimeter

(mScm). MilliSiemens per centimeter (mS/cm) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum*

Length: NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Matrix spike duplicate

(msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Microsoft Public License

(mspl). The licensing for the measure or data set is managed under the Microsoft Public License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/mspl/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Moore swab passive sample depreciated

(mspsDep). Moore swab passive sample. Deprecated in version 2, please do not use. *Part Type:* categories *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Major sewer pipeline

(mSwrPpl). Major sewer pipeline *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Mycobacterium tuberculosis

(mTuberculosis). Mycobacterium tuberculosis *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tuberculosisGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mu

(mu). B.1.621 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

murine coronavirus

(muCo). Measure of the amount of murine coronavirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* betaCoronaGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

murine coronavirus spike target

(muCoMat). Murine coronavirus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Multiple fraction

(mul). Multiple fractions were analyzed separately and aggregated together post-analysis. This fractionID is intended for use for archival data and should not be used for newly added new moving forward (2022). Please also specify in the notes section which fractions were used for the multiple fractions (ex. solid and liquid) to avoid loss of information. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Mulan Permissive Software License, Version 2

(mulanPSL20). The licensing for the measure or data set is managed under version 2 of the Mulan Permissive Software License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/mulanpsl-2.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Multi-Community-level Surveillance

(multiComLev). The scope of the surveillance covers multiple communities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Multiple Purpose

(multiple). A measure or sample taken for multiple purposes, not easily captured by the other purpose categories. Useful for parent samples where various subsamples will have different purposes/ *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

MultiQC

(multiQC). A QC pipeline tool for sequencing data that aggregates QC results from multiple sources (e.g., FastQC, SAMtools) into a single report, useful in large pipelines. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* https://seqera.io/multiqc/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mumps

(mumps). Mumps *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mumpsGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mumps Group

(mumpsGrp). A group of measures/methods related to the mumps virus. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mumpsGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Municipalities or communes

(municipalLevel). Municipalities or communes *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* na-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Municipality

(municp). A complete municipality, this specifies an entire metropolitan area, either a city, town, etc. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Municipality-level Aggregation at Site

(muniLevel). Specifies that a sewershed/site represents an entire municipality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mutations class

(mutation). Measures and methods related to mutations. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* mutation *Nomenclature:* mutation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 2.3.0.

Mutation panels class

(mutationPanel). Measures and methods related to a panel or list of more than one mutation from the same sequence read. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* mutationPanel *Nomenclature:* mutationPanel *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

MilliVolt

(mvolt). milliVolt (mV) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Mycoplasma Group

(mycoplasmaGrp). A group of measures/methods related to mycoplasma bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mycoplasmaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Mykrobe

(mykrobe). Mykrobe. Focus: Rapid detection of resistance, MLST, and serotyping. Applications: Mycobacterium tuberculosis and other pathogens. Features: Fast processing and species-specific database compatibility. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/Mykrobe-tools/mykrobe Website: https://www.mykrobe.com/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

N sars-cov-2 gene target

(n). N sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENEPIO:0100153 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Combined N1 and N2 sars-cov-2 gene target

(n1n2). Combined N1 and N2 sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant n211i mutation

(n211i). Omicron Variant n211i mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

N50

(n50). The length of the shortest read that, together with other reads, represents at least 50% of the nucleotides in a set of sequences. Provide the N50 value in Mb. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Omicron Variant n679k mutation

(n679k). Omicron Variant n679k mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant n856k mutation

(n856k). Omicron Variant n856k mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant n969k mutation

(n969k). Omicron Variant n969k mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Not applicable

(NA). The field for which the expected value is not a property of the described object. Missing value indicator for missing data with no explanation. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation not applicable

(naAggr). Not applicable for aggregations. Used for parts for which an aggregation value is not applicable or appropriate. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation scale not applicable

(naAggrScale). Not application for aggregation sets. Used for parts for which an aggregation scale value is not applicable or appropriate. *Part Type:* aggregationScales *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation set not applicable

(naAggrSet). Not application for aggregation sets. Used for parts for which an aggregation set value is not applicable or appropriate. *Part*

Type: aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

No amplification control

(nac). Denotes a no amplification control replicate sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Class not applicable

(naClass). Class is not applicable. Use this for all parts that don't have classes (most non-measure or method parts) *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Compartment not applicable

(naCompartment). Compartment not applicable. *Part Type:* compartments *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Compartment set not applicable

(naCompartmentSet). Compartment not applicable. *Part Type:* compartmentSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Domain not applicable

(naDomain). Not applicable. Use 'not applicable' when there is no domain for the part *Part Type:* domains *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Group not applicable

(naGroup). Used when there is no group; ie. group is not applicable. Use 'not applicable' when there is no group for the part *Part Type:* groups *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Name

(name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the 'name' field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details). Name of any entity. Use a prefix to distinguish names from different report tables. See fully specified name (FSN) list. i.e. Si-name = Site name, Po-name = Polygon name, Or-name = Organization name, Me-name = Method-name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

English name for countries

(nameEngl). English-language name of a given country. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Official state name

(nameOfficial). Official english-language name of a given state. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Not a number

(nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, …) Missing values indicator for when a numeric value is expected but not given. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Nomenclature not applicable

(naNomenclature). Not applicable. Use 'not applicable' when there is no nomenclature for the part *Part Type:* nomenclatures *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NanoPlot

(nanoPlot). A QC pipeline tool for sequencing data that does visualizations for quality assessment of long-read data, particularly from Oxford Nanopore. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/wdecoster/NanoPlot *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Specimen not applicable

(naSpecimen). Non applicable specimen. Use 'not applicable' when there is no specimen/set for the part *Part Type:* specimens *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specimen set not applicable

(naSpecimenSet). A specimen set for when specimen/specimen set is not applicable. Use 'not applicable' when there is no specimen/set for the part *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Native Name

(natName). The native name of the language, i.e. what the language is called by its speakers. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

Unit not applicable

(naUnit). Not appliable for units. *Part Type:* units *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

Unit set not applicable

(naUnitSet). Not applicable for unit sets. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NB.1.8.1 variant (Nimbus)

(nb181V). The Nimbus variant of SARS-CoV-2 (NB.1.8.1), descendant of the recombinant variant XDV.1.5.1. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

Group: nimbusGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

number of base-pairs sequenced

(nBPSeq). The number of total base pairs generated by the sequencing process. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

National Center for Biotechnology Information

(ncbi). NCBI header *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NCBI Format

(ncbiForm). Dataset was originally recorded and/or stored in NCBI format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ncbi.nlm.nih.gov/biosample/docs/packages/SARS-CoV-2.wwsurv.1.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nomenclaturre from the NCBI

(ncbiNom). Nomenclaturre from the National Center for Biotechnology Information *Part Type:* nomenclatures *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NCBI - notes

(ncbiNotes). NCBI notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:*

genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NCBI's Pathogen Detection Isolates Browser

(ncbiPDIB). Database that tracks AMR in pathogens and provides resistance profiles for pathogens worldwide. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ncbi.nlm.nih.gov/pathogens/isolates/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

number of contigs

(nContig). The number of contigs (contiguous sequences) in a sequence assembly. Provide a numerical value. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ncov-tools

(ncovtools). Tools and plots for perfoming QC on coronavirus sequencing results. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/jts/ncov-tools *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

University of Illinois/NCSA Open Source License

(ncsa). The licensing for the measure or data set is managed under the University of Illinois/NCSA Open Source License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/ncsa/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

National Database of Antibiotic Resistant Organisms (NDARO)

(ndaro). A database maintained by the USCDC with genomic data on AMR organisms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category*

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NEBNext Ultra II DNA Library Prep Kit

(nebnextUltraII). NEBNext Ultra II DNA Library Prep Kit by New England Biolabs. A high-efficiency library prep kit for low DNA input, ideal for whole-genome and target enrichment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V1a Long Primer Set

(nebVarSkipV1aLong). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a long. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/nebiolabs/VarSkip *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V1a short Primer Set

(nebVarSkipV1aShort). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a short. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/nebiolabs/VarSkip *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V2a Primer Set

(nebVarSkipV2a). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2a. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/nebiolabs/VarSkip *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V2b Primer Set

(nebVarSkipV2b). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce ef-

fects of variants with the attributes of version 2b. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/nebiolabs/VarSkip *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Negative experimental control

(negCon). A sample or experimental condition where the expected outcome should not occur, intended to check the original sample matrix for contamination, false positives, or unintended effects. An example would be testing for viral RNA or DNA in a sample known to be free of that virus. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Neighbourhood

(neigh). A municipal neighbourhood, this specifies a sub-section of a larger municipality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Local administrative units or neighborhoods

(neighborLevel). Local administrative units or neighborhoods *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Neighbouring relationship

(neighbour). Locations/polygon are neighbouring eachother. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Neighbourhood-level Aggregation at Site

(neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a municipaility. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population of newly vaccinated persons

(newVax). Population of newly vaccinated persons A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NextClade nomenclature

(nextclade). Specifies variant or genetic nomenclature as set out by NextClade. *Part Type:* nomenclatures *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Nextera XT DNA Library Preparation Kit

(nexteraXT). Nextera XT DNA Library Preparation Kit by Illumina. A fast and efficient library prep kit for small genomes and amplicons, uses transposase-based fragmentation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nextstrain Software

(nextstrain). A lineage or clade analysis software tool for real-time tracking of pathogen evolution, with tools for clade and lineage analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://nextstrain.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nanograms per liter

(ngL). nanograms per liter (ng/L) *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness*

Set: NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NGMLR (Next-Generation Mapping and Long-Read Alignment)

(ngmlr). NGMLR (Next-Generation Mapping and Long-Read Alignment). A long-read specific mapper. Specialized for long-read platforms like PacBio and Nanopore. Best for: Structural variant analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/philres/ngmlr *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Normalized geometric mean

(ngmn). Geometric mean, normalized. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Neisseria gonorrhoeae

(nGonorrhoeae). Neisseria gonorrhoeae *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* gonococcusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Next-Generation Sequencing (NGS) platforms or intruments

(ngsInst). Next generation sequencer instruments and platforms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Ammonia and Ammonium as Nitrogen

(nh3nh4). Ammonia and Ammonium combined concentration, as Nitrogen *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:*

seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Ammonium Nitrogen

(nH4N). Ammonium nitrogen concentration, as N. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Night

(night). Sample was collected at night, between sunset and sunrise. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

niid_2019-ncov_n sars-cov-2 gene target

(niid19). niid_2019-ncov_n sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 Nimbus Variant Group

(nimbusGrp). A group of measures/methods related to the SARS-CoV-2 Nimbus Variant. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* nimbusGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nano-molar

(nM). the unit of nanomolar. *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

No quality concerns

(noConcern). A flag to indicate there is are no quality concern about the measure or sample. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sample not labelled

(noLabel). Sample had no label *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

No liquid concentration, liquid recombined with separated solids

(noliquid). No liquid concentration, liquid recombined with separated solids *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Nomenclature

(nomenclature). A classification system to report the measure class. Only applicable to variants, mutations, and diseases. Currently only used for class = variant, mutation, or disease. Valid options are currently restricted to 'NextClade', 'Pangolin', 'WHO', or 'ICD'. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* nomenclatures *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Nomenclatures

(nomenclatures). A classification system to report the measure class. See partID = nomenclatureID. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

No sample storage medium used

(none). No sample storage medium used *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

No rain

(noRain). Qualitative category for the weather measure, specifying no rainfall for a given day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Purpose is normalization

(norm). The purpose of a measure or sample is for normalization. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Normalization Calculation Type

(normalization). A transformation of data to have a mean of zero and a standard deviation of one, commonly used to compare values across different datasets or units. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NORMAN

(norman). NORMAN header *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Norman Format

(normanForm). Dataset was originally recorded and/or stored in Norman format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* na-

Class *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.norman-network.com/nds/sars_cov_2/downloadDCT.php *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NORMAN - notes

(normanNotes). Norman notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Norovirus

(noro). Norovirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Norovirus G1

(noroG1). Norovirus genogroup 1 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Norovirus G2

(noroG2). Norovirus genogroup 2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Norovirus GI Group

(noroGIGrp). A group of measures/methods related to norovirus GI. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGIGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA

Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Norovirus GII Group

(noroGIIGrp). A group of measures/methods related to norovirus GII. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGIIGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Norovirus Group

(noroGrp). A group of measures/methods related to noroviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

No Seperation or Concentration

(noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. *Part Type:* categories

Domain: naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Notes

(notes). A note used to describe details that are not captured in other attributes There is no recommended structure of a note. Use notes as needed. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample missing time stamp

(noTime). Sample is missing the autosampler time; incomplete metadata on collection. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Novoalign

(novoalign). Novoalign. A specialized read mapper. Commercial aligner known for high accuracy. Best for: Applications requiring precise alignments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://www.novocraft.com/products/novoalign/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NovoPlasty

(novoPlasty). A sequencing software that is an assembler tailored for organellar genomes (mitochondrial and chloroplast). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/ndierckx/NOVOPlasty *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Number per 100 kilo-base-pairs

(nPerKbp). This unit expresses the frequency of an event (such as a mutation, binding site, or feature) per 100,000 base pairs (kbp) of DNA or RNA. It normalizes counts across genomic regions of different lengths, making comparisons more meaningful. *Part Type:* units *Domain:* bio *Speciment*

Parts

ID: saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Not reported

(nr). A value could have been recorded, however, it was not. Missing value indicator for data that is absent because it was not reported. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Not reported, Not applicable missing set

(nrNAMissingnessSet). Not reported, Not applicable missing set. *Part Type:* missingnessSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

MinusRT

(nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sarbecovirus-specific N sars-cov-2 gene target

(nSarbec). Sarbecovirus-specific N sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 nsp1 Gene target

(nsp1). SARS-CoV-2 nsp1 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100158 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp10 Gene target

(nsp10). SARS-CoV-2 nsp10 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100167 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp11 Gene target

(nsp11). SARS-CoV-2 nsp11 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100157 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp15 Gene target

(nsp15). SARS-CoV-2 nsp15 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompart-

mentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100171 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp16 Gene target

(nsp16). SARS-CoV-2 nsp16 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100172 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp2 Gene target

(nsp2). SARS-CoV-2 nsp2 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100159 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp3 Gene target

(nsp3). SARS-CoV-2 nsp3 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100160 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp4 Gene target

(nsp4). SARS-CoV-2 nsp4 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100161 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp5 Gene target

(nsp5). SARS-CoV-2 nsp5 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100162 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp6 Gene target

(nsp6). SARS-CoV-2 nsp6 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100163 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp7 Gene target

(nsp7). SARS-CoV-2 nsp7 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100164 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp8 Gene target

(nsp8). SARS-CoV-2 nsp8 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

Group: sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100165 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp9 Gene target

(nsp9). SARS-CoV-2 nsp9 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100166 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Non-template control

(ntc). Denotes a non-template control sample replicate. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NTC Amplification Detected

(ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Control-plate Flag - NTCs

(ntcFlag). quality indicator for when there is observed amplicifation in the non-template controls (NTCs) of a PCR reaction. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 3.0.0.

number of total reads

(nTotRead). The total number of non-unique reads generated by the sequencing process. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA

Unit Set: unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

No target present

(ntp). Denotes a sample replicate/control with no target present. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Nephelometric turbidity unit

(ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see "turbidity" under measureIDs). Nephelometric turbidity units (NTU) are based on white light (400–680nm) and 90° incident angle. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Nuclisens automated magnetic bead extraction kit

(nucAuto). Nucleic acid extraction performed using the nuclisens automated magnetic bead extraction kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

nucleomag (ref. 744220.4) using kingfisher automated instrument

(nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Nuclisens manual magnetic bead extraction kit

(nucManu). Nucleic acid extraction performed using the nuclisens manual magnetic bead extraction kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Null

(NULL). A logical representation of a statement that is neither TRUE nor FALSE. Missing value indicator when the value is neither TRUE nor FALSE. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 3.0.0.

ISO 3166-1 numeric country code

(numCode). The ISO 3166-1 numeric code, a three-digit country code which is identical to that developed and maintained by the United Nations Statistics Division, with the advantage of script (writing system) independence, and hence useful for people or systems using non-Latin scripts. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 3 *Maximum Length:* 3 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Number of NTCs per Run

(numNTC). The number of no-template controls included in each PCR instrument run. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

number of unique reads

(nUniRead). The number of unique reads generated by the sequencing process. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

National Wastewater Surveillance System

(nwss). NWSS header *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:*

genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

US-CDC NWSS Format

(nwssForm). Dataset was originally recorded and/or stored in the US-CDC's NWSS format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://covid.cdc.gov/covid-data-tracker/#wastewater-surveillance *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

NWSS - notes

(nwssNotes). NWSS notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

NWSS - process

(nwssProcess). NWSS process *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Water

(nww). Non-wastewater, coming from any kind of water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

coronavirus OC43

(oc43). Measure of the amount of coronavirus OC43. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

oc43 spike target

(oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Ocean, natural water body

(ocean). Ocean, natural water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Other Collection depreciated

(oColDep). Other type of collection method. Add description to collectionOther. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (https://github.com/Big-Life-Lab/PHES-ODM/issues), or at phesd_odm@ohri.ca *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Odour Control Unit

(ocu). Odour Control Unit ventilation extends the life of a sewer by reducing the amount of maintenance the pipeline needs, making management of the network much more efficient. The filters used in the Odour Control Unit and ventilation stacks absorb gases such as hydrogen sulphide, which is a common source of odours from sewerage systems. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Office

(office). A workplace where administrative, managerial, or clerical tasks are performed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:01001221 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SIL Open Font License 1.1

(ofl11). The licensing for the measure or data set is managed under the SIL Open Font License 1.1. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/ofl-1.1/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Original Data Format Set

(ogFormSet). The category set for recording the possible original data formats to be recorded in the originalFormat field in the datasets table. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* ogFormSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Lab Analysis

(ola). Offline laboratory analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Omicron BA.1

(omicr1). Omicron B.1.1.529 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.2

(omicr2). Omicron BA.2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.2.75

(omicr275). Omicron BA.2.75 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:*

seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.4

(omicr4). Omicron BA.4 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.5

(omicr5). Omicron BA.5 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 Omicron Variant Group

(omicronGrp). A group of measures/methods related to the SARS-CoV-2 Omicron Variant. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpeci-

menSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NCIT:C169076 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Onset date

(onsDate). Earliest that symptoms were reported for this case. This data is often not known and reported. In lieu, episode is used. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Online Sensor

(onse). Online sensor An online sensor *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Ontology reference

(ontologyRef). Ontology reference for a part. This field contains a link to an existing ontology reference for the part. ODM content spans several existing ontologies. ODM does not strive to generate a new ontology, rather ODM seeks to harmonize and extend dictionaries for application in environmental and public health surveillance. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 200 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Value out of range

(oor). Value is outside of the allowable range for quality control. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Open license not otherwise described

(open). The licensing for the measure or data set is managed under an open license not otherwise described. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Orthophosphates

(ophos). Ortho-phosphate concentration. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Optical calibrator sample

(opt). Denotes a sample control or replicate used for optical calibration. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Surface water

(opWa). An outdoor accumuation of water either on the surface of the earth, no other additional details specified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Organization table Shorthand

(or). The abbreviated short name used to reference the The table that contains information about a laboratory. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Other residential building

(orb). Individual residential buildings or institutions not captured in other categories *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

OR Boolean aggregation

(orBoo). "OR" aggreation. If any value in the aggregation is "TRUE" then the OR aggregation is also "TRUE". If all values in the aggregation is "FALSE" then the OR aggregation is also "FALSE". *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Order

(order). The order a single calculation/data treatment takes within the full container pipeline/workflow. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf10 Gene target

(orf10). SARS-CoV-2 orf10 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100181 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf14 Gene target

(orf14). SARS-CoV-2 orf14 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100182 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ORF1a sars-cov-2 gene target

(orf1a). ORF1a sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENEPIO:0100156 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ORF1ab sars-cov-2 gene target

(orf1ab). ORF1ab sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENEPIO:0100155 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ORF1b sars-cov-2 gene target

(orf1b). ORF1b sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 orf3a Gene target

(orf3a). SARS-CoV-2 orf3a Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

Group: sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100173 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf3b Gene target

(orf3b). SARS-CoV-2 orf3b Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100174 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf6 (ns6) Gene target

(orf6). SARS-CoV-2 orf6 (ns6) Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100175 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf7a Gene target

(orf7a). SARS-CoV-2 orf7a Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100176 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf7b (ns7b) Gene target

(orf7b). SARS-CoV-2 orf7b (ns7b) Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100177 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf8 (ns8) Gene target

(orf8). SARS-CoV-2 orf8 (ns8) Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100178 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf9b Gene target

(orf9b). SARS-CoV-2 orf9b Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENE-PIO:0100179 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf9c Gene target

(orf9c). SARS-CoV-2 orf9c Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENE-PIO:0100180 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Organism

(organism). Organism class Identify class = ‘organism‘ for when a part identifies an organism and partType = ‘groups‘. Indivdual measures should be recorded with a class for the specific measure type. i.e. allele, variant, mutation, etc. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Organization ID

(organizationID). A unique identifier for the organization to which the reporter is affiliated. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.1.0. Last updated: 3.0.1.

Organization table

(organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. or *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Organizations table column order

(organizationsOrder). Specifies the order of the columns in a Organizations table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organziation table required headers

(organizationsRequired). Specifies the columns required in a Organizations table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organization level

(orgLevel). The geographic level of an organization. There are six levels based on International Standard Classification of Administrative Units (ISCU). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* nrNAMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organization level set

(orgLevelSet). Categories of organization levels. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organization sector

(orgSector). The sector of an organization *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgSectorSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* nrNAMissingnessSet *Minimum Value:*

NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organization sector set

(orgSectorSet). Cateogries of organization sectors. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgSectorSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organization Type

(orgType). Specifies the type or purpose of a given organization. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* nrNAMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Organization type set

(orgTypeSet). The set for storing organization types. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgTypeSet *Unit Set:* naUnitSet

Aggregation Scale: naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample origin

(origin). An attribute of a sample specifying the origin. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* originSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Original Data Format

(originalFormat). The original structure or model used to record and store the data. This helps indicate if data have been transformed or mapped into the ODM structure. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* ogFormSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample Origin set

(originSet). The set for storing the valid categorical values of sample origin. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* originSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Oxidation reduction potential (ORP)

(orp). Oxidation-reduction potential (ORP) measures the ability of a lake or river to cleanse itself or break down waste products, such as contaminants and dead plants and animals. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* electricPotentSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

OrthoFinder Software

(orthoFinder). OrthoFinder - For orthogroup identification and phylogenetic tree building, often useful in evolutionary clade studies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:*

software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/davidemms/OrthoFinder *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Orthopox Virus Group

(orthoGrp). A group of measures/methods related to orthopox viruses (excluding variolla viruses). *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* orthoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Open Science Foundation (OSF)

(osf). Open Science Foundation project/data storage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://osf.io *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Open Software License 3.0

(osl30). The licensing for the measure or data set is managed under the Open Software License 3.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/osl-3.0/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Other Collection depreciated

(otco). Other type of collection method. Add description to collectionOther. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (https://github.com/Big-Life-Lab/PHES-ODM/issues), or at phesd_odm@ohri.ca *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Other aggregation scale

(othAgg). Specifies an aggregation scale that can't be described as either "qualitative" or "quantitative". *Part Type:* aggregationScales *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Other

(other). Other Other category. A categorical response for several variables in version 1. Also accompanied by a free text field. Depreciated in version 2, with common text fields added as new categories in version 2.0.0 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation set

(otherAggrSet). Aggregation set used for unitless measures. *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation depricated

(otherDep). Other aggregation method. Add description to aggregationOther Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (https://github.com/Big-Life-Lab/PHES-ODM/issues), or at phesd_odm@ohri.ca *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Other (or proprietary) Format

(otherForm). Dataset was originally recorded and/or stored in a format not otherwise described. Please name (and optionally describe) the data format in the "notes" section when using this value. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Access to other prov depricated

(otherProvDep). If this is 'no', this data will not be available to other data providers not listed before. If missing, data will be available to other

data providers not listed before *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Other report table set

(otherReportTableSet). Additional tables that form the full data model. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Variants Other

(otherV). Used for reporting variants detected for which a specific measureID doesn't already exist. The ODM team will periodically migrate collected responses in this category into set measureIDs. Please write in an official name for the new variant that was detected, and specify which nomenclature you're using with the nomenclatureID. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet

Reference Link: NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Other Site - sample depreciated

(otsisaDep). Other type of site. Add description to typeOther. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (https://github.com/Big-Life-Lab/PHES-ODM/issues), or at phesd_odm@ohri.ca *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Other Site - Site depreciated

(otsisiDep). Other site type. Add description to typeOther *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Other Unit depricated

(otunDep). Other measurement of viral copies or wastewater treatment plant parameter. Add description to UnitOther. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (https://github.com/Big-Life-Lab/PHES-ODM/issues), or at phesd_odm@ohri.ca *Part Type:* units *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Value is an outlier

(out). Value is an outlier and may be of questionable quality. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Outbreak declaration

(outb). Public health action type used to indicate outbreak status. Given that when outbreaks occur, full data on case counts may not be available or completely accurate, using this measure indicates that case counts may be approximate. The datetime for the measure helps indicate that start

and end periods for an outbreak. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

End of Outbreak

(outbEnd). Indicates an outbreak has ended. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Outbreak - on-going

(outbOngoing). Indicates an outbreak is on-going. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Outbreak class

(outbreak). Measures and methods relating to public health outbreaks. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* outbreak *Nomenclature:* outbreak *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 3.0.0.

Outbreak declaration Value Set

(outbreakSet). set for the valid values of the outbreak measure. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* outbreakSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Declared outbreak or Outbreak start

(outbStart). Indicates an outbreak began. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Overlapping relationship

(overlap). Locations/polygon have overlapping portions. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Delta Variant p100l mutation

(p100l). Delta Variant p100l mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant p13l mutation

(p13L). Omicron Variant p13l mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:*

seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Delta Variant p2046l mutation

(p2046l). Delta Variant p2046l mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Delta Variant p2287s mutation

(p2287s). Delta Variant p2287s mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant p3395h mutation

(p3395h). Omicron Variant p3395h mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Delta Variant p681r

(p681r). Delta Variant p681r mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-CompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Parts Look-up table Shorthand

(pa). The abbreviated short name used to reference the Look up table containing all parts in of the data model. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* na-CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

polymerase activation

(pAct). Describes the polymerase activation cycle in a PCR process. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Paired Layout

(pairLay). Specifies the paired layout for a sequencing method *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Pangolin nomenclature

(pangolin). Specifies variant or genetic nomenclature as set out by the Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin). *Part Type:* nomenclatures *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:*

naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Pangolin Software

(pangolinSoft). A lineage or clade analysis software tool used for lineage assignment in SARS-CoV-2 and other viral genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/cov-lineages/pangolin *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Papilomavirus Group

(papilomavirusGrp). A group of measures/methods related to papilomaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* papilomavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Paraxanthine (PARA)

(para). A metabolite of the common central nervous system stimulant caffeine, measred levels of paraxanthine have been found to be less affected by the genetic heterogeneity and population structure than caffeine is, and it may serve as a useful population biomarker in wastewater. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Parainfluenza Group

(parafluGrp). A group of measures/methods related to parainfluenza viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* parafluGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Parapoxvirus Orf Virus Spike Target

(parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup

Class: naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Parent dataset ID

(parDatasetID). The datasetID that is a parent to another datasetID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Parechovirus group

(parechoGrp). A group of measures/methods related to parechoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* parechoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Parent sample ID

(parent). If this sample has been pooled into one big sample for analysis this indicates the sample of the larger pooled sample. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.1.0. Last updated: 2.0.0.

Parent Site ID

(parSiteID). The siteID that is a parent to another siteID; usually the sub-site will be contained in the parentSite. An example would be surface testing in a LTC facility. The LTC facility would be the parentSiteID, and the various rooms/surfaces would be the sub-sites, or child-sites. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Part description

(partDesc). The description of the part. Provides description of the part, used for tranlsation. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Part identifier

(partID). The unique identify of any entity within the dictionary. Every entity in the ODM has a partID. The partID must be unique with no duplcates. partIDs are short. partIDs that are constructed by different part attributes can be up 28 characters (check max), but each part attibute should be 1 to 5 characters. partIDs are machine readible, but a knowledgable user can understand what they represent. partID are used, for example, as a header in an Excel input table. Numbers are allowed but there no other special characters other than ‘‘. “ is a reserved character that is used to generate a partID using a compoent or table attributes. A partID for a subComponent is automatically generated using attributes of a component. For example, the partID for the compoent ‘SARS-CoV-2‘ is ‘covid‘. ‘Covid‘ can have many subComponents including different groups (Covid-19-al, Covid-19-va, ovid-pr (allele, variant or protein) or units and aggregatrions (i.e. covid-al-N1-mean-cpl representing ovid allele N1, mean observation of viral copies per litre of effluent). A similar approach to naming subComponent is use for naming parts in a reprotTable. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Part instruction

(partInstr). Additional notes and instructions on how a part is used and/or defined. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 200 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Parts Look-up table

(parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. pa *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Parts table column order

(partsOrder). Order of headers in the Parts table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Parts table required headers

(partsRequired). Required headers in the Parts table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Part Support

(partSupport). Parts designed to support the metadata definition of other parts in the parts table. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Part type column (Reported)

(partType). The recorded part type for every part in the part table. This is the attribute in the parts table, not to be confused with partTypes, the part type. *Part Type:* attributes *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* partTypes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Part type input (wide table)

(partTypeInput). The partID for the part type being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* partTypes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Part type name (wide table)

(partTypeName). The part type being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* partTypes *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Part types part type

(partTypes). Part types describe the purpose or use of the part. Enivornment data has three main part types: measure (i.e. covN1 viral measures, wasteawater flow rate, temperature), method (e.g. how the measure was taken), and attribute (such as a site name). See description of each of the part types within setID = partTypeCatSets. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Passive Sample - General

(passiveGen). Used to specify a passive sampling method not otherwise specified was used to collect the sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Pasteurized sample

(pasteur). Binary indicator for whether a sample was pasteurized as part of its processing. *Part Type:* methods *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp

Class: standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Pathogenwatch

(pathogenwatch). Pathogenwatch. Focus: Integrates MLST, serotyping, and resistance typing with a user-friendly interface. Applications: Primarily used for Salmonella and Escherichia coli. Features: Combines typing results with interactive visualization. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://next.pathogen.watch/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PATRIC/RAST Database

(patricRast). Database that hosts resistance gene annotations within their microbial genome data resources. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* patricbrc.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA

Minimum Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PBPfinder

(pbfinder). PBPfinder. Used for typing and serotyping of Streptococcus pneumoniae through analysis of penicillin-binding proteins and capsular genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* GitHub: https://github.com/rpetit3/pbptyper *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Phosphate Buffered Saline (PBS)

(pbs). An isotonic solution for general sample preservation, used when immediate freezing is available. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Primary Clarifier Effluent depreciated

(pceDep). Effluent obtained after primary clarifiers. Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those.

Part Type: categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Postal or Zip Code

(pCode). The zip code or postal code for a given address, specifying a specifc geographic area. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qPCR Class

(pcr). Measures and methods relating to qPCR. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PCR Action/Activity

(pcrAct). Describes a given PCR cycle for delineating more method information. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* pcrActSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

PCR action/activity set

(pcrActSet). The set capturing containing all of the valid methods for the PCR activity cycles. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* pcrActSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

PCR Quanitification Cycles

(pcrCycles). A count unit of how many Polymerase Chain Reaction (PCR) cycles it took to detect a real signal from a sample. Equivalent to the PCR cycle number at which a sample's reaction curve intersects the threshold line. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet

Aggregation Scale: quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PCR method

(pcrmeth). Description of the PCR method. Description of the PCR method used *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* pcrSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

PCR quality set

(pcrQualitySet). Quality set for PCR measures. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PCR Sequencing Selection Method

(pcrSeq). Specifies the PCR selection method for sequencing, ie. that a predetermined primer was used. Primer should be specified if this is selected.

Part Type: categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

PCR Method set

(pcrSet). The set capturing containing all of the valid methods for the PCR method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* pcrSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Primary Clarifier Sludge depreciated

(pcs). Sludge produced by primary clarifiers. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Porcine Circovirus 1 (PCV-1)

(pcv1). Porcine Circoviruses (PCV) are the smallest viruses replicating autonomously in eukaryotic cells. The virions are non-enveloped and spherical with a diameter of 16-18 nm and the covalently closed and single-stranded DNA genomes comprise less than 1800 nucleotides. Porcine circovirus type 1 (PCV1) is not linked with a disease. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* circoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Porcine Circovirus 2 (PCV-2)

(pcv2). Porcine Circoviruses (PCV) are the smallest viruses replicating autonomously in eukaryotic cells. The virions are non-enveloped and spherical with a diameter of 16-18 nm and the covalently closed and single-stranded DNA genomes comprise less than 1800 nucleotides. Porcine circovirus type 2 (PCV2) is the etiological agent of Postweaning Multisystemic Wasting Syndrome (PMWS), a new emerging and multifactorial disease in swine. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* circoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Number of people

(peeps). Unit specifying a number of people. *Part Type:* units *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Primary clarifier effluent

(pEfflu). Effluent obtained after primary clarifiers *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Polyethyleneglycol (PEG) precipitation

(peg). Peg precipitation *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PEHaplo

(pehaplo). A sequencing software that is an assembler that considers heterozygosity in diploid genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/chjiao/PEHaplo *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Percent

(perc). Percentage. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

percent read contamination

(percContam). The percent of the total number of reads identified as contamination (not belonging to the target organism) in a sequence dataset. Provide the percent contamination value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA

Unit Set: percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Percent unit set

(percentUnitSet). Unit set for percentages. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

percent Ns across total genome length

(percNLength). The percentage of the assembly that consists of ambiguous bases (Ns). Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Percent recovery

(percRec). Percent of the surrogate recovery for a recovery efficiency control assay (as a unit). Use this for reporting the results of any recovery control assay. *Part Type:* units *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Persons for square kilometre

(personPerKm). Persons per square kilometre. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Persons per square mile

(personPerMile). Persons per square mile. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum*

Length: NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PGAP (Prokaryotic Genome Annotation Pipeline)

(pgap). PGAP (Prokaryotic Genome Annotation Pipeline). Focus: Annotation pipeline that integrates MLST and antigen typing. Applications: Broad bacterial pathogens. Features: Provided by NCBI, designed for high-throughput workflows. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NCBI: https://www.ncbi.nlm.nih.gov/refseq/annotation_prok/ GitHub: https://github.com/ncbi/pgap *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

pH

(ph). pH measurement *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* waterQualityGrp *Class:* pHClass *Nomenclature:* pHClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* 1 *Maximum Value:* 14 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Public Health Actions Report Table Shortname

(pha). The abbreviated short name used to reference the table for recording information on public health actions. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PHA4GE Format

(pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/pha4ge/Wastewater_Contextual_Data_Specification *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Access to phac

(phac). If this is 'no', the data will not be available to employees of the Public Health Agency of Canada - PHAC. If missing, data will be available to employees of the Public Health Agency of Canada - PHAC. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Public Health Action ID

(phActionID). Unique identifier for public health actions. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public Health Actions Report Table

(phActions). Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. pha *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health actions table column order

(phActionsOrder). Specifies the order of the columns in the public health actions table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health actions table required headers

(phActionsRequired). Required headers in the public health actions table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health advisory

(phAdvise). A public health action type wherein a public health advisory is deseminated to the public. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public Health Advisory Value Set

(phAdviseSet). A set of valid categories for the public health action field, where the action type is 'publi health advisory'. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* phAdviseSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PHAGE

(phage). PHAGE header *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Bacteriophage Group

(phageGrp). A group of measures/methods related to bacteriophages. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* organism *Nomenclature:*

organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

PHAGE - notes

(phageNotes). PHAGE notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Phagetyping Results

(phagetype). The phagetyping results from an organism. Please record in numerical code for the profile. ie. convert lysis profiles into numerical codes for easier classification. For instance: binary presence/absence profile (e.g., 11001 for five phages) is converted into a unique numerical identifier for the phage type. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Phandango

(phandango). Phandango. A visualization tool that integrates serotype predictions with phylogenetic analyses for population studies. Often used alongside other serotyping tools. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* CLI & web: https://github.com/jameshadfield/phandango Web: https://jameshadfield.github.io/phandango/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Pharmaceutical manufacturing plant

(pharmPl). An industrial building in which pharamceutical drugs are synthesised and processed on an industrial scale. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

pH class

(pHClass). Measures and methods relating to pH. *Part Type:* classes *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* pHClass *Nomenclature:* pHClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet

Aggregation Scale: seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Public health emergency (outbreak)

(phEmerg). Indicates a public health emergency from an outbreak. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Phenol chloroform

(phenCl). Nucleic acid extraction performed using phenol chloroform. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PHES-ODM Version 1 Format

(phesODMFormV1). Dataset was originally recorded and/or stored in PHES-ODM version 1 format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.phes-odm.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PHES-ODM Version 2 Format

(phesODMFormV2). Dataset was originally recorded and/or stored in PHES-ODM version 2 format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.phes-odm.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PHES-ODM Version 3 Format

(phesODMFormV3). Dataset was originally recorded and/or stored in PHES-ODM version 3 format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.phes-odm.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Pseudomonas virus phi6

(phi6). Measure of the amount of pseudomonas virus phi6. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

phi6 spike target

(phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Country national phone prefix

(phone). International dialing code for the country. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Total phosphorous

(phos). Total phosphorous *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Total Phosphates

(phostot). Total phosphates *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

PHRED quality score

(phred). PHRED Quality Score For Sequencing *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *On-*

tology Reference: NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Physical property

(phy). A physical property or object not characterized by life or chemistry. *Part Type:* domains *Domain:* phy *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PhyloPhlAn Software

(phyloPhIAn). A lineage or clade analysis software tool, specialized in high-resolution phylogenetic analysis, typically used for microbial clade analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://huttenhower.sph.harvard.edu/phylophlan/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PhyloSuite Software

(phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://dongzhang0725.github.io/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PhyML Software

(phyML). A lineage or clade analysis software tool that builds phylogenetic trees using maximum likelihood methods, with clade confidence assessments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.atgc-montpellier.fr/phyml/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Physical class

(physical). Measures and methods related to generic physical properties. *Part Type:* classes *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA

Unit Set: volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Picard MarkDuplicates

(picard). A deduplication method within the Picard suite that marks duplicate reads in BAM files based on mapped location. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://broadinstitute.github.io/picard/ (Picard toolkit includes MarkDuplicates) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Picobirnavirus

(picobirna). The single genus of the Picobirnaviridae family, Picobirnavirus, members of which have been identified in the feces of humans, rabbits, and a variety of other species of mammals, reptiles, and birds. Picobirnaviruses have been increasingly recognized with the advent of deep sequencing analysis of fecal specimens from many species of animals, and distinct genetic subgroups are now described. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* picobirnaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Picobirnavirus Group

(picobirnaGrp). A group of measures/methods related to picobirnaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* picobirnaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Pipeline ID

(pipelineID). A primary key linked to a single measure (may be used multiple times), it is the shorthand for the data transformation pipeline used. Serves as a data pipeline identifier. Can be used to link multiple data treatments together - rows of differe related treatments will share the same pipelineID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PIQMIe

(piqmie). A comprehensive QC and contamination assessment pipeline for metagenomic datasets and sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PiSeqQC

(piSeqQC). A QC pipeline tool for sequencing data for microbiome and metagenomic sequencing data, including quality filtering and contaminant removal. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/piseqqc/ (genomic QC) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Primary key

(pK). Primary key for a table. All report tables have a primary key. Each row in a report table has unique identifier recorded in the primary key. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Plasmodium

(plasmodium). Plasmodium *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* malariaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Platanus

(platanus). A sequencing software that is an assembler, optimized for large, diploid genome assemblies, particularly plants. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/bioinfomatics-i/platanus link pending retrieval *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Plumbing drain

(pluDra). An artificial channel which transports unwanted water or waste liquids away from their source, either to a more useful area, a receptacle, or into sewers or stormwater mains as waste discharge to be released or processed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PMMoV- and flow-normalized mean

(pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Mostly used for reporting specific alleles (N1, N2, E, etc.) *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PMMoV Group

(pmmovGrp). A group of measures/methods related to the Pepper Mild Mottle Virus (PMMoV). Used to describe the organism information for

general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* pmmovGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

PMMoV-normalized mean

(pmmovNorm). Mean measure normalized to amount of PMMoV. Mostly used for reporting specific alleles (N1, N2, E, etc.) *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PMMoV Standarized

(pmmovStand). This data treatment standardizes the measurement value to concentration levels of pepper mild mottle virus (PMMoV). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

PMMV forward primer (ABI)

(pmmvABIFor). PMMV forward primer (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* pmmovGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

PMMV probe (ABI)

(pmmvABIProbe). PMMV probe (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* pmmovGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

PMMV reverse primer (ABI)

(pmmvABIRev). PMMV reverse primer (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* pmmovGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Polygon table Shorthand

(po). The abbreviated short name used to reference the The table that contains information about the geometry of a geographic area. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Post-Grit depreciated

(pogr). Raw wastewater after a treatment plant's headworks. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Polygon License

(poLic). The license for the availability of the polygon shapefile. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* licSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Policy and political sector or organization

(policy). Describes organizations whose core focus is on policy or political activity. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Poliovirus Group

(polioGrp). A group of measures/methods related to polioviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polioGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Polygon

(poly). A measure made on a compartment or property within a polygon. An example would be the population of a polygon; this specimen is used for measures at the polygon level, where site or population might not be entirely appropriate. *Part Type:* specimens *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon ID

(polygonID). Unique identifier for the polygon. A polygon is a geographic are representing the capment area of an environmental sample. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Polygon ID Object

(polygonIDObject). The polygon ID Object in a polygon relationship. The polygon relationship should be read as " 'subject' is 'relationshipID' to 'object' ". *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polgygon ID Subject

(polygonIDSubject). The polygon ID subject in a polygon relationship. The polygon relationship should be read as " 'subject' is 'relationshipID' to 'object' ". *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon Relationships Table

(polygonRelationships). Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. por *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Polygon relationships table column order

(polygonRelationshipsOrder). Specifies the order of the columns in the polygon relationships table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon relationships table required headers

(polygonRelationshipsRequired). Required headers in the polygon relationships table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon relationship ID

(polygonRelID). Unique identifier for each row in the polygon relationships table. Provisional PK. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon table

(polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. po *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Polygons table column order

(polygonsOrder). Specifies the order of the columns in a Polygons table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Polygon table required headers

(polygonsRequired). Specifies the columns required in a Polygons table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Polyomavirus Group

(polyomaGrp). A group of measures/methods related to polyomaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polyomaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Polygon Population

(polyPop). An attribute of a polygon, which specifies the population of that polygon. A rough estimate of the number of human residents. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.3.0.

Polygon Relationship Set

(polyRelSet). Value set for polygon relationships. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* polyRelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon or site specimen set

(polySiSpecimenSet). A specimen set that inculdes polygon or site specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* polySiSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Polygon specimen set

(polySpecimenSet). A specimen set that inculdes only a polygon specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* polySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Pooled

(pooled). Is this a pooled sample, and therefore composed of multiple child samples obtained at different sites *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Population

(pop). An measure or observation for a geographic area or population. Examples include human compartment measures such as case numbers, hospitalization rates for diseases or surface or air compartment measures such as snow coverage or ambient temperature. *Part Type:* specimens *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Populated area type set

(popAreaSet). Set of valid values used to describe the type of a populated area. *Part Type:* mmaSets *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* popClass

Nomenclature: popClass *Ontology Reference:* NA *Category Set ID:* popAreaSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Populated area type

(popAreaType). Type of populated area being sample (ie. urban, rural) *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* popAreaSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population assessment method

(popAs). Method for assessing the population count for a site/polygon. *Part Type:* methods *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* popMetSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population Class

(popClass). Measures and methods relating to population (ie. Measures of population, location). *Part Type:* classes *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Type of date for case reporting depreciated

(popDateTypeDep). Type of date used for confirmed cases. Typically, report or episode are reported. Onset and test date is not usually reported within aggregate data. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* methodConcSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Population density

(popDensity). Measure of population density of a site. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* popDensUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet

Reference Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population density unit set

(popDensUnitSet). Unit set for measures of population density of a site. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* popDensUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population equivalents

(popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a signle person would use. *Part Type:* units *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Population group

(popGrp). A group of measures/methods related to population-level factors. Examples might be case numbers, hospitalization rates, etc. *Part*

Parts

Type: groups *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Population Interval Set

(popIntSet). The collection of categorical inputs for population interval measures. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* popIntSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population assessment method set

(popMetSet). The set for valid inputs for the population assessment method. *Part Type:* mmaSets *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* popMetSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population or polygon specimen set

(poPolySpecimenSet). A specimen set that inculdes population or polygon specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* poPolySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population Served

(popServ). An measure of a site, which specifies the population of/population served by a given site. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.3.0.

Population Served - Interval

(popServRange). Population served by a site, when reported as an interval. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* popIntSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality*

Set: genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population unit set

(populationUnitSet). Unit set for hospital-related measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Polygon Relationships Table Short Name

(por). The abbreviated short name used to reference the table for recording the relationships between polygons. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Porechop

(porechop). A sequencing data processing application that is specifically designed for adapter trimming in Oxford Nanopore Technologies data.

Part Type: categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/rrwick/Porechop *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Port or Harbour

(port). A harbor is any sheltered body of water where boats or ships may moor or anchor. A port is an installation that has been built around a harbor with facilities for loading and unloading such vessels. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Population or sample set

(poSaSpecimenSet). A specimen set that inculdes population or sample specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* poSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Positive experimental control

(posCon). A sample or experimental condition where the expected outcome is known to occur, intended to confirm that the experimental setup is working properly. An example would be a wastewater sample spiked with a known quantity of SARS-CoV-2 virus. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Population or site set

(poSiSpecimenSet). A specimen set that inculdes population or site specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* poSiSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Population specimen set

(poSpecimenSet). A specimen set that inculdes only a population specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* poSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PostgreSQL License

(postgreSQL). The licensing for the measure or data set is managed under the PostgreSQL License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/postgresql/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Percent positive

(pp). Percent positive of sample measures. Can use for Moore swabs, etc. *Part Type:* units *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

parts per million

(ppm). Parts per million. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

PMMoV-CP

(ppmv). Pepper mild mottle virus capsid protein gene region *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* pmmovGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Percent positivity rate

(pprt). Percent positivity rate of tests conducted within a day in a given region. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum*

Value: 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Percent primary sludge

(pps). Percentage of total solids, for primary sludge. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

parts per thousand

(ppt). Parts per thousand. *Part Type:* units *Domain:* phy *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Protocol relationships table Shorthand

(pr). The abbreviated short name used to reference the The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Parts

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Precipitation (from solution)

(prec). The formation of a solid from a dissolved substance in a solution, typically induced by chemical reactions or changes in temperature/pH. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Precipitation - general

(precip). General measure of precipitation, type not specified. *Part Type:* measurements *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Precipitation class

(precipitation). Measures and methods related to precipitation. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* precipitation *Nomenclature:* precipitation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Precipitation unit set

(precipitationUnitSet). Unit set for percipitation measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Storage temperature prior to concentration

(preConcTemp). The temperature at which a sample was stored between collection and concentration. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference*

Parts

Link: NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* -100 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Storage time prior to concentration

(preConcTime). Length of time for which a sample is stored between collection and concentration. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Predicted data

(predicted). Predicted data, data generated by predictove models or algorithims, not taken directly from sample measures. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Predictive Modeling Calculation Type

(predictiveModels). A statistical or machine learning approach used to estimate future values or outcomes based on historical data patterns. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Storage temperature prior to extraction

(preExtractTemp). The temperature at which a sample was stored between concentration and extraction. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* -100 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Storage time prior to extraction

(preExtractTime). Length of time for which a sample is stored between concentration and extraction. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation*

Scale: seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

preQC (from Meraculous)

(preQC). A QC pipeline tool for sequencing data that evaluates data quality before assembly, particularly for large genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

presampling activity

(presampAct). A measure for recording any relevant activities that occur upstream of the sampling source. For example, recording that the river one is sampling from flows through farmland, or that filtration and/or sedimentation occurred at the wastewater treatment plant before the sample was collected. *Part Type:* measurements *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* presampSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Presampling activity category set

(presampSet). The set of valid input values for reporting pre-sampling activity. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* presampSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Pre-sampling weather

(preSampWeath). Weather leading up to, but not including, the day of sampling. *Part Type:* measurements *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* weathSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Pretreatment

(pretreat). Was the sample chemically treated in anyway with the addition of stabilizers or other Pretrement method can be describe using a method. See methodID. *Part Type:* measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Set ID: booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Primary clarifer

(primClar). A large settling tank that removes solids and floating materials from wastewater before secondary treatment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501468 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Genetic primer

(primer). Method ID used for indicating the primer used for a PCR or sequencing assay. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* primerSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Genetic primer set

(primerSet). The set for genetic primers used in sequencing or PCR assays. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* primerSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

PRINSEQ

(prinseq). A QC pipeline tool for sequencing data for assessing and filtering sequences based on complexity, quality scores, and GC content. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/prinseq/prinseq *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Prinseq-lite

(prinseqLite). A sequencing data processing application that filters sequences based on complexity and removes low-quality reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:*

https://prinseq.sourceforge.net *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Primate T-lymphotropic virus 1

(priTlym1). Human T-cell lymphotropic virus type 1, Primate T-lymphotropic virus 1, or human T-lymphotropic virus (HTLV-I or HTLV-1), also called the adult T-cell lymphoma virus type 1, is a deltaretrovirus of the human T-lymphotropic virus (HTLV) family. Latin species name: Deltaretrovirus priTlym1. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaretroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Primate T-lymphotropic virus 2

(priTlym2). Human T-cell lymphotropic virus 2, or Primate T-lymphotropic virus 2 (HTLV-II or HTLV-2), is a deltaretrovirus of the human T-lymphotropic virus (HTLV) family. Latin species name: Deltaretrovirus priTlym2. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaretroGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Private sector

(priv). The category of organization type used for private sector or non-profit groups that are not otherwise captured by the academic category. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Private data - not for disemination

(private). The measure or data set is private data - not for disemination. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Protocols table Shorthand

(pro). The abbreviated short name used to reference the the table that contains the summary information and details about a given protocol. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Processing group

(procGrp). A group of measures/methods related to processing samples for analysis. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Environmental survey or profiling

(profil). Purpose of sampling/measure is to record characteristics and profile a given environment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Program decription tables

(programDescr). Tables used to describe surveillance and testing programs. Program description tables record metadata on the organizations, locations, and protocols. Information include the name, location, and other contact information.These tables are usually completed once and they are updated only when contact information changes. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Prokka (with serotyping integration)

(prokka). Prokka (with serotyping integration) While primarily an annotation tool, Prokka outputs can be paired with databases for identifying serotypes of certain bacterial pathogens. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/sanger-pathogens/Roary *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Prokka + Roary Pipeline (Nextflow)

(prokkaRoary). Prokka + Roary Pipeline. Focus: Genome annotation (Prokka) with MLST and serotyping integration via Roary. Applications:

Broad compatibility with bacterial pathogens. Features: Facilitates core-genome MLST and accessory gene analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/lifebit-ai/roary *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

promega automated tna kit

(promAuto). Nucleic acid extraction performed using the promega automated tna kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

promega wastewater large volume tna capture kit - depreciated

(promegaLVTNA). promega wastewater large volume tna capture kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.2.0. Last updated: 3.0.1.

promega ht tna kit

(promHt). Nucleic acid extraction performed using the promega ht tna kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

promega manual tna kit

(promManu). Nucleic acid extraction performed using the promega manual tna kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

promega wastewater large volume tna capture kit

(promWW). Nucleic acid extraction performed using the promega wastewater large volume tna capture kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Proportion of total

(prop). Proportion as a precent of total. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Proportion of variant in sample

(propV). Proportion of a variant as percent of total variants. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Proteins class

(protein). Measures and methods related to proteins. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* protein *Nomenclature:* protein *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference*

Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol ID

(protocolID). A unique identifier for a given protocol. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol ID container

(protocolIDContainer). Unique identifier for the protocol and the steps and other protocols that make it up. Protocol ID Container in popuated by a protocolID (partID = protocolID) *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol ID object

(protocolIDObj). The object of the relationship between one protocol and another protocol or step, within a given protocol ID container. Populate

this field using Protocol ID (partID = protocolID). Together with ‘protocolIDSub‘ or ‘stepIDSub‘ and ‘relationshipID‘, the protocol relationship is defined as: [protocolIDSubject or stepIDSubject] [relationshipID] [protocolIDObject or stepIDObject]. Ex: stepIDSubject precedes protocolIDObject. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol ID subject

(protocolIDSub). The subject of the relationship between one protocol and another protocol or step, within a given protocol ID container. Populate this field using Protocol ID (partID = protocolID). Together with ‘protocolIDObj‘ or ‘stepIDObj‘ and ‘relationshipID‘ the row of ‘protocolRelationships‘ should say: [protocolIDSubject or stepIDSubject] [relationshipID] [protocolIDObject or stepIDObject]. Ex: stepIDSubject precedes protocolIDObject. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol relationships table

(protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a proceedure) and measureIDs (a measure). An example of a method is centrifugation; where the centriguation rotation speed is described as a measure. The short name for the table (partID) can be found in the instructions field. pr *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Synthetic ID for the protocolRelationships table

(protocolRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the protocolRelationships table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Protocol relationships table column order

(protocolRelationshipsOrder). Specifies the order of the columns in the Protocol Organization table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol Relationship table required headers

(protocolRelationshipsRequired). Specifies the columns required in the Protocol Organization table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol Relationships set

(protocolRelSet). set for valid values of relationshipID in the protocolRelationships table. Use only for protocolRelationships table relationshipID. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* protocolRelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocols table

(protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. pro *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocols table column order

(protocolsOrder). Specifies the order of the columns in the Protocols table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocols table required headers

(protocolsRequired). Specifies the columns required in the Protocols table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol steps table

(protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. ps *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Protocol steps table column order

(protocolStepsOrder). Specifies the order of the columns in a Protocol Steps table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol steps table required headers

(protocolStepsRequired). Specifies the columns required in a Protocol Steps table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol table set

(protocolTableSet). Tables holding information on the methods used for sample collection or measurement. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol version

(protocolVersion). Specifies the version of a method set. Version of the method set. Semantic versioning is recommended. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:*

integer *Missingness Set:* genMissingnessSet *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Access to prov ha

(provHA). If this is 'no', this data will not be available to provincial health authorities. If missing, data will be available to provincial health authorities. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Provisional report

(provisional). A provisional or interm report. Use for measurement that are not yet finalized. Typically this purpose is not publicly reported. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Province-level Aggregation at Site

(provLevel). Specifies that a sewershed/site represents a sub-national state, province, or region. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Protocol steps table Shorthand

(ps). The abbreviated short name used to reference the The table for collecting metadata on individual steps in a protocol, methodological process, or assay. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Pseudomonas

(pseudomonas). Pseudomonas *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* pseudomonasGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA

Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Pseudomonas Group

(pseudomonasGrp). A group of measures/methods related to pseudomonas bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* pseudomonasGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Primary clarifier sludge

(pSludge). Sludge produced by primary clarifiers *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Pumping station

(pStat). Pumping station - these stations transport sewage or various types of water from one place to another, to facilitate its movement toward

treatment plants. Sometimes also referred to as "lift stations". *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Post-grit

(pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but priort to a primary clarifier) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Practical salinity unit

(psu). practical salinity unit (PSU) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Pretreatment description - depreciated

(ptDescDep). If preTreatment then describe the treatment that was performed. Deprecated in version 2, please do not use. Use pretreatment methodID and specify further in summary and/or notes, if necessary. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Number of positive tests

(ptot). Number of positive tests conducted within a day in a given region. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Public Administration

(pubAdm). An organisation type that describes governmental organizations that manage or administer programs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:*

naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public Authority

(pubAuth). An organization type describing a public agency with authority over a given domain. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health agency

(pubHealth). Public health agency. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Access to public

(public). If this is 'no', this data will not be available to the public. If missing, data will be available to the public. *Part Type:* attributes *Domain:*

naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

PubMLST

(pubMLST). PubMLST. Focus: Web-based platform for MLST and serotyping analyses. Applications: Neisseria, Campylobacter, Salmonella, and more. Features: Combines curated databases with user-uploaded sequences. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://pubmlst.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Puro virus

(puro). Measure of the amount of puro virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* lentiGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Puro virus spike target

(puroMat). Puro Virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Purpose

(purpose). The reason the measure or sample was taken. See allowed categories: report, quality control, validation study, test *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* purposeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Purpose set

(purposeSet). Purpose set for a sample or measure. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* purposeSet *Unit Set:* naUnitSet

Aggregation Scale: naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Puumala virus (PUUV) hantavirus

(puuv). Puumala virus (PUUV) is the main cause of hemorrhagic fever with renal syndrome (HFRS) in Europe and Russia. Puumala virus is transmitted by the bank vole (Clethrionomys glareolus). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Poliovirus type 2

(pv2). Poliovirus type 2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polioGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Peptone Water with Glycerol

(pwWg). A buffer solution/medium used in environmental sampling, especially for preserving microorganisms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Human Polyomavirus (PyV)

(pyv). Studies reported human Polyomaviruses (PyV) (mainly strains BK and JC) contaminating water and food. These strains are, respectively, associated with nephropathy and progressive multifocal leukoencephalopathy. Others link them to common respiratory illnesses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polyomaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

BK Polyomavirus (BKV)

(pyvBK). BKPyV, or human polyomavirus BK, is defined a polyomavirus and an etiological agent associated with nephropathy. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

anyCompartmentSet *Group:* polyomaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

JC Polyomavirus (JCV)

(pyvJC). JCPyV, or human polyomavirus JC, is defined a polyomavirus and an etiological agent associated with progressive multifocal leukoencephalopathy, characterized by demyelination in the central nervous system, and has been detected in certain tumors, suggesting a potential but unproven link to cancer development. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polyomaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

q19e omicron-variant gene target

(q19e). q19e omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

q493r omicron-variant gene target

(q493r). q493r omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

q498r omicron-variant gene target

(q498r). q498r omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

q954h omicron-variant gene target

(q954h). q954h omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-

CompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quaility assurance method

(qaqc). Quality assurance and quality control method. Description of the quality control steps taken *Part Type:* methods *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* seqQCSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

QC3

(qc3). A comprehensive QC pipeline for NGS sequencing data that provides summary statistics on sequence quality and contamination. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/nhoffman/seq_qa_tools (quality control tools suite) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing Quality Control Method

(qcMethod). Method for sequencing quality control or assessment. *Part Type:* methods *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* seqQCSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Quality concerns

(qf1). A flag to indicate there is a quality concern, not otherwise sepcified. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

qiagen allprep dna/rna kit

(qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen digital PCR

(qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen ez1 virus mini kit v2.0

(qgEz1). Nucleic acid extraction performed using the qiagen ez1 virus mini kit v2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep powerfecal dna/rna kit

(qgPwrFecal). Nucleic acid extraction performed using the qiagen allprep powerfecal dna/rna kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:*

procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep powerviral dna/rna kit

(qgPwrViral). Nucleic acid extraction performed using the qiagen allprep powerviral dna/rna kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen powerwater kit

(qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen qiaamp buffers with epoch columns

(qgQiAmp). Nucleic acid extraction performed using the qiagen qiaamp buffers with epoch columns. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen rneasy kit

(qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen rneasy powermicrobiome kit

(qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep dna/rna kit depreciated

(qiAllprep). qiagen allprep dna/rna kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.2.0. Last updated: 3.0.1.

qiagen qiaamp dsp viral rna mini kit

(qiampDSP). qiagen qiaamp dsp viral rna mini kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

QIAseq FX DNA Library Kit

(qiaSeqFX). QIAseq FX DNA Library Kit by Qiagen. Alibrary prep kit that uses enzymatic fragmentation, suitable for a variety of applications, including whole-genome sequencing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Quantitative Real-Time PCR

(qpcr). Real-time PCR, also called 'quantAggScale' PCR *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

qPCR instruments (quantitative PCR)

(qPCRinst). A quantitative PCR instrument, to detect and quantify specific DNA/RNA targets. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

qProfiler2

(qProfiler2). A QC pipeline tool for sequencing data that produces reports with detailed QC metrics for aligned and unaligned reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/qprofiler2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Quality reports table Shorthand

(qr). The abbreviated short name used to reference the The table for recording the various quality metrics and indicators for samples and measures. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Qualitative

(qualAggScale). The qualitative aggregation scale. *Part Type:* aggregationScales *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet

Aggregation Scale: qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality control

(qualityControl). A measure or sample taken for the purpose of quality control. Measures with this category are take to assess quality control. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality flag

(qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample or measure. Types of quality flag vary on context; please see the qulaityFlagSet to be confirm. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* qualityIndicators *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicators

(qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality Indicator Set Header

(qualityIndSet). The quality set that corresponds to a given part. Only applicable for samples and measures. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* qualityIndSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicator sets

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical

Missingness Set: genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality report ID

(qualityReportID). A unique identifier for a given quality report. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality reports table

(qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. qr *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality rerpots table column order

(qualityReportsOrder). Specifies the order of the columns in the Quality Reports table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quality report table required headers

(qualityReportsRequired). Specifies the columns required in the Quality Reports table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quantitative

(quantAggScale). The "quantAggScale" aggregation scale. *Part Type:* aggregationScales *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Quarantine recommendation

(quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

R squared

(r2). R-squared value of the calibration curve. Used for storing calibration curve information, potentially also applicable for other curve types. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

r203m delta-variant gene target

(r203m). r203m delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

R346T Mutation

(r346t). The FLiRT/SLip variant mutation R346T. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Raindance digital PCR

(rainDpcr). Describes a PCR analysis done using Raindance's digital PCR technology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

dPCR Rain Percentage

(rainPerc). The percentage of droplets tha fall between the major positive and negative population in digital droplet PCR. *Part Type:* measurements

Domain: bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Rainy

(rainy). Qualitative category for the weather measure, specifying a rainy day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Random sampling surveillance program

(randomSurv). A surveillance sampling strategy in which baseline is established at the beginning of a study or project by the selection of sample units via random sampling. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Random sequencing selection method

(ranSeq). Specifies the random selection method for sequencing No primer set should be used if this is selected. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Ratio

(ratio). Ratio (unitless) Report as a real number or fration. i.e 10:2 ratio is reported as 5. The specifics of the ratio (the numerator and the demoninator) are described in the measure. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Raw data

(raw). Raw data, without adjustment or additional treatment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Raw wastewater

(raws). Raw wastes water sample *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Raw Sequence Data Processing Method

(rawSeqProc). The software/library/pipeline used to process the raw sequencing data. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* rawSeqProcSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Raw Sequence Data Processing Method Set

(rawSeqProcSet). The category set of valid innput values for the software/library/pipeline used to process the raw sequencing data. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:*

anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* rawSeqProcSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Raw sewage at site

(rawWW). Wastewater without any form of treatment *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Raw sewage downstream from a site

(rawWWdown). Downstream from a site. See partType = rawWWup. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Raw sewage upstream from a site

(rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjuctiion with downstream sample. For example, if the site is a long-term care home, but ther is not access to the building or property cleanout. Use two sameple, one sample upstream and one sample downstream. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

RaxML Software

(raxML). A lineage or clade analysis software tool, popular for rapid maximum likelihood-based phylogenetic tree building with clade assignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://cme.h-its.org/exelixis/web/software/raxml/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

IP2 rdrp sars-cov-2 gene target

(rdrpIP2). IP2 rdrp sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompart-

mentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

IP4 rdrp sars-cov-2 gene target

(rdrpIP4). IP4 rdrp sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing read mapping software name

(readMapper). The name of the bioinformatics software tool used to align short DNA or RNA sequence reads (obtained from high-throughput sequencing technologies like Illumina, PacBio, or Oxford Nanopore) to a reference genome or transcriptome. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* readMapperSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:*

NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing read mapping software set

(readMapperSet). The set of valid input values for the sequence read mapping software. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* readMapperSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Date sample recieved

(recDate). The date the sample was received at the laboratory for analysis. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Recombinant Lineage Variant

(recomb). A catch-all measure for viruses of non-specified and recombinant lineages, defined as those virsues wherein viruses of two different parent strains coinfect the same host cell and interact during replication to generate

virus progeny that have some genes from both parents. Recombination generally occurs between members of the same virus type (e.g., between two influenza viruses or between two herpes simplex viruses). This is particularly common in the evolution of coronaviruses and sarbecoviruses. Please bundle with a more general pathogen measure in a common measure set, so that it is clear to what species the recombinant virus belongs. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Recovered patients

(recov). Units for describing a population measure of patients who have recovered from a given disease. Unit for a population or disease measure to explain population-level clinical effects. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Redundans

(redundans). A sequencing software that is a genome assembler that reduces redundancy, useful for fragmented assemblies. *Part Type:* cate-

gories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/Gabaldonlab/redundans *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Refugee camp

(refCamp). A temporary, often makeshift shelter for persons displaced by war, political oppression, or for religious beliefs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Reference link

(refLink). Link to the reference material for a part. May link to literature on a method, measure, etc. Link to standard operating procedure for a measure or part. Part reference is a reference to a technical document that describes the part in detail. The reference could be a URL, DOI, or reference to a techincal report. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

Missingness Set: genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 255 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Region

(region). Specifies a region that combines multiple urban areas, and/or large rural areas. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Regular Pathogen Surveillance

(regular). A measure or sample taken for surveillance or epidemiology. A 'regular' measure is the default. Missing data will be recoded to this purpose. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Regular reports table set

(regularReportTableSet). Tables used for daily reporting of new measurements and information on sample collection. *Part Type:* dictSets *Domain:*

naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Relationship between entities

(relationshipID). Attribute for specifying the relationship between a sample subject and object. Together with ‘sampleIDSubject‘ and ‘sampleRelID‘, a row of the ‘sampleRelationships‘ should say: [sampleIDSubject] is a [sampleID] of [sampleIDObject] *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* relSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Measure relevance end date

(relDateEnd). The end date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Measure relevance start date

(relDateStart). The start date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Relative humidity

(relHum). The unit of relative humidity, or the air-water mixture. The ratio of the partial pressure of water vapor in the mixture to the equilibrium vapor pressure of water over a flat surface. of pure water at a given temperature. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* humid *Nomenclature:* humid *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* relHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Relative humidity unit set

(relHumidUnitSet). Unit set for relative humidity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* relHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Relationship Not Reported

(relNR). A relationship ID used in relationship tables across the ODM when two entities are related or connected in some way, but the actual nature of that relationship is not clear or reported. This is mostly used when mapping data from other data formats wherein protocol relationships (for example) do not report clear temporal relationships or order to method steps. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

General Relationship Set

(relSet). set for valid values of relationshipID across all fields and tables. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* relSet

Unit Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Representative grab sample

(repGrab). A single large representative grab sample. Deprecated in version 2, please do not use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Replicate Type set

(replicateSet). The set for storing valid categorical values of replicate type. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* replicateSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

replicate number

(repNum). The replicate number for a Ct or Cq value - used for specifying out a protocol standard curve. Only applies and used for aggregated

standard curves, or curves that are used across multiple plates. Otherwise, these details can be captured in a measure report and specified by measure index. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardCurve *Nomenclature:* standardCurve *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Primary reporting authority ID

(repOrg1). The primary or most responsible authority for rountine surveillance reports or findings, or where the site is located. Use the ‘organizations‘ table to describe attributes such as the name and address of the organziation. Use ‘orgType‘, ‘orgLevel‘ and ‘orgSector‘ to describe additional attributes. For example,whether the organization is a government agency (‘orgType‘), local (‘orgLevel‘), or public health (‘orgSector). If the attributes are not specified, the default is version 1.1.0 ‘publicHealthDepartment‘ defined as ’The public health department or region where the site is located. See also ‘healthReg‘ if there is a separate regional health care delivery authority.‘ *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Secondary reporting authority ID

(repOrg2). The secondary, additional or alternative authority for rountine surveillance reports or findings, or where the site is located. Use the ‘organizations‘ table to describe attributes such as the name and address of the organziation. Use ‘orgType‘, ‘orgLevel‘ and ‘orgSector‘ to describe additional attributes. For example,whether the organization is a government agency (‘orgType‘), local (‘orgLevel‘), or public health (‘orgSector). If the attributes are not specified, the default is version 1.1.0 ‘healthRegion‘, The health planning authority where is site is located. defined as ‘The public health department or region where the site is located.’ *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Reportable

(reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.1.0.

Report date

(reportDate). The date a measure was reported. This date is the first date the laboratory or enity reported the measure findings to the public health or other enity who ordered the measure or is responsible for action. Use the analyses end date if the measure is part of a research study or other purpose that does not have a reporting entity. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Reporter ID depreciated

(reporterIDDep). Unique identifier for the person or organization that is reporting the data. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.1.0. Last updated: 2.0.0.

Reporter table depreciated

(reportersDep). The table that contains information about a reporter of a sample, method, measure, or attribute. The short name for the table (partID) can be found in the instructions field. NA - depricated *Part Type:*

tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Report table input (wide table)

(reportTableInput). The short name for the listed source table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* shortName *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Report table name (wide table)

(reportTableName). The report table that the wide name calls from. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* tables *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 40 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Replicate Type

(repType). Attirbute of a sample, specifying whether the sample is unique, or a replicate. And if it is a replicate, what type of replicate is it? *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* replicateSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Reservoir

(res). An artificial body of water, often contained by a dam, constructed for the purpose of water storage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Resuspend COSCa filter collection

(resCosca). Nucleic acid extraction via resuspension of a sample collected using the COSCa ball method. See partID = cosca for additional details. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet

Reference Link: NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Research sector or organization

(research). Describes organizations whose focus is on research generation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Research purposes

(researchPurp). Purpose of sampling/measure is for research. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ResFinder Database

(resFinderDtbase). nomenclaturre from the National Center for Biotechnology Information *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category*

Parts

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* genepi.food.dtu.dk/resfinder *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ResFinder Tool

(resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/genomicepidemiology/resfinder *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Residents per square kilometre

(resPerKm). Residents per square kilometre. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Residents per square mile

(resPerMile). Residents per square mile. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Restaurant

(restaurant). A commercial establishment that prepares and serves food and beverages to customers. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:01000934 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Restricted data

(restrict). Missing data is witheld because it is restricted access. Missing value indicator for data that has been classified as resiticted, and not for sharing. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Results tables

(results). Tables used to record samples, measures and quality reports. These tables are updated whenever a new sample is taken or a measure is reported. Quality reports are used to report quality assurance and quality control for samples and measures. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Resuspension method

(resuspension). Describes the method used for resuspending material. *Part Type:* methods *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* resusSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Resuspension method set

(resusSet). The set to describe valid categorical values for the resuspension method. *Part Type:* mmaSets *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* resusSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Retained Element

(retainedElement). The element retained after centrifugation, filtration, solid separation, etc. *Part Type:* methods *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* retElSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Retained Element Set

(retElSet). The set for enumerating the valid possible values of the retained element method. *Part Type:* mmaSets *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* retElSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical

Missingness Set: NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Retention pond

(retPond). Retention pond *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Review of records

(rev). A review of records for determining site/polygon population. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Rickettsia

(rickettsia). Rickettsia *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rickettsiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:*

seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Rickettsia Group

(rickettsiaGrp). A group of measures/methods related to ricketsia parasites. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rickettsiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

River, natural water body

(river). River, natural water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

RNA Template

(rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

rRNA Depletion Method

(rnaDepl). Removal of background RNA for the purposes of enriching the genomic target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

RNAlater

(rnaLater). A buffer solution/medium the stabilizes RNA and DNA in samples, effective for preserving nucleic acids in wastewater. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Ribonuclease P (RNase P)

(rnaseP). Ribonuclease P (RNase P) (usually measured as a human fecal indicator) *Part Type:* measurements *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Road

(road). A paved or unpaved pathway designed for vehicular and pedestrian travel. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:00000064 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Roadside

(roadside). The area adjacent to a road, including sidewalks, shoulders, or drainage ditches. *Part Type:* categories *Domain:* naDomain

Speciment ID: naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:01000447 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Role of contact

(role). Specifies the organizational role of a given contact. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Rotavirus

(rotavirus). Rotavirus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rotavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Rotavirus Group

(rotavirusGrp). A group of measures/methods related to rotaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rotavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Routine surveillance

(routSurv). Standard, ongoing collection of public health data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Rate per 100,000

(rP100). Units for describing a population measure of a rate of case incidence per 100,000 people of a given disease. Unit for a population or disease measure to explain population-level clinical effects. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Revolutions per minute (RPM)

(rpm). RPM stands for "Revolutions per minute." This is how centrifuge manufacturers generally describe how fast the centrifuge is going. The rotor, regardless of its size, is revolving at that rate. *Part Type:* units *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Raw post-pasteurized wastewater

(rppw). Raw wastewater sample post-pasteurization *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Resistant strain identified

(rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. *Part Type:* categories *Domain:* naDomain *Spec-*

iment ID: naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Respiratory syncytial virus A and B combined

(rsvAB). Human Respiratory Syncytial Virus Type A (RSV A) and Type B (RSV B). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NCIT:C184696 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.3.

Respiratory syncytial virus A

(rsvAMe). Human Respiratory Syncytial Virus Type A (RSV A). Refer to Group = ‘rsv‘ and ‘rsv‘ for measure that are apply to either RSV A or RSV B. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NCIT:C184696 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.3.

Respiratory syncytial virus B

(rsvB). Human Respiratory Syncytial Virus Type B (RSV B). Refer to Group = 'rsv' and 'rsv' for measure that are apply to either RSV A or RSV B. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NCIT:C184697 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.3.

Respiratory syncytial virus (RSV) Group

(rsvGrp). Human Respiratory Syncytial virus (RSV). Refer to Group = 'rsvA' and 'rsvB' for measure that are specific to RSV A or RSV B, respectively. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NCIT:C14267 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.1.2.

Respiratory syncytial virus

(rsvMe). Human Respiratory Syncytial virus (RSV), generic measure. Refer to Group = 'rsvA' and 'rsvB' for measure that are specific to RSV A or RSV B, respectively. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* anyCompartmentSet *Group:*

rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NCIT:C14267 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.1.2.

RSV N-gene

(rsvN). Human Respiratory syncytial Virus, N-gene region. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.3. Last updated: 2.1.3.

reverse transcription

(rt). Describes the reverse transcription cycle in a PCR process. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

RT-qPCR intruments

(rtqPCRinst). Real-time quantitative PCR instruments, used when detecting RNA viruses (an additional a reverse transcription step). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Rubella

(rubella). Rubella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rubellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Rubella Group

(rubellaGrp). A group of measures/methods related to the rubella virus. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rubellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum*

Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Rural

(rural). Rural populated area type *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

s2083i omicron-variant gene target

(s2083i). s2083i omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

s371l omicron-variant gene target

(s371l). s371l omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation*

Scale: seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

s373p omicron-variant gene target

(s373p). s373p omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

s375f omicron-variant gene target

(s375f). s375f omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

s477n omicron-variant gene target

(s477n). s477n omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample

(sa). A measure made on a compartment or property from a sample of a substance. *Part Type:* specimens *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Saffold Virus Group

(saffoldGrp). A group of measures/methods related to saffold virus. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA

Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus (SAFV)

(safv). Saffold virus (SAFV) is an emerging human cardiovirus associated with respiratory and gastrointestinal infection, and, more recently, to symptoms related to the endocrine, cardiovascular, and neurological systems. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 1 (SAFV-1)

(safv1). Strain 1 of the saffold virus (SAFV-1). The only strain with global distribution. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 2 (SAFV-2)

(safv2). Strain 2 of the saffold virus (SAFV-2) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 3 (SAFV-3)

(safv3). Strain 3 of the saffold virus (SAFV-3) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 4 (SAFV-4)

(safv4). Strain 4 of the saffold virus (SAFV-4) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference*

Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 5 (SAFV-5)

(safv5). Strain 5 of the saffold virus (SAFV-5) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompart-mentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 6 (SAFV-6)

(safv6). Strain 6 of the saffold virus (SAFV-6) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompart-mentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 7 (SAFV-7)

(safv7). Strain 7 of the saffold virus (SAFV-7) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 8 (SAFV-8)

(safv8). Strain 8 of the saffold virus (SAFV-8) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saffoldGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Salivirus A (Salivirus aklasse)

(saliA). Salivirus A (Salivirus aklasse) has been identified in humans and chimpanzees and may cause acute gastroenteritis in humans, having been detected in 0% to 8.7% of fecal samples collected from gastroenteritis in different human populations. Salivirus is ubiquitous in wastewater of human origin and river water specimens worldwide and represents a potential indicator human RNA virus for monitoring of environmental samples.

Parts

Part Type: measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Salivirus Group

(saliGrp). A group of measures/methods related to salivirus. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* saliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Salinity

(salinity). Measurement of salinity/salt content *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* salinityUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Salinity unit set

(salinityUnitSet). Unit set for salinity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* salinityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Salmonella

(salmonella). Salmonella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* salmonellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Salmonella Group

(salmonellaGrp). A group of measures/methods related to salmonella bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* salmonellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

SalmonellaTypeFinder

(salTypeFin). SalmonellaTypeFinder A specialized tool for predicting Salmonella serotypes based on genomic data, similar to SeqSero. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* Source: https://bitbucket.org/genomicepidemiology/salmonellatypefinder *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample material

(saMaterial). Type of sample. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sampleMatSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sample concentrate

(samConc). Sample concentrate. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sampling Event

(sampleEvent). In settings where a person goes out and collects multiple samples, but more accurate location data is not recorded, this is used to group samples from that outing, or 'sampling event'. Use for the shared sampling event as a single sample, all independent samples would be child samples of the event, with a 'child' relationship ID. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample ID

(sampleID). Unique identifier for a sample. Suggestion:siteID-date-index. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Sample ID object

(sampleIDObject). Populated by ‘sampleID‘ - this specifies the object of a sample relationship. Use ‘sampleID‘ for this field. Together with ‘sampleIDSub‘ and ‘relationshipID‘ the row of the ‘sampleRelationships‘ should say: [sampleIDSubject] is a[relationshipID] of [sampleIDObject] *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample ID subject

(sampleIDSubject). Populated by ‘sampleID‘ - this specifies the subject of a sample relationship. Use ‘sampleID‘ for this field. Together with ‘sampleIDSub‘ and ‘relationshipID‘ the row of the ‘sampleRelationships‘ should say: [sampleIDSubject] is a[relationshipID] of [sampleIDObject] *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample material set

(sampleMatSet). set for the types of material that can be found in a sample. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sampleMatSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample quality set

(sampleQualitySet). Quality set for a sample. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample relationships table

(sampleRelationships). Table for recording the relationships between samples.Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field. sar *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:*

results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Synthetic ID for the sampleRelationships table

(sampleRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the sampleRelationships table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sample relationships table column order

(sampleRelationshipsOrder). Specifies the order of the columns in a Sample Relationships table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample relationships table required headers

(sampleRelationshipsRequired). Specifies the columns required in a Sample Relationships table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample relationships set

(sampleRelSet). set for valid values of relationshipID in the sampleRelationships table. Use only for sampleRelationships table relationshipID. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sampleRelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample report table

(samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site.Samples can be combined, split, stored and reused. The ‘Sample relationships‘ (sampleRelationships) is used to describe the relationships between samples. The short name for

the table (partID) can be found in the instructions field. sas *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sample shed

(sampleShed). A geographic area, physical space, or structure. A sample is taken from a sampleshed for a representative measurement of a substance(s). Examples: Airplane, Long-term care home, Neighbourhood, University campus, Municipality *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* shedSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Samples table column order

(samplesOrder). Specifies the order of the columns in a Samples table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1

Maximum Value: NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample table required headers

(samplesRequired). Specifies the columns required in a Samples table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Collection other depreciated

(sampleTypeOther). Description for other type of method not listed in collection. depreciated. *Part Type:* methods *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* othAgg *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

SAMtools rmdup

(samRmdup). A deduplication method that identifies and removes PCR duplicates based on alignment data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.htslib.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SAMtools

(samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.htslib.org/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample volume

(samVol). The volume of a given sample. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.2.0. Last updated: 3.0.0.

Sapovirus

(sapovirus). Sapovirus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sapovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sapovirus Group

(sapovirusGrp). A group of measures/methods related to sapoviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sapovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sample relationships table Shorthand

(sar). The abbreviated short name used to reference the Table for recording the relationships between samples. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

Missingness Set: NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

SARS-CoV-2

(sarsCov2). A group of measures/methods related to the SARS-CoV-2 virus. SARS-CoV-2 measures have the following classes: proteins, alleles, variants, mutations, diseases. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NCIT:C169076 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample report table Shorthand

(sas). The abbreviated short name used to reference the The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Sample specimen set

(saSpecimenSet). A specimen set that inculdes only a sample specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sparse coverage

(sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. If there are multiple issues to flage, use the multiple issues flag and explain the details in the notes section. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Secondary clarifier effluent depreciated

(sce). Effluent obtained after secondary clarifiers. Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Standard curve frequency

(scf). A measurment for specifying the frequecy over which a standard curve (or 'Master Curve') is used. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 3.0.1.

School

(school). A school serving students in the kindergarten to 12th grade range *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

School closure

(schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. *Part Type:* categories *Domain:* naDomain *Speci-*

ment ID: naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

sciencell viral rna isolation kit

(sciencellRNA). sciencell viral rna isolation kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sequencing script version set

(scriptSet). The set for script versions *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* scriptSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Genetic sequencing script version

(scriptVersion). Used to specify the script or script version used to extract summary information (i.e. coverage and mutation frequency statistics, etc.) from the sequencing output. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* scriptSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Secondary clarifier sludge depreciated

(scsDep). Sludge produced by secondary clarifiers. Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Standard deviation

(sd). Standard deviation. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

Missingness Set: NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Normalized standard deviation

(sdn). Standard deviation, normalized. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sludge dryer

(sDryer). A facility or equipment used to reduce moisture content in wastewater sludge for easier handling and disposal. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501473 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sterile Distilled Water with Sodium Thiosulfate

(sDWwST). Sterile Distilled Water with Sodium Thiosulfate - Used to neutralize chlorine for microbiological analysis in wastewater samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sets look-up table Shorthand

(se). The abbreviated short name used to reference the Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Sea, natural water body

(sea). Sea, natural water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Secondary clarifer

(secClar). A tank in wastewater treatment that removes biological solids (e.g., microbial flocs) after aeration. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501471 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Seconds

(seconds). The unit of time, seconds. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

See unit (aggregation scales)

(seeUnitAggScale). A value for aggregation scale to be used when the aggregation scale depends on that specified in the parts list entry for the unit. When you encounter this value, see the unit being used for that entry and follow that aggregation scale entry. *Part Type:* aggregationScales *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet

Aggregation Scale: naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

See unit (data type)

(seeUnitData). The data type entry when the data type for a given entry is specified by the unit used. Only used for measures, which is where the data type entry is used to validate the entry in the value field. For these cases, however, the data type is more dependant on the unit than the measure , and so this entry directs users to consult the data type of the unit. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

See unit (value)

(seeUnitVal). A value for maximum or minimum value in the dictionary, use when the maximum or minimum value is determined by the unit. Used for measures when the constraints on maximum and minimmum value are specified by the unit, not the measure. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Secondary clarifier effluent

(sEfflu). Effluent obtained after secondary clarifiers *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Access to self

(self). If this is 'no', this data will not be shown on the portal when this reporter logs in. If missing, data will be available to this reporter. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Semi-solid

(semSol). A state of matter consisting of molecules in a non-rigid structure that can retain its shape and volume but that is not resistant to such change. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Date sample was sent

(sentDate). Date that the sample was sent from the collection site to the lab. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Seoul virus (SEOV) hantavirus

(seov). Seoul virus (SEOV) is one of the main causes of hemorrhagic fever with renal syndrome (HFRS). Seoul virus is transmitted by the brown rat (Rattus norvegicus) and the black rat (Rattus rattus). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Septic tank wastewater

(septage). Wastewater from within a septic tank *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Septic tank

(septTnk). Septic tank *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sequence Assembly Software

(seqAss). The name of the software/toolkit/pipeline used for assembling sequences from reads. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqAssSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

sequence assembly length

(seqAssLen). The length of the genome generated by assembling reads using a scaffold or by reference-based mapping. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequence Assembly Software Set

(seqAssSet). The valid set of categorical values for sequence assembly software methods. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqAssSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequence Contaminated

(seqContam). Sequence is contaminated. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* na-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

SeqKit rmdup

(seqKitRmdup). A deduplication method that works within SeqKit for duplicate removal in FASTA/FASTQ files. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/shenwei356/seqkit *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SeqKit stats

(seqKitStats). Part of SeqKit, a QC pipeline tool for sequencing data that providing a summary of sequence metrics like length, GC content, and quality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://bioinf.shenwei.me/seqkit/usage/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing Layout

(seqLay). The layout of genetic material used in sequencing. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqLaySet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing Layout set

(seqLaySet). The set for the layout of genetic material used in sequencing *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqLaySet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SeqMan Pro (Lasergene)

(seqManPro). Sequencing software that is for de novo sequence assembly and consensus calling. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.dnastar.com/software/lasergene/ (homepage) — happy to fetch exact link *Data Type:* varchar *Missingness*

Set: NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing QC Pipeline

(seqQC). The quality control pipeline for sequencing or PCR data. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqQCSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing QC Pipeline Set

(seqQCSet). The category set of valid innput values for the software/library/pipeline used to do quality checks on sequencing or PCR data. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqQCSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing quality set

(seqQualitySet). Quality set for sequencing measures *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment*

Set: anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing selection method

(seqSel). The primer sequence selection method used in sequencing. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqSelSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing selection method set

(seqSelSet). The set for the selection method used in sequencing *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqSelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SeqSero2

(seqSero2). SeqSero2. Specifically designed for Salmonella serotyping using raw sequence reads, assemblies, or even complete genomes. Provides results based on antigenic formulas or serotype names. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.denglab.info/SeqSero2 GitHub: https://github.com/denglab/SeqSero2 *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing Strategy

(seqStrat). The sequencing strategy used for an analysis. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqStratSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing Strategy set

(seqStratSet). The set for the sequencing strategy used for an analysis *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:*

sequence *Ontology Reference:* NA *Category Set ID:* seqStratSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

seqtk

(seqtk). A lightweight sequencing data toolkit for FASTQ and FASTA manipulation, including trimming and subsampling. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/lh3/seqtk (homepage of tool) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SeqTyping

(seqTyping). SeqTyping. Focus: Simultaneous MLST and serotyping for Escherichia coli and Salmonella. Applications: Integrated with bacterial genome typing databases. Features: Compatible with short-read sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Genetic sequences class

(sequence). Measures and methods related to genetic sequencing. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

serial dillution

(serDil). Describes a serial dilution process for standard curve generation for PCR. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Serial dilution

(serialDilution). The serial dilution method for assessing inhibition. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* dilution *Nomenclature:* dilution *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Serotyping Method

(seroMeth). The method used to determine the serovar. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seroMethSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Serotyping Method Set

(seroMethSet). The set of categorical inputs for populating the the serotyping method field. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seroMethSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SerotypeFinder

(serotypeFin). SerotypeFinder. A web-based tool that predicts serotypes for Escherichia coli and other bacteria by detecting genes encoding O-antigens and H-antigens. Developed by the Center for Genomic Epidemi-

ology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* Web tool: https://cge.cbs.dtu.dk/services/SerotypeFinder/ CLI: https://github.com/Papos92/ecoli_serotyper *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Serological Variant (Serovar)

(serovar). The serovar of the organism. Only include this information if it has been determined by traditional serological methods or a validated in silico prediction tool e.g. SISTR. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sewer Sediments Depreciated

(seseDep). Sediments obtained in sewer. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite Set ID

(setCompID). A composite ID generated by concatennating the 'setID' and 'partID' of a given row in the sets table. This allows for a unique primary key and robust relational database structure. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 60 *Part Status:* active. First released: 2.2.2. Last updated: 3.0.1.

Set ID

(setID). The unique identifier of a value set. A set is a group of units, attributes, categories, specimens, or compartments that can be used for a measure, method or attribute. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sets look-up table

(sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. se *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sets table column order

(setsOrder). Specifies the order of the columns in the Sets table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sets table required headers

(setsRequired). Required headers in the Sets table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Settled solids

(settsol). Amount of settled solids from a wastewater sample. May be a volume or a weight, see the unitID for a given measure row for details on a given sample. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Set type

(setType). The type of set. i.e. quality set, aggregation set, unit set *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* setTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Set Type Set

(setTypeSet). The mmaSet for defining the possible values of setType. Previously undefined but now made explicit in this set. *Part Type:* mmaSets

Domain: naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* setTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Severity indicator

(severity). An indicator of the severity or seriousness of a quality flag. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sevSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Severity set

(sevSet). A set for severity indicators. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sevSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sewage equivalent

(sewEq). Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sewer network file link depreciated

(sewerNetworkFileBLOB). Link to a file that has any detailed information about the sewer network associated with the site (any format). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Sewage travel time

(sewTrTi). A measure of sewage travel time, often approximate, from sewage source to the sampling site. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data*

Type: integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Shaker aggitation speed

(shaker). The speed/aggitation level for a shaker plate/shaker platform. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* speed *Nomenclature:* speed *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* speedUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Shasta

(shasta). A sequencing software that is a fast assembler optimized for nanopore long-read data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://paoloshasta.github.io/shasta/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sampleshed set

(shedSet). The set for all valid values of sampleshed. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-

CompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* shedSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Shigella

(shigella). Shigella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* shigellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Shigella Group

(shigellaGrp). A group of measures/methods related to shigella bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* shigellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ship

(ship). A cruise ship or other ship. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Shipped on ice

(shipOnIce). Was the sample kept cool while being shipped to the lab *Part Type:* methods *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

ShortBRED Software

(shortBRED). Software tool that screens for known AMR genes in shotgun metagenomic sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://huttenhower.sph.harvard.edu/shortbred/ *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Short names

(shortName). Shortened names for tables and other important parts for use in wide names. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Read Lengths Shorter Than Expected

(shortRead). Read lengths are shorter than expected. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Shorthand or Short Name Set Type

(shortSets). Sets used to group together short names for tables or part types in ODM. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Short Name Set

(shrtNameSet). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). *Part Type:* shortSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Sites table Shorthand

(si). The abbreviated short name used to reference the The table that contains information about a site; the location where an environmental sample was taken. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Sickle

(sickle). A sequencing data processing application that is a quality-based trimming tool for Illumina data with single-end and paired-end support. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/najoshi/sickle *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Single

(sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Single Layout

(sinLay). Specifies the single layout for a sequencing method *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Singleplex, probe-based, one-step RT-qPCR

(sinProbeOne). Describes a PCR method that is singleplex, probe-based, and one-step RT-qPCR. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Site or sample specimen set

(siSaSpecimenSet). A specimen set that inculdes site or sample specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Site specimen set

(siSpecimenSet). A specimen set that inculdes only a site specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Salmonella In Silico Typing Resource (SISTR)

(sistr). Salmonella In Silico Typing Resource (SISTR). Used for in silico serotyping of Salmonella enterica based on whole-genome sequencing. Combines genomic data with the traditional White-Kauffmann-Le Minor serotyping scheme. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* CLI: https://github.com/phac-nml/sistr_cmd Web app: https://lfz.corefacility.ca/sistr-app/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Site

(sit). A measure made on a compartment or property at a site. An example is the wastewater flow rate, taken at a wasteawater treatment plant. *Part Type:* specimens *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Site ID default

(siteDef). Used as default when a new sample is created by this reporter. See ID in Site table. Deprecated in version 2, please do not use. Just populate standard SiteID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Site features group

(siteFeat). A group of environmental measures/methods and those pertaining to the features of a site. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Site ID

(siteID). Unique identifier for the location where a sample was taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Level of Aggregation of a Sampling Site

(siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type of region is represented by the base sewershed. This can be used to pool together or average results across similar sewersheds, and avoid trying to average different scales of sewershed together without a correction for size. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* siteLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Site Level Category Set

(siteLevelSet). The category set containing all valid entries for the siteLevel field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* siteLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Site measure ID

(siteMeasureID). Unique identifier for wide table only. Use when all measures are performed on a single sample. Depreciate in version 2. siteMeasures *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Sites table

(sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an eviromental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the infomation changes often. The short name for the table (partID) can be found in the instructions field. si *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* programDescr *Nomenclature:* programDescr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sites table column order

(sitesOrder). Specifies the order of the columns in a Sites table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet

Parts

Compartment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sites table required headers

(sitesRequired). Specifies the columns required in a Sites table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Site Type

(siteType). Type of site or institution where sample was taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* siteTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Site set

(siteTypeSet). set for the type of sampling site. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* siteTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Skewer

(skewer). A sequencing data processing application that is a fast tool for adapter trimming and quality trimming in Illumina data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/relipmoc/skewer *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Skimmed milk flocculation

(skimMilkFloc). Skimmed milk flocculation *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Slow-flowing

(slFlow). A quality of a body of water wherein there is a slow flow. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample Limit of Detection (LOD)

(slod). The minimum level of a target within a sample that would be consistently detectable considering all sample processing steps, from sample concentration leading up to and including amplification and quantification steps of RT-qPCR. In this Protocol, the SLOD is the concentration factor-adjusted ALOD, which provides a theoretical estimate of the minimum concentration in the original sample that would yield consistent detection of the target, assuming no method losses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 3.0.0.

slope

(slope). Slope value of the calibration curve. Used for storing calibration curve information, potentially also applicable for other curve types. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater Sludge - non-specified

(sludgeNS). Sample material is wastewater sludge - whether primary, secondary or other is unspecified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Slurry

(slur). An quality in which the fluid like material is more viscous due to the suspension of insoluble solid particles. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

Missingness Set: NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Siemens per meter

(sm). Siemens per meter (S/m) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SMALT

(smalt). SMALT. A highly parallelized mapper. High-speed aligner for genomic DNA reads. Best for: Applications requiring flexibility with non-standard parameters. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sourceforge.net/projects/smalt/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SMARTer ThruPLEX Plasma-seq Kit

(smarterThruPLEX). SMARTer ThruPLEX Plasma-seq Kit by Takara Bio. A library prep kit optimized for low-input DNA, including cell-free DNA

for liquid biopsy studies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Skim Milk–Glycerol Medium

(smgm). A buffer solution/medium that protects bacteria in environmental samples, preventing freeze-thaw damage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Smoothing Calculation Type

(smoothing). A technique used to reduce short-term fluctuations in data to better reveal underlying trends or patterns, such as using moving averages or splines. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Snap

(snap). Snap. A highly parallelized mapper. Ultrafast, designed for genomic and RNA-seq applications. Best for: Large-scale sequencing projects. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/amplab/snap (alignment tool) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SNAPP Software

(snapp). A lineage or clade analysis software tool in BEAST for species delimitation and clade analysis in population genomics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.beast2.org/snapp/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sewer network file link depreciated 2

(snfl). Link to a file that has any detailed information about the sewer network associated with the site (any format). Depreciate in version 2. This attribute has been changed to referenceLink. Use po_referenceLink to specify polygon link to sewer network file. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Snowy

(snowy). Qualitative category for the weather measure, specifying a snowy day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sin Nombre virus (SNV) hantavirus

(snv). Sin Nombre virus (SNV) is the most common cause of hantavirus pulmonary syndrome (HPS) in North America. Sin Nombre virus is transmitted mainly by the western deer mouse (Peromyscus sonoriensis). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hantaGrp *Class:* organism

Nomenclature: organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Soap2

(soap2). Soap2. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://soap.genomics.org.cn/soap2.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Soap3

(soap3). Soap3. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* Reference: http://soap.genomics.org.cn (includes SOAP3 info) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SOAPdenovo

(soapDenovo). A sequencing software that is an assembler for short-read data, suited to large and complex genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://soap.genomics.org.cn/soapdenovo.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Social distancing measures

(socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Software Class

(software). Measures and methods related to software. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Solid fraction (general)

(sol). Solid fraction of a sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Solid Fraction (Dry)

(solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

Solids/Pellet retained

(solid). The solids or pellet is retained after solid separation/centrifugation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet

Compartment Set: naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Solid

(solidMat). The state in which a substance has no tendency to flow under moderate stress; resists forces (such as compression) that tend to deform it; and retains a definite size and shape. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Solid seperation

(solidSep). Process used to separate solid and liquid phases of the sample. Solid seperation is used either prior to or in the absence of the concentration method specified in 'methodConc'. *Part Type:* methods *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* solidSeparationSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Solid separation set

(solidSeparationSet). set for the separation of solids. *Part Type:* mmaSets *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* solidSeparationSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Solid fraction (Wet)

(solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.3.0. Last updated: 2.3.0.

SortMeRNA

(sortMeRNA). A sequencing data processing application that is used for ribosomal RNA filtering in metatranscriptomic data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:*

software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/sortmerna/sortmerna *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wide name source

(source). The database or table sourced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Source Code

(sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps. It is possible to record the full code as text, or to record it as a URL to where code is stored. Likely a different URL than the refLink field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Source Protocol ID

(sourceProtocol). A protocol that served as a basis for another protocol. This may be due to version changes, or a referencing a protocol that was later adapted. Populate with protocolID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Protocol step source ID

(sourceStep). Specifies the protocol step which serves as a basis for a given protocol step. Populate with a protocol step ID (stepID). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sovereign status of a country

(sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

SPAdes

(spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://cab.spbu.ru/software/spades/ (via SPbU) — can confirm official mirror *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Specific humidity

(specHum). Measure for specific humidity, the unit is the ratio of the mass of water vapour and the mass of total air. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* humid *Nomenclature:* humid *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* specHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specific humidity unit set

(specHumidUnitSet). Unit set for specific humidity. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* specHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specifies

(specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Use only for protocolRelationships table relationshipID. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specimen

(specimen). The substance or thing upon which the observation was made. Specimens include: site, sample, person and population. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* specimens *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:*

NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specimen input (wide table)

(specimenInput). The partID for the specimen being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* specimens *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Specimen name (wide table)

(specimenName). The specimen referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* specimens *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Specimens

(specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See

partID = specimentID. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specimen Set Header

(specimenSet). An idenfication of a set of specimens that can be applied for a measure or method. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* specimenSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Specimen sets

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Spectrophotometers or fluorometers

(spectroFluoro). Spetrometer and fluorometer instruments; may be used to assess concentration and purity (e.g., NanoDrop™, Qubit™). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Speed class

(speed). Measures and methods relating to speed. *Part Type:* classes *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* speed *Nomenclature:* speed *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* windSpeedUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Speed Unit Set

(speedUnitSet). Unit set for reporting speeds (centrifugation speed, etc.) *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* speedUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sucrose Phosphate Glutamate (SPG) Buffer

(spg). A buffer solution/medium that stabilizes viruses, including in wastewater samples, by preventing RNA degradation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Spike matrix and recovery

(spike). The spike matrix and recovery method for assessing inhibition. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Spike Concentration

(spikeConc). Concentration of the recovery efficiency target in a spike matrix and recovery assay. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Category Set ID: NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 Spike gene (orf2)

(spikeGene). SARS-CoV-2 Spike gene (orf2) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100154 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Spike material

(spikeMat). Material into which the recovery efficiency control target is spiked. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* spikeMatSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Spike material set

(spikeMatSet). set for spikeMat (aterial into which the recovery efficiency control target is spiked). *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* spikeMatSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Recovery efficiency spike target

(spikeTarget). Method specifying the recovery efficiency control target. This matches on to the the spike material method ID. Should typically be indexed as a step proceeding the spikeMaterial methodID step. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* spikeTargetSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Recovery efficiency spike target set

(spikeTargetSet). The set capturing containing all of the valid categories for the recovery efficiency control (or spike) target. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:*

NA *Category Set ID:* spikeTargetSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample spilled

(spill). Sample contents spilled from container. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Spring

(spr). A surface landform which provides an egress for groundwater or steam to flow out of the ground. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sequence Read Archive (SRA)

(sra). Sequence Read Archive (SRA). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.ncbi.nlm.nih.gov/sra/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SRST2 Software

(srst2). Software tool for analyzing antimicrobial resistance using short read sequences. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/katholt/srst2 or https://katholt.github.io/srst2/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

SSAKE

(ssake). A sequencing software that is a simple de novo assembler for highly overlapping short reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* https://www.bcgsc.ca/resources/software/ssake *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Streptococcus Serotyping Tool (SSI)

(SSI). Streptococcus Serotyping Tool (SSI) A web-based platform for serotyping Streptococcus pneumoniae based on capsular polysaccharide synthesis loci. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* Product/antisera info: https://ssidiagnostica.com/solutions/antisera/streptococcus-antisera/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Secondary clarifier sludge

(sSludge). Sludge produced by secondary clarifiers *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Social services shelter

(sss). Other type of social services shelter *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Stabilization pond

(stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment to reduce the organic content and remove pathogens from wastewater. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Stagnant

(stag). A quality of a body of water wherein it has no current or flow. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Statistical Analysis of Metagenomic Profiles (STAMP) Software

(stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://kiwi.cs.dal.ca/Software/STAMP or https://beikolab.cs.dal.ca/software/STAMP *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Standard for Data Adjustment

(standard). A field where one can categorically record the standard to which something is being standardized (ie. PMMoV, Crassphage, Flow, etc.) or smoothed (ie. bayesian smoothing, central average smoothing, 7-days, time, etc.). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* allStandardSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Standard concentrations class

(standardConc). Measures and methods relating to standard conentrations. *Part Type:* classes *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Standard curve class

(standardCurve). Measures and methods relating to generating or recording a standard curve. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* standardCurve *Nomenclature:* standardCurve *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Standardization Calculation Type

(standardization). A method used to scale data to a common range or distribution, often to enable fair comparisons across different variables, time periods, or locations. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Staphylococcus Group

(staphGrp). A group of measures/methods related to staphylococcus bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* staphGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

STAR (Spliced Transcripts Alignment to a Reference)

(star). STAR (Spliced Transcripts Alignment to a Reference). A general-purpose read mapper. Fast aligner designed for RNA-seq, supports spliced alignment. Best for: Transcriptome data analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/alexdobin/STAR *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

StarAMR Software

(starAMR). Software tool that is used to detect AMR genes in genome assemblies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.rcac.purdue.edu/software/staramr *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Departments, states, or provinces

(stateProvLevel). Departments, states, or provinces *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

State, Province, or Region

(stateProvReg). The state, province, or region where a site or organization is located; part of the address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* geoRefMissingnessSet *Minimum Value:* NA *Maximum*

Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 3.0.1.

Status

(status). Whether the part is still active and can be used in the most current ODM version. Values are 'active' or 'inactive'. The status of the part or list. 'active' means the part is used in the dictionary version. 'inactive' means the part has been retired and not longer used in the version. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* statusSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Status set

(statusSet). A set for partID = Status to indicate whether a part is in current use or not. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* statusSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Standard sample

(std). Denotes a standard sample replicate. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Standard concentration unit set

(stdConcentrationUnitSet). Unit set for concentration measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Standard Curve Calculation Method

(stdCurveMet). Describes the specific approach used for calculating a standard curve. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* stdCurveSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Standard Curve Calculation Set

(stdCurveSet). The set capturing containing all of the valid methods for the PCR standard curve calculations. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardCurve *Nomenclature:* standardCurve *Ontology Reference:* NA *Category Set ID:* stdCurveSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Shiga-toxin-producing Escheria coli (STEC)

(stec). Shiga-toxin-producing Escheria coli (STEC). *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Storage temp

(sTemp). Temperature that the sample is stored at in Celsius. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment*

Set: anyCompartmentSet *Group:* procGrp *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* float *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Protocol Step ID

(stepID). The unique identifier for a specific protocol step. Protocol Steps are the component parts of a larger protocols, the latter being linked to specific measure reports. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Step ID Object

(stepIDObj). The object of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Populate this field using Protocol Step ID (partID = stepID). Together with ‘protocolIDSub‘ or ‘stepIDSub‘ and ‘relationshipID‘ the row of ‘protocolRelationships‘ should say: [protocolIDSubject or stepIDSubject] [relationshipID] [protocolIDObject or stepIDObject]. Ex: stepIDSubject precedes protocolIDObject. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Step ID Subject

(stepIDSub). The subject of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Populate this field using Protocol ID (partID = stepID). Together with 'protocolIDSub' or 'stepIDSub' and 'relationshipID' the row of 'protocolRelationships' should say: [protocolIDSubject or stepIDSubject] [relationshipID] [protocolIDObject or stepIDObject]. Ex: stepIDSubject precedes protocolIDObject. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Method step parent ID

(stepProvenanceID). A method step that served as a basis for another method step. This may be due to version changes, or a referencing a method set that was later adapted. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

Missingness Set: genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 2.0.0.

Protocol step version

(stepVer). Specifies the version of a given protocol step. Version of the method step. Semantic versioning is recommended. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Standard Error

(stEr). The standard error of a series of measurements. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Stercobilin

(stercobilin). Stercobilin is a tetrapyrrolic bile pigment and is one end-product of heme catabolism. It is the chemical responsible for the brown color of human feces and was originally isolated from feces in 1932. *Part*

Type: measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sample Storage Medium

(stoMed). The medium used to store a sample before final analysis. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* stoMedSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample Storage Medium Set

(stoMedSet). The set of valid categorical inputs for the stoMed field. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* stoMedSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Stormy Weather

(stormy). Stormy weather *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sewer network file blob

(storTempDef). A file blob that has any detailed information about the sewer network associated with the site (any format). Deprecated in version 2, please do not use. Refer to WKT and EPSG instead. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* blob *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 65535 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Storage time

(stoTim). Length of time that a sample was in storage. *Part Type:* measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet

Reference Link: NA *Data Type:* float *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Stream

(str). A watercourse which is linear and flows across the solid portion of a planetary surface. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Strain ID

(strainID). The strain identifier for a given organism. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

StrainPhlAn Software

(strainPhlAb). A lineage or clade analysis software tool within MetaPhlAn for strain-level lineage analysis from metagenomic data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://segatalab.cibio.unitn.it/tools/strainphlan/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Streptococcus Group

(strepGrp). A group of measures/methods related to streptococcus bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* strepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Streptococcus pneumoniae

(strepPneu). Streptococcus pneumoniae *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* strepGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA

Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sodium Thiosulfate Solution

(sts). A buffer solution/medium that neutralizes residual chlorine in wastewater samples, ensuring microbial viability. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Summary worksheet Shorthand

(su). The abbreviated short name used to reference the Summary sheet of the dictionary.xlxs file. sheet support *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.2.2. Last updated: 3.0.0.

Subread

(subread). Subread. A general-purpose read mapper. Includes the subread-align algorithm for mapping DNA and RNA reads. Best for: High-throughput data with a balance of speed and accuracy. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* http://subread.sourceforge.net/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Subsample (General)

(subSamp). A general replicate type for a subsample not otherwise defined. Use when additional details about the replicate are not available. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Suburban

(suburban). Suburban populated area type *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sub-variant or lineage

(subVar). A unit used to report a specific genetic lineage, or to specify that a reported variant is a sub-variant of another. Combine in a measure report if necessary. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sucralose

(suc). Sucralose (usually measured as a human fecal chemical indicator) *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Sudan virus, Orthoebolavirus sudanense

(sudanV). Sudan virus (species Orthoebolavirus sudanense) causes Sudan virus disease. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ebolaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Rolling sum of previous 14 days

(sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* poSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Summary

(summ). Short description of the assay and how it is different from the other assay methods. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Summary worksheet

(summary). Summary sheet of the dictionary.xlxs file. The summary sheet contains versioning and changelog. *Part Type:* dictionarySupport *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sunny

(sunny). Qualitative category for the weather measure, specifying a clear and sunny day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

SureSelect XT HS2 DNA Library Preparation Kit

(sureSelectXThs2). SureSelect XT HS2 DNA Library Preparation Kit by Agilent. A high-sensitivity library prep kit with target capture capabilities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Surface compartment

(surf). A measure or observation made from a substance on a surface. *Part Type:* compartments *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* surfaceCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Other surface

(surface). Surface other than floor or desk. See also categories for floor and desk. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment set

(surfaceCompartmentSet). A compartment set for measures and methods in the surface compartment. *Part Type:* compartmentSets *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* surfaceCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Surface and water compartment set

(surfaceWaterCompartmentSet). A compartment set for measures and methods in the surface or water compartments. *Part Type:* compartmentSets *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* surfaceWaterCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Surface swab

(surfSw). Surface swab. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

Parts

Category Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Surveillance alert

(survAlert). A public health action type wherein authorities have made a decision about surveillance and communicated the alert. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Alert Value Set

(survAlertSet). A set of valid categories for the public health action field, where the action type is 'surveillance alert'. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* survAlertSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Level

(survLevel). The scale or level of surveillance being done at a site. Ie. Is it institutional, is it only for a single building, or is it for a whol municipality. Mostly for use when a polygon is not reported. But situations of community surveillance, ideally a polygon should also be supplied. *Part Type:* measurements *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* miscMeas *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* survLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Level Set

(survLevelSet). The list of valid categories for the survLevel measure. *Part Type:* mmaSets *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* survLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sewage truck

(swgTrck). Sewage truck *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Swift 2S Turbo DNA Library Kit

(swift2STurbo). Swift 2S Turbo DNA Library Kit by Swift Biosciences. A fast library prep kit workflow with robust performance for low-input DNA. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sewer sediment

(swrSed). Sediments obtained in sewer *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Sewer catchment area

(swrSet). Sewer catchment area. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Synthetic sample

(synthetic). A synthetic or artificially generated sample. Synthetic samples are artificially created by mixing known quantities of target substances or organisms with clean water, often in a laboratory setting. These samples are used as controls, benchmarks, or calibration standards during the analysis process to ensure accurate and reliable results. For instance, a synthetic sample containing a known concentration of a specific pollutant might be used to calibrate analytical equipment or to test the efficiency of a new detection method. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

t19r delta-variant gene target

(t19r). t19r delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA

Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

t3646a delta-variant gene target

(t3646a). t3646a delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

t547k omicron-variant gene target

(t547k). t547k omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

t9i omicron-variant gene target

(t9i). t9i omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Tables

(tables). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. An example of a table is ‘site‘ a collection of attributes such as site name and address to describe where environment samples are taken. PHES-ODM has report tables, but users can create their own tables as well. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Table column set

(tableSet). The set for valid inputs in table columns. These categories are used in the parts list for columns named after tables to indicate the position and function of a given part in the entity relationship diagram of

the data model. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* tableSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Table Support

(tableSupport). Parts designed to support the metadata definition oftables in the parts table. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wide name measurement and linkage tag

(tag). A tag used in wide names to clarify relationship and linkage in the flattened, single table format. If a column doesn't have tag value at the end, then it means it applies to all groups, while one with a tag only applie to fields with the same tag value. For example, a value under qr_qualityFlag (with no tag) applies to fields in the group with tag == .odm10 and all other groups. If there's a column called qr_qualityFlag.odm10, however, then the group with that .odm10 tag uses the value from qr_qualityFlag.odm10 instead of from qr_qualityFlag (like wat_sa_nr_hMe_hUn_hAg_NR_value.odm10 and mr_unit.odm10, for

example). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 8 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.1.

Taï Forest virus, Orthoebolavirus taiense

(taiforestV). Orthoebolavirus taiense (formerly Taï Forest ebolavirus) is a rare viral species that causes Taï Forest virus disease in humans. It is one of four orthoebolaviruses known to cause illness in people, with only one confirmed human infection ever recorded. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ebolaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Tanapox

(tanapox). Tanapox (a virus from the genus Yatapoxvirus) was first seen among individuals in the flood plain of the Tana River in Kenya during two epidemics (1957 and 1962) of acute febrile illness accompanied by localized skin lesions. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tanapoxGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set*

ID: NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Tanapox Group

(tanapoxGrp). A group of measures/methods related to tanapox viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tanapoxGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

TaqPath N sars-cov-2 gene target

(taqpatN). TaqPath N sars-cov-2 mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

TaqPath S sars-cov-2 gene target

(taqpatS). TaqPath N sars-cov-2 mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Targeted surveillance program

(targetSurv). A surveillance sampling strategy in which an aspired outcome is explicitly stated. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Targetted surveillance initiated

(targSurv). Monitoring focused on a specific population, location, or risk factor. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Taxonium Software

(taxonium). Taxonium - A scalable tool for viewing and analyzing large phylogenetic trees, including clade annotations. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Total Dissolved Solids (TDS)

(tds). Total dissolved solids *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* measQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Technical replicate

(techRep). A sample that comes from the same biological or environmental source (e.g., the same extracted DNA, the same RNA aliquot, or the

same water sample). Helps detect inconsistencies due to pipetting errors, instrument fluctuations, or reagent inconsistencies, rather than biological variation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Sample temperature

(temp). Temperature of the sample measured in degrees Celcius *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* waterQualityGrp *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Temperature class

(temperature). Measures and methods related to temperatures. *Part Type:* classes *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:*

NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Temperature unit set

(temperatureUnitSet). Unit set for temperature measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Template Sheet Set

(templateSheetSet). Worksheets in the full generic ODM surveillance template (all tables). *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Template Set

(tempSet). The organizing set for templates. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

Reference: NA *Category Set ID:* tempSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Nucelic Acid Template Type

(tempType). Specifies whether a PCR or sequencing used RNA or DNA as the template for the reaction. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* tempSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Nucleic acid template volume

(tempVol). The volume of DNA or RNA template used for PCR. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Airport terminal

(terminal). Airport terminal sample shed category type *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Test date

(tesDate). Date that the covid-19 test was performed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Number of tests performed

(test). Number of tests performed. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Protocol testing

(testing). A measure or sample taken to test a new method. These measures are typically used for internal lab uses and not reported to external partners. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Tetracycline Anti-microbial resistance Group

(tetAMRGrp). The group for measures and methods pertaining to tetracycline-related anti-microbial resistance. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tetAMRGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

TetW Tetracycline-resistance gene target

(tetW). The tetW tetracycline anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tetAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:*

geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Thermal cyclers

(thermCyc). A thermal cycler instrument, used to perform temperature-controlled reactions for PCR. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

thermo magmax microbiome ultra nucleic acid isolation kit

(thermMag). Nucleic acid extraction performed using the thermo magmax microbiome ultra nucleic acid isolation kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

thermo magmax viral/pathogen nucleic acid isolation kit

(thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Threat designation

(threatDes). A public health action type wherein a threat level is determined and communicated by authorities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Threat designation Value Set

(threatDesSet). A set of valid categories for the public health action field, where the action type is 'threat designation'. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* threatDesSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Public health threat targeted by action

(threatTarget). The pathogen or variant for which the designation or action is being taken. Populated by a 'measurement' part type. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* measurements *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ThruPLEX DNA-seq Kit

(thruPLEX). ThruPLEX DNA-seq Kit by Takara Bio. A low-input library prep kit with fast, three-step protocol. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Transport hub - General

(tHub). A tansport hub not otherwise specified. i.e. a place where passengers and cargo are exchanged between vehicles or/and between transport

modes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Time class

(timeClass). Measures and methods relating to time. *Part Type:* classes *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 3.0.0.

Time proportional sample

(timePr). A time proportional composite sample generally collected by an autosampler. Use collectionPeriod to describe how many hours the sample was taken. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Time standardized

(timeStand). This data treatment standardizes the measurement value against time. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Time unit set

(timeUnitSet). The unit set for measures of time. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Total Kjeldahl Nitrogen

(tkn). A measure of Total Kjeldahl Nitrogen; ie. the sum of nitrogen bound in organic substances, nitrogen in ammonia (NH3-N) and in ammonium (NH4+-N) in the chemical analysis of soil, water, or waste water. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category*

Set ID: NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Country code top-level domain

(tld). The internet top-level domain generally used or reserved for a country, sovereign state, or dependent territory identified with a country code. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 3 *Maximum Length:* 3 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Total Nitrogen

(tn). Total nitrogen concentration, as N. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

TopHat

(tophat). TopHat. A general-purpose read mapper. An older RNA-seq aligner, splicing-aware. Replaced by HISAT2 in most workflows. Best for: Historical RNA-seq studies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ccb.jhu.edu/software/tophat/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Total amount or count - the sum

(total). The total number or final count of cases, or other defined metric. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* poSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Time Proportional 24hr sample

(tp24s). A time proportional 24-hour composite sample generally collected by an autosampler. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Treponema pallidum

(tPallidum). Treponema pallidum *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* treponemaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Translation look-up table Shorthand

(tr). The abbreviated short name used to reference the Look up table for translations of the description, label, and instruction for all parts. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Traditional Serotyping methods

(tradSero). Traditional Serotyping methods used for serotyping. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Train

(train). A series of railroad cars moved as a unit by a locomotive or by integral motors. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Synthetic ID for the translations table

(translationID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the translations table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Translation look-up table

(translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. tr *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Translation table column order

(translationsOrder). Specifies the order of the columns in the Translation table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Translation table required headers

(translationsRequired). Required headers in the Translations table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Transportation vehicle - general

(transp). A vehicle, i.e. a mobile machine, transporting people or cargo, of a type not otherwise specified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Passive (trap) sampling

(trap). A composite sampler that passively collects a sample without use of electricity or a battery. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:*

NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Travel ban

(travBa). A restriction prohibiting travel to or from specific locations. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Travel hub surveillance - general

(travelSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Travel warning

(travWa). A notice advising against travel to certain areas due to health risks. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:*

NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Treated

(treat). A quality which denotes an altered state of an item resulting from purposeful interventions or processes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Treatment ID

(treatmentID). A unique identifier for a single calculation/data treatment, a single data treatment identifier. Can be grouped together into a pipeline, which are then linked to a measure. This is done by having all related treatments share the same pipelineID, and specifying the order of the treatments in the pipeline using the order field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

TreeTime Software

(treeTime). A lineage or clade analysis software tool for phylodynamic analysis, often for molecular clock dating and clade assignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://evol.bio.lmu.de/_statgen/software/treetime/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Treponema Group

(treponemaGrp). A group of measures/methods related to treponema bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* treponemaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Trichomonas Group

(trichomonasGrp). A group of measures/methods related to trichomonas bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* trichomonasGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA

Unit Set: naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

TrimGalore!

(trimGalore). A QC pipeline tool for sequencing data that integrates Cutadapt and FastQC to assess sequence quality and remove adapters in one step. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/FelixKrueger/TrimGalore *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Trimmomatic

(trimmomatic). A sequencing data processing application that trims adapters and low-quality bases from Illumina sequencing reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.usadellab.org/cms/?page=trimmomatic *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Trinity

(trinity). A sequencing software that is an assembler designed specifically for RNA-seq data, creating transcriptome assemblies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/trinityrnaseq/trinityrnaseq *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

TE Buffer (Tris-EDTA)

(trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater Triturator

(triturator). The location where wastewater transportation vehicles unload wastewater. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

trizol, zymo mag beads w/ zymo clean and concentrator

(trizol). Nucleic acid extraction performed using the trizol, zymo mag beads w/ zymo clean and concentrator method. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

trizol, garnet bead beating, alcohol precipitation

(trizolEtOH). trizol, garnet bead beating, alcohol precipitation *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

trizol and RNA purification kit

(trizolRNA). trizol and RNA purification kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompart-

mentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Train Station

(trStat). A place on a railroad line where trains regularly stop so that passengers can get on or off. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

TRUE

(TRUE). Boolean data type = TRUE Use only "TRUE" (case sensitive) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 4 *Maximum Length:* 4 *Part Status:* active. First released: 1.0.0. Last updated: 2.3.0.

TruSeq DNA PCR-Free Library Prep Kit

(truSeqDNA). TruSeq DNA PCR-Free Library Prep Kit by Illumina. A high-quality library prep kit without PCR amplification, reducing bias. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Total solids concentration

(ts). Total solids concentration *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Tryptic Soy Broth (TSB)

(tsb). Tryptic Soy Broth (TSB) - A nutrient-rich medium for bacterial survival, sometimes used for short-term storage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Total suspended solids

(tss). Total suspended solids *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Concentration of total suspended solids

(tssConc). Total suspended solids concentration of the wastewater. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Torque Teno Virus

(ttv). Torque teno virus (TTV) is the type species in the genus Anellovirus. The viruses are small (30–50 nm) and non-enveloped with a circular single-

stranded DNA genome that is approximately 3.8 kb in size. More than 90% of adults worldwide are said to be infected with TTV. The viruses have not been conclusively shown to cause disease in humans, although they have been associated with some acute respiratory illnesses in infants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ttvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Torque Teno Virus Group

(ttvGrp). A group of measures/methods related to torque teno viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ttvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.1. Last updated: 3.0.1.

Tuberculosis Group

(tuberculosisGrp). A group of measures/methods related to tuberculosis. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tuberculosisGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:*

naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Francisella tularensis (tularemia) Group

(tularemiaGrp). A group of measures/methods related to Francisella tularensis. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tularemiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Turbidity

(turb). A measure for the turbidity of water, or a liquid sample, quanitfying the relative clarity or opcaity of a liquid. Highly indicative of water quality. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* turbidity *Nomenclature:* turbidity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* turbidityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Turburdity class

(turbidity). Measures and methods relating to water and wastewater turbidity. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* turbidity *Nomenclature:* turbidity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* turbidityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Turbidity unit set

(turbidityUnitSet). Unit set for turbidity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* turbidityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Trichomonas vaginalis

(tVaginalis). Trichomonas vaginalis *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* trichomonasGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Tube weight empty

(tWeighE). The weight of the tube used for analysis while empty. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Tube weight full

(tWeighF). The weight of the tube used for analysis while full of analyte. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Type other depreciate

(tyOtDep). Description for other type of sample not listed in *Part Type:* methods *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:*

Parts

naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* othAgg *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Type other depreciate2

(tyOtDep2). Description of the site when the site is not listed. See siteType. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

University campus

(uCampus). Universityor college campus - comprising an entire campus or part of a campus. See also 'Higher Education Domitory". *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Ugene

(uGene). Sequencing software that offers alignment and consensus sequence generation features. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://ugene.net/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Micrograms per gram

(ugG). Micrograms per gram *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Micrograms per litre

(ugL). Micrograms per litre *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Micrograms per milligram

(ugmg). Concentration unit of micrograms per milligram. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Micro-litres

(uL). The unit of microlitres. *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ultracentrifuges

(ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Standard centrifuges are a separate instrument type option. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

Set: naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Micromho per centimeter

(umhocm). Micromho per centimeter (mho/cm) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Unique Molecular Identifier (UMI) Tagging

(umiTag). A deduplication method that adds unique tags to individual DNA fragments, allowing identification and removal of duplicate reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://www.illumina.com/techniques/sequencing/ngs-library-prep/multiplexing/unique-molecular-identifiers.html *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

UMI-tools

(umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/CGATOxford/UMI-tools *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Undisclosed or Not Provided

(undisc). A value has been recorded, however it was not included in the dataset. Missing value indicator for data that has not been shared or disclosed with outside parties. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Unicycler

(unicycler). A sequencing software that is a hybrid assembler for bacterial genomes, combining short and long reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:*

naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/rrwick/Unicycler *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Unique sample

(unique). A unique sample, not duplicated. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Unit

(unit). The units of a measurement. Different units that are used to describe measurement values. Units are combined into UnitSetIDs. Please requests new units by creating an issue in the ODM repository. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* units *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Unit input (wide table)

(unitInput). The partID for the unit being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* units *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Unitless measure

(unitless). A unit for unitless measures, like pH. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Unitless unit set

(unitlessUnitSet). Unit set for measurements that does not have units. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Unit name (wide table)

(unitName). The unit referenced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* units *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Units

(units). The unit of the measurement. Every measurement must have a unit. Meaning, ‘units‘ are a mandatory field whenever a measurement is recorded. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Unit set

(unitSet). An idenfication of a set of units that can be used for a measure or method. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* unitSets *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Unit sets

(unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of 'yes' and 'no'; and set B could contain the values of 'yes', 'no', and 'maybe.' partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused. *Part Type:* partTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Unknown sample

(unkn). Denotes an unknown sample replicate type. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

The Unlicense

(unlicense). The licensing for the measure or data set is managed under The Unlicense. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/unlicense/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ultracentrifugation

(untracent). Ultracentrifugation Should typically be linked to a lower limit, and some indication of data spread (ie. standard deviation), and a mean/median measure. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Untreated

(untreat). A quality which denotes an absence of purposeful intervention or processes on an item. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale

Quality Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Upper limit of a 95% confidence interval

(upperCI95). Specifies the the upper limit of a 95% confidence interval. A catch-all category for upstream wastewater sampling sites, including major sewer pipelines and pumping stations. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Upstream sites

(upstream). A general site type for upstream wastewater sampling sites. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.1.0. Last updated: 2.0.0.

Urban

(urban). Urban populated area type *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Ureaplasma

(ureaplasma). Ureaplasma *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ureaplasmaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Ureaplasma Group

(ureaplasmaGrp). A group of measures/methods related to ureaplasma bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ureaplasmaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Urobilin or urochrome

(urobilin). Urobilin or urochrome is the chemical primarily responsible for the yellow color of urine. It is a linear tetrapyrrole compound that, along with the related colorless compound urobilinogen, are degradation products of the cyclic tetrapyrrole heme. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingness-Set *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Micro-Siemens per centimetre

(uSCm). Micro-siemens per centimetre. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Ultrafast Sample placement on Existing tRees (UShER) Software

(usher). A lineage or clade analysis software tool that adds new genomes to an existing phylogenetic tree, widely used for SARS-CoV-2 clade assignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/yatisht/usher *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

U site measure ID

(uSiteMeasureID). Unique identifier for each measurement for a site. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 2.0.0.

Coordinated universal time (UTC) zone

(utc). UTC – Time zone. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Parts

Set ID: NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Coordinated universal time (UTC) zone in daylight savings

(utcDST). Time zone during Daylight Saving Time. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Utilities sector or organization

(utilities). Describes organization that manage or provide utilities services, whether water, gas, heat, etc. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Universal Transport Medium (UTM)

(utm). Universal Transport Medium (UTM) - Used for microbial preservation in various environmental samples, including wastewater. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

V1104L Mutation

(v1104l). The FLiRT/SLip variant mutation V1104L *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

v2930l delta-variant gene target

(v2930l). v2930l delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Vacuum sludge sampling

(vac). Intrument type is a grab sampler that takes a sample at a designated depth with minimal disturbance to surrounding layers. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Validation study

(validationStudy). A meaure or sample taken for a validation study. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Value Treatment

(valTreat). A field which specifies what kinds of data treatments or the nature of the measurement value. The options are raw, derived, estimate, and predicted. *Part Type:* attributes *Domain:* naDomain *Speciment ID:*

naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* valTreatSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Value treatment value set

(valTreatSet). Valid set of values for the value treatment set. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* valTreatSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Value

(value). Value of a measure, observation or attribute. Only used for the dictionary entries of parts. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 100 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

VanA-A Vancomycin-resistance gene target

(vanAA). The VanA-A vancomycin anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* vanAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/ *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Vancomycin Anti-microbial resistance Group

(vanAMRGrp). The group for measures and methods pertaining to vancomycin-related anti-microbial resistance. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* vanAMRGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Vancomycin resistance

(vanc). Vancomycin resistant bacteria. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:*

seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Variable character data type

(varchar). The data type for variable character data. Measured by sequencing. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Frequency of variants detected

(varFreq). A description of the frequency of a variants detected. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Variants class

(variant). Measures and methods relating to variants. *Part Type:* classes *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* variant *Nomenclature:* variant

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Varicella

(varicella). Varicella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* varicellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Varicella Group

(varicellaGrp). A group of measures/methods related to varicella viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* varicellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Population with 1 dose of vaccine

(vax1). The population with exactly 1 dose of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 1+ vaccine dose(s)

(vax1p). Specifies the portion of the population with 1 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Population with 1+ dose(s) of vaccine

(vax1plus). The population with 1 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Population with 2 or more doses of vaccine

(vax2). The population with exactly 2 dose of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 2+ vaccine doses

(vax2p). Specifies the portion of the population with 2 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Population with 2+ or more doses of vaccine

(vax2plus). The population with 2 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Population with 3 or more doses of vaccine

(vax3). The population with exactly 3 dose of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.2.0.

Proportion of population with 3+ vaccine doses

(vax3p). Specifies the portion of the population with 3 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:*

naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Population with 3+ or more doses of vaccine

(vax3plus). The population with 3 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Population with 4 or more doses of vaccine

(vax4). The population with exactly 4 dose of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 4+ vaccine doses

(vax4p). Specifies the portion of the population with 4 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Population with 4+ or more doses of vaccine

(vax4plus). The population with 4 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Change to Vaccine Schedule

(vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Velvet

(velvet). A sequencing software that is a de novo assembler optimized for short-read data, often used in microbial genomics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/dzerbino/velvet *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

ODM V1 category

(version1Category). ODM V1 category *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 location

(version1Location). ODM V1 location *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 table

(version1Table). ODM V1 table *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ODM version 1 to 2 changes

(version1to2Changes). Changes for part between ODM v1 and V2 *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 variable

(version1Variable). ODM V1 variable mapping row in working document parts list. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Vertical grab sampling

(vertGrb). Intrument type is a grab sampler in which the container for the sample is mounted on the end of a rod, which is suitable for collecting waste from a tank. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Vibrio

(vibrio). Vibrio *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* vibrioGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData

Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Vibrio Group

(vibrioGrp). A group of measures/methods related to vibrio bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* vibrioGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Viral passage experiment

(viralPass). A research sampling strategy in which samples are selected in order to perform a viral passage experiment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Miscellaneous viruses group

(virusMisc). A group of measures/methods related to miscellaneous viruses. The miscallenous viruses are often measured for normalization or standard-

ization and have only one measure or method. When a virus has many measures, they will be given their own groupID in updated dictionary versions. *Part Type:* groups *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.2.0.

Variant of concern

(voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for assigning this threat level. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Variant of interest

(voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Size in volume

(vol). Total volume of water or sludge sampled. Used for water or air testing *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* airWaterCompartmentSet *Group:* colGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* sampleQualitySet *Reference Link:* NA *Data Type:* integer *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Volume proportional sample

(volPr). A volume proportional sample generally collected by an autosampler. The sampling takes the same wastewater volume at variable time intervals, after a defined volume of wastewater has passed the sampling point. This is also called constant volume, variable time (CVVT). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Volume unit set

(volumeUnitSet). Unit set of volume measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Volatile suspended solids

(vss). Volatile suspended solids *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Volatile suspended solids - ignition

(vssIg). A water quality measure, captured by via the loss on ignition of the mass of measured total suspended solids. This ignition generally takes place in an oven at a temperature of 550 °C to 600 °C. It represents the amount of volatile matter present in the solid fraction of the measured solution. *Part Type:* measurements *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* waterCompartmentSet *Group:* measGrp *Class:*

standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Vesicular stomatitis virus (VSV) target

(vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

VSV forward primer (ABI)

(vsvABIFor). VSV forward primer (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* vsvGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

VSV probe (ABI)

(vsvABIProbe). VSV probe (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* vsvGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

VSV reverse primer (ABI)

(vsvABIRev). VSV reverse primer (ABI) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* vsvGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Vesicular Stomatitis Virus (VSV) Group

(vsvGrp). A group of measures/methods related to Vesicular Stomatitis Virus (VSV). Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* vsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Verotoxin-producing Escherichia coli (VTEC)

(vtec). Verotoxin-producing Escherichia coli (VTEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Viral Transport Medium (VTM)

(vtm). A buffer solution/medium the preserves viral samples during transport, commonly used for wastewater viral studies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

variant under monitoring

(vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat

level. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Water compartment

(wat). A measure or observation made from a substance in the water, including wastewater. *Part Type:* compartments *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

water concentrating buffer (R2042-1)

(watConcBuff). water concentrating buffer (R2042-1) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Water depreciated

(water). Non-wastewater, coming from any kind of water body. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.0.0. Last updated: 2.0.0.

Water compartment set

(waterCompartmentSet). A compartment set for measures and methods in the water compartment. *Part Type:* compartmentSets *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Water Quality Group

(waterQualityGrp). A group of measures/methods related to water quality. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* waterQualityGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Water-based Transit Hub

(waterTH). A transport hub is a place where passengers and cargo are exchanged between water-based vehicles and/or between water-based transport modes. Used when not greater detail can be provided *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.3. Last updated: 2.2.3.

Wastewater temperature

(watTemp). Temperature of the wastewater. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Weather (time of sampling)

(weath). A measure for weather captured through qualitative categories; part of a larger suite of weather measures that may be useful when col-

lecting samples from outdoor sources. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* weathSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Weather class

(weather). Measures and methods relating to weather. *Part Type:* classes *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Weather set

(weathSet). A set of the valid qualitative categories for the qualitative weather measure. *Part Type:* mmaSets *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* weathSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Weeks

(weeks). A unit of measuring time in weeks, or periods of seven days. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Well

(well). A cylindrical hole, pit, or tunnel drilled or dug down to a depth from which water, oil, or gas can be pumped or brought to the surface. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

West Nile

(westNile). West Nile *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Whole genome sequencing

(wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

WHO nomenclature

(who). Specifies variant or genetic nomenclature as set out by the World Health Organization. If there are multiple issues to flage, use the multiple issues flag and explain the details in the notes section. *Part Type:* nomenclatures *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wide 95% interval

(wI). The 95% interval is too wide, low confidence in results. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Com-*

partment Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Specified attribute (wide table)

(wideAttribute). Unique identifier for an attribute in a wide table only. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Compartment set for wide names

(wideCompartmentSet). Compartment set for wide names. For wide names. *Part Type:* compartmentSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* wideCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.2.0. Last updated: 3.0.0.

Fraction set for wide names

(wideFractionSet). Fraction set for wide names. For wide names. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* wideFractionSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Measure identification (wide table)

(wideMeasure). Unique identifier for a measure in a wide table only. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 60 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wide Name

(wideName). Unique identifier for wide table only. Use when all measures are performed on a single sample at the same time and same laboratory. Suggestion: siteID_sampleID_LabID_reportDate_ID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wide name table

(wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field. wn *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wide name table order

(wideNamesOrder). Column for indicating the order of the fields in the wide names table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Wide name table required

(wideNamesRequired). Column for indicating which fields in the wide names table are mandatory. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Wide name type

(wideNameType). The type of wide name generated. Possible options are measure, protocol or attribute. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Specified protocol (wide table)

(wideProtocol). Unique identifier for a protocol in a wide table only. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Speciment set for wide names

(wideSpecimenSet). Speciment set for wide names. For wide names. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* wideSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Wind Speed

(wind). A measure for wind speed; part of a larger suite of weather measures that may be useful when collecting samples from outdoor sources. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* airCompartmentSet *Group:* siteFeat *Class:* speed *Nomenclature:* speed *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* windSpeedUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wind speed unit set

(windSpeedUnitSet). Unit set for wind speed measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* windSpeedUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum*

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Whole Metagenome Sequencing

(wms). A DNA sequencing assay that intends to provide information on the DNA sequences of multiple genomes (a metagenome) from different organisms present in the same input sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wide name table Shorthand

(wn). The abbreviated short name used to reference the The table for wide names. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

Sample stored incorrectly

(wrongStorage). Sample was stored inappropriately. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Parts

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Sample stored at wrong temperature

(wrongTemp). Sample was stored at an inappropriate temperature. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

World Sphere (W-SPHERE)

(wSphere). World Sphere header *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

wSphere Format

(wSphereForm). Dataset was originally recorded and/or stored in wSphere format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://sphere.waterpathogens.org/about *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

World Sphere (W-SPHERE) notes

(wSphereNotes). W-Shere notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Delta Variant wt214 gene target

(wt214). Delta Variant wt214 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Maximum Length: NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Wastewater Treatment Agency

(wta). An organization type that includes those organizations who manage wastewater treatment programs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

WTDBG (aka wtdbg2)

(wtdbg2). A sequencing software that is an assembler for long-read data that generates contigs rapidly. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://github.com/ruanjue/wtdbg2 *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Do What The F*ck You Want To Public License { #wtfpl }

(wtfpl). The licensing for the measure or data set is managed under the Do What The F*ck You Want To Public License.* Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Set: naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/wtfpl/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Wastewater Treatment Plant Operator

(wtpo). An organization type that includes those organizations who run and operate wastewater treatment facilities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Whole Virome Sequencing

(wvs). A whole metagenome sequencing assay that intends to provide information on multiple genome sequences from different viruses present in the same input sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Weight for weight

(ww). weight for weight (% w/w) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater aerobic digestion

(wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101199 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater anaerobic digestion

(wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101200 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

wastewater comminution process

(wwCominuated). wastewater comminution process occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101719 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge removal

(wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101201 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge dewatering

(wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:*

naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101202 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge drying

(wwDry). Wastewater sludge drying occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101718 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater filtration

(wwFilt). Wastewater filtration occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater grit removal

(wwGrit). Wastewater grit removal occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater microbial treatment

(wwMic). Wastewater microbial treatment occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewtaer primary sedimentation

(wwPriSed). Wastewtaer primary sedimentation occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

Length: 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater screening process

(wwScreen). Wastewater screening process occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* GENEPIO:0101198 *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater secondary sedimentation

(wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater treatment plant

(wwtp). A general site type for wastewater treatment plants. Used as a catch-all category for industrial or municipal wastewater treatment plants that carry combined or sanitary sewage, or lagoons. *Part Type:*

categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Wastewater treatment efficiency assessment

(wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Back-up wastewater treatment site

(wwtpBack). Indicates a wastewater treatment plant where multiple labs are or were sampling, and where secondary samples are being taken taken. Maps to units of either million gallons per day, or population equivalents. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* siteFeat *Class:* capacity *Nomenclature:* capacity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:*

0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater treatment plant designed capacity

(wwtpCap). A measure for the designed capacity of a wastewater treatment plant, in terms of how much water it was designed to be able to hold and process. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* colGrp *Class:* capacity *Nomenclature:* capacity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* capacityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Industrial wastewater treatment plant

(wwtpInd). Industrial wastewater treatment plant *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Municipal wastewater treatment plant for combined sewage

(wwtpMuC). Municipal wastewater treatment plant for combined sewage *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass

Nomenclature: naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 1.0.0. Last updated: 2.0.0.

Municipal wastewater treatment plant for sanitary sewage only

(wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* genQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater treatment

(wwTrt). Wastewater treatment occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

XEC Variant

(xecV). The XEC variant of SARS-CoV-2, a subvariant of the Omicron strain. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* seqQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Relative Centrifugal Force (RCF) or x g units

(xg). RCF (Relative Centrifugal Force) denotes the degree of force exerted on a sample. RCF is quantified in multiples of the gravitational acceleration that is standard at the Earth's surface (x g). Thus, the terms RCF and XG are often used interchangeably in centrifugation protocols. *Part Type:* units *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

y505h omicron-variant gene target

(y505h). y505h omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation*

Scale: seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Years

(years). A unit for indicating a length of time in years. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

Yersinia enterocolitica

(yEnterocolitica). Yersinia enterocolitica *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* yersiniaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Yersinia Group

(yersiniaGrp). A group of measures/methods related to yersinia bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* yersiniaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Zenodo

(zenodo). Zenodo open data storage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://zenodo.org *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: 3.0.0. Last updated: 3.0.0.

Zika

(zika). Zika *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* seeUnitData

Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

zLib License

(zlib). The licensing for the measure or data set is managed under the zLib License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* https://choosealicense.com/licenses/zlib/ *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

Zones look-up table Shorthand

(zo). The abbreviated short name used to reference the Look up table for the possible sub-national region or zone inputs. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.2. Last updated: 2.2.2.

English name of country sub-domains

(zoneName). The english-language name for a given country sub-domain. Preprogrammed into dictionary tables, not editable by users. *Part Type:*

attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Zones look-up table

(zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. zo *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Zones table column order

(zonesOrder). Specifies the order of the columns in the zones table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

Zones table required headers

(zonesRequired). Required headers in the zones table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.1.0. Last updated: 2.1.0.

zymo quick-rna viral kit #r1035

(zymo1035). zymo quick-rna viral kit #r1035 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

zymo quick-rna viral 96 kit #r1041

(zymo1041). zymo quick-rna viral 96 kit #r1041 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.2.0. Last updated: 2.2.0.

zymo environ water rna kit (cat. r2042)

(zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit (cat. r2042). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

zymo quick-rna fungal/bacterial miniprep #r2014

(zymoQuick). Nucleic acid extraction performed using the zymo quick-rna fungal/bacterial miniprep #r2014 kit. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* pcrQualitySet *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: 2.0.0. Last updated: 2.0.0.

zymo environ water rna kit (cat. r2042) - depreciated

(zymoWatRNA). zymo environ water rna kit (cat. r2042) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **depreciated**. First released: 2.2.0. Last updated: 3.0.1.

Sets

Dictionary v3.0.1 Documentation v3.0.1

Sets are lists of categories and other parts. For example, "Collection category set" (`collectSet`) (collectSet) contains a list of the different collection types including: `mooreSw` (Moore swab), `grb` (Grab sample), `flowPr` (Flow proportional sample), etc.

Sets can have parts that are reused. For example, there are different quality measures for sample collection (e.g. `Sample not collected`), PCR measures (`Inhibition preset`), and sequencing measures (`Low depth of coverage`), but all quality sets share the `No quality concerns` indicator.

Public Health Action Type Value Set

(actionTypeSet). A set of valid categories for the public health action type field.

Threat designation (threatDes). A public health action type wherein a threat level is determined and communicated by authorities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public health advisory (phAdvise). A public health action type wherein a public health advisory is deseminated to the public. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance alert (survAlert). A public health action type wherein authorities have made a decision about surveillance and communicated the alert. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Control measure implementation (contMeasImp). A public health action type wherein authorities have begun implementing infection control measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial resistance (AMR) classification (amrClass). A public health action type wherein threat level classification has been done on a strain of antimicrobial resistant (AMR) microbes, and communicated to the public. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Outbreak declaration (outb). Public health action type used to indicate outbreak status. Given that when outbreaks occur, full data on case counts may not be available or completely accurate, using this measure indicates that case counts may be approximate. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Aggregations

(aggregations). Statistical measures used to report a measure. Each measure reported as a number should be reported with an aggregation. The default aggregation is `sin`, which corresponds to a single measurement.

AND Boolean aggregation (andBoo). "AND" aggreation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Cumulative count (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Daily count (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

EpiWeek Mean (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flow-normalized mean (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Geometric mean (gmn). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

See Header for Aggregation (hAg). An indicator to show in a wide-name that aggregation information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Lower limit of a 95% confidence interval (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Maximum value (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Arithmetic mean (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Median (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized arithmetic mean (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Minimum value (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation not applicable (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Normalized geometric mean (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

OR Boolean aggregation (orBoo). "OR" aggreation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation depricated (otherDep). Other aggregation method. Add description to aggregationOther Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

PMMoV- and flow-normalized mean (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PMMoV-normalized mean (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard deviation (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized standard deviation (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Single (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Standard Error (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rolling sum of previous 14 days (sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Total amount or count - the sum (total). The total number or final count of cases, or other defined metric. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Upper limit of a 95% confidence interval (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation scales

(aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative.

Aggregation scale not applicable (naAggrScale). Not application for aggregation sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation scale (othAgg). Specifies an aggregation scale that can't be described as either "qualitative" or "quantitative". Status: active. First released: 2.0.0. Last updated: 2.0.0.

Qualitative (qualAggScale). The qualitative aggregation scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quantitative (quantAggScale). The "quantAggScale" aggregation scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See unit (aggregation scales) (seeUnitAggScale). A value for aggregation scale to be used when the aggregation scale depends on that specified in the parts list entry for the unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation sets

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean.

Boolean aggregation set

(booleanAggrSet)Aggreagation set for boolean. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

AND Boolean aggregation (andBoo). "AND" aggreation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

OR Boolean aggregation (orBoo). "OR" aggreation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Single (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Linear scale aggregation set

(linearAggrSet)The aggregation set that contains all aggregations that exist on the linear scale. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Cumulative count (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Daily count (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

EpiWeek Mean (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flow-normalized mean (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Lower limit of a 95% confidence interval (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Maximum value (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Arithmetic mean (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Median (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized arithmetic mean (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Minimum value (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

PMMoV- and flow-normalized mean (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PMMoV-normalized mean (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard deviation (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized standard deviation (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Single (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Standard Error (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rolling sum of previous 14 days (sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Total amount or count - the sum (total). The total number or final count of cases, or other defined metric. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Upper limit of a 95% confidence interval (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Logarithmic scale aggregation set

(logAggrSet)The aggregation set that contains all aggregations that exist on the logarithmic scale (rather than linear or qualitative). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Flow-normalized mean (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Geometric mean (gmn). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Lower limit of a 95% confidence interval (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Maximum value (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Minimum value (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized geometric mean (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

PMMoV- and flow-normalized mean (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PMMoV-normalized mean (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Single (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Standard Error (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Upper limit of a 95% confidence interval (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation set not applicable

(naAggrSet)Not application for aggregation sets. Used for parts for which an aggregation set value is not applicable or appropriate. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Aggregation not applicable (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation set

(otherAggrSet)Aggregation set used for unitless measures. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Cumulative count (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Daily count (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

EpiWeek Mean (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flow-normalized mean (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Geometric mean (gmn). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

See Header for Aggregation (hAg). An indicator to show in a wide-name that aggregation information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Lower limit of a 95% confidence interval (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Maximum value (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Arithmetic mean (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Median (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized arithmetic mean (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Minimum value (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation not applicable (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Normalized geometric mean (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Standard deviation (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Normalized standard deviation (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Single (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Standard Error (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rolling sum of previous 14 days (sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Total amount or count - the sum (total). The total number or final count of cases, or other defined metric. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Upper limit of a 95% confidence interval (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Aggregation sets

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean.

Boolean aggregation set (booleanAggrSet). Aggreagation set for boolean. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Linear scale aggregation set (linearAggrSet). The aggregation set that contains all aggregations that exist on the linear scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Logarithmic scale aggregation set (logAggrSet). The aggregation set that contains all aggregations that exist on the logarithmic scale (rather than linear or qualitative). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation set not applicable (naAggrSet). Not application for aggregation sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation set (otherAggrSet). Aggregation set used for unitless measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

All Public Health Actions Set

(allActionsSet). A set of all valid categories for public health action, regardless of action type.

End of Outbreak (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Outbreak - on-going (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Declared outbreak or Outbreak start (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Public health emergency (outbreak) (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Variant of concern (voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Variant of interest (voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

variant under monitoring (vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

De-escalated variant (dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel warning (travWa). A notice advising against travel to certain areas due to health risks. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel ban (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mask recommendation (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Quarantine recommendation (quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hand hygiene advisory (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Targetted surveillance initiated (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Increased surveillance (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Routine surveillance (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Decreased surveillance (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Stay-at-home order (homeOrder). A directive requiring people to remain at home except for essential activities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Border closure (borderClos). A measure shutting entry points to limit cross-border movement and disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

School closure (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lockdown (lockdown). Broad restrictions on movement and activities within a region to control disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mask mandate (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Social distancing measures (socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Critical priority pathogen (cpp). A microorganism with resistance to multiple drugs and a high threat to human health. Status: active. First released: 3.0.0. Last updated: 3.0.0.

High priority pathogen (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Medium priority pathogen (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Resistant strain identified (rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Change to Vaccine Schedule (vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data Adjustment Standard Value Set

(allStandardSet). Set of valid input values for the standard field.

PMMoV Standarized (pmmovStand). This data treatment standardizes the measurement value to concentration levels of pepper mild mottle virus (PMMoV). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Crassphage Standarized (crassStand). This data treatment standardizes the measurement value to concentration levels of crassphage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flow Standarized (flowStand). This data treatment standardizes the measurement value to flow rates. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bayesian Smoothing applied (bayesSmooth). This data treatment smooths the measurement value using bayesian smoothing techniques. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Central average smoothing applied (caSmooth). This data treatment smooths the measurement value using central average smoothing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

7-day smoothing of values (day7Smooth). This data treatment smooths the measurement value across 7-days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Time standardized (timeStand). This data treatment standardizes the measurement value against time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gaussian distribution stanrdized/Normalized (gauss). Standardize the data to a gaussian/normal distribution, such that the data have a mean of zero and a standard deviation of one. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial Resistance (AMR) Classification Value Set

(amrClassSet). A set of valid categories for the public health action field, where the action type is 'antimicrobial resistance (AMR) classification'.

Critical priority pathogen (cpp). A microorganism with resistance to multiple drugs and a high threat to human health. Status: active. First released: 3.0.0. Last updated: 3.0.0.

High priority pathogen (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Medium priority pathogen (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Resistant strain identified (rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AMR Software Set

(amrSoftSet). The valid set of AMR analysis software categories.

ARG-ANNOT Annotation Tool (argAnnotSoft). Software annotation tool for antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ResFinder Tool (resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CARD Resistance Gene Identifier (RGI) (cardRGI). Software tool that is a part of the Comprehensive Antibiotic Resistance Database (CARD) used for annotation and prediction of AMR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DeepARG Software (deepARG). Software tool that predicts AMR genes using deep learning on metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AMRFinderPlus Software (amrFinderPlus). Software tool that was developed by NCBI to detect AMR genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MetaPhlAn Software (metaPhIAn). Software tool that profiles microbial communities and can provide resistance gene insights. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ABRicate Software (abricate). Software tool for screening bacterial genomes against multiple resistance databases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

StarAMR Software (starAMR). Software tool that is used to detect AMR genes in genome assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ShortBRED Software (shortBRED). Software tool that screens for known AMR genes in shotgun metagenomic sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SRST2 Software (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Attributes

(attributes). Attributes describe the who, where, when, and why of environmental surveillance. There are attributes for domain, specimen, compartment, or table. Attributes are one of the three main components or ways to report environment surviellence data. The other two components are measures and methods.

Accessions Index ID (accessIndexID). Provisional ID to act as a primary key for each row of the accessions table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wide Name (wideName). Unique identifier for wide table only. Use when all measures are performed on a single sample at the same time and same

laboratory. Suggestion: siteID_sampleID_LabID_reportDate_ID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Accession Number in Repository (accessNum). The accession number for the data entry in the given data repository or hosting platform. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Address ID (addressID). A unique identifier for an address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Alias ID depreciated (aliasIDDep). Alias id Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Assay ID (asID). Links with the AssayMethod used to perform the analysis. Use instrument.ID for measures that are not viral measures. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Assay method id default depreciated (amDefDep). Used as default when a new measurement is created for this lab. See ID in AssayMethod table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Analysis date (aDate). Date the measurement was performed in the lab. Status: depreciated. First released: 1.0.0. Last updated: 2.1.0.

Analysis date end (aDateEnd). Date the measurement or analysis was completed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Analysis date start (aDateStart). Date the measurement or analysis was started. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Calculation ID (calculationID). A unique identifier and primary key for every row of the calculations table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Address Line 1 (addL1). Line 1 (the street name, number and direction) for a given address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Foreign Key Alias ID (fKAliasID). The primary key that is being referenced by another name in another table as a foreign key. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Composite Set ID (setCompID). A composite ID generated by concatenating the 'setID' and 'partID' of a given row in the sets table. This allows for a unique primary key and robust relational database structure. Status: active. First released: 2.2.2. Last updated: 3.0.1.

Aggregation scale (aggregationScale). A scale used for an aggregation. Only applicable for measures and units. Status: active. First released: 2.0.0. Last updated: 3.0.1.

Aggregation (aggregation). Statistical measures used to report a measure. Each aggregation has a corresponding value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

character length (charLength). The number of characters used for the wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Domain (domain). Domain is the highest level of describing of a measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Alias depreciated (aliasDep). ID of an assay that is the same or similar. A comma separated list. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Contact ID (contactID). A unique identifier for a given contact person. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Access to all org (allOrgs). If this is 'no', this data will not be available to any partner organization. If missing, data will be available to the all organizations. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Cphd ID (cphid). Unique identifier for the table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Aggregation set (aggregationSet). The aggregation set for a unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Custody Contact ID (custodyCont). A unique identifier for data custodians. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Description (descr). A detailed description of a measure, method, or attribute. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wide name source (source). The database or table sourced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Data custodian ID (custodyID). The data custodian of a database. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dataset ID (datasetID). The name of the dataset that stores information for MeasureReport, SampleReport and other reporting tables. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Specimen Set Header (specimenSet). An idenfication of a set of specimens that can be applied for a measure or method. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Compartment Set Header (compartmentSet). An idenfication of a set of compartments that can be applied for a measure or method. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Group (group). Unique identifier for a group of measures. Mostly applicable for measures, methods, units, and aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Capital city endonym (capitalEndonym). The name locals use for their country's capital. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Capital city exonym (capitalExonym). The English name foreigners use for the country's capital. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Funder contact ID (funderCont). A unique identifier for a funder. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Class (class). A unique identifier for a class, which is akin to a sub-group; it's a way of grouping parts within a given group. A group can have one or more classes to describe different parts of the class. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measure identification (wide table) (wideMeasure). Unique identifier for a measure in a wide table only. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Address Line 2 (addL2). Line 2 (the unit number) for a given address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nomenclature (nomenclature). A classification system to report the measure class. Only applicable to variants, mutations, and diseases. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Collection Approximate Time Period (collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Collection Date (time not included) (collDate). Sample collection date, where time is reported in a separate field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Collection date time (collDT). For grab samples this is the date, time and timezone the sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Collection date time end (collDTEnd). For integrated time average samples this is the date, time and timezone the sample was finished being taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Collection date time start (collDTStart). For integrated time averaged samples this is the date, time and timezone the sample was started being taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Collection number (collNum). The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Collection period and number (collNumPer). Composite collection number.period. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

Collection period (collPer). Collection period. The time period over which the sample was collected, in hours. Alternatively, use collectionStart and collectionEnd. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample collection type (collType). The type of collection. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Column name depreciiated (columnNameDep). Name for the column Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Compartment (compartment). The attribute identifying the substance from which where a sample was taken. For more information, see partID = compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specified protocol (wide table) (wideProtocol). Unique identifier for a protocol in a wide table only. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Specified attribute (wide table) (wideAttribute). Unique identifier for an attribute in a wide table only. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Method (method). A procedure for collecting a sample or performing a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Contact name (contactName). Contact person or group, for the lab. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Measure, Method, or Attribute Set Header (mmaSet). The set for a measure, method, or attribute. Only applicable for categorical fields, and the categories that populate them. The use has meean extended to include 'partType' values as well, to codify instances where a catgeorical variable takes any part of a certain part type. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit set (unitSet). An idenfication of a set of units that can be used for a measure or method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Funding agency ID (funderID). The funding agency of the dataset. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality Indicator Set Header (qualityIndSet). The quality set that corresponds to a given part. Only applicable for samples and measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

City (city). The city where a site or organization is located; part of the address. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Country endonym (countryEndonym). The name locals use for their country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Country exonym (countryExonym). The English name foreigners use for the country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Covid-19 population measurement date (cphDate). date of reporting for covid-19 measure. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Instrument ID (instrumentID). A unique identifier for an instrument. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Lab ID (labID). Unique identifier for a laboratory. Status: depreciated. First released: 1.0.0. Last updated: 2.1.0.

Lab ID default depricated (labDefDep). Used as default when a new sample is created by this reporter. See ID in Lab table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Host Data Repository or Bank (dataHost). The external repository or database/bank in which a sequence (or other external data) is stored. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dataset creation date (datasetDate). Specifies the date a given dataset was created. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Language ID (lang). Language code for translation purposes. Specifies the langage for each translation, other than the default English. Uses the ISO-6393 code. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Missingness Set (missingnessSet). Missingness sets for measures, methods or attributes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Date (dateDep). Date Status: depreciated. First released: 1.0.0. Last updated: 3.0.0.

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Access to details deprecated (detailsDep). More details on the existing confidentiality requirements of this measurement. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Wide name type (wideNameType). The type of wide name generated. Possible options are measure, protocol or attribute. Status: active. First released: 2.2.0. Last updated: 2.2.0.

European Nucleotide Association Mapping Column (enaMap). ENA header Status: active. First released: 2.0.0. Last updated: 2.0.0.

European Nucleotide Association (ENA) - notes (enaNotes). ENA notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

Enumeration for set values (enumeration). The numeric value that corresponds to a given value in a set, defined in the sets table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

EpiWeek Number (epiWeek). The number of the epi week in which a sample what collected, or to which a measure would apply. Status: active. First released: 3.0.0. Last updated: 3.0.0.

EpiWeek Start Date (epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start dat resolves the possible ambiguity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Year of the EpiWeek (epiYear). The year in which the epi week is occuring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Measure Report ID (measureRepID). Unique identifier for a measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

File location of polygon (fileLocation). The location of the file containing the geometry of the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

First name of contact (firstName). Specifies the first name of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Fraction analyzed (fraction). Fraction of the sample that is analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Report table name (wide table) (reportTableName). The report table that the wide name calls from. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Report table input (wide table) (reportTableInput). The short name for the listed source table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

License (license). The license of a dataset. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Part type name (wide table) (partTypeName). The part type being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Measure set report set ID (measureSetRepID). Unique identifier that links together a group of related measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site Type (siteType). Type of site or institution where sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample shed (sampleShed). A geographic area, physical space, or structure. A sample is taken from a sampleshed for a representative measurement of a substance(s). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Type of geography (geoType). Type of geography that is represented by the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Well-known text (geoWKT). Well-known text of the polygon Status: active. First released: 1.0.0. Last updated: 3.0.1.

Version of Data Hosting Platform/Repository (hostVersion). The version of the data repository or hosting platform being used. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Part type input (wide table) (partTypeInput). The partID for the part type being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Measure (measure). A measurement or observation of any substance including a biological, physical or chemical substance. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Instrument Type (insType). Type of instrument used to perform the measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Describe other instrument type, if applicable (insTypeOth). Description of the instrument in case it is not listed in instrumentType. Status: active. First released: 1.0.0. Last updated: 2.0.0.

ISO639-1 (iso6391). The first part of the ISO 639 series of international standards for language codes. Part 1 covers the registration of two-letter codes. There are 183 two-letter codes registered as of June 2021. The registered codes cover the world's major languages. Status: active. First released: 2.0.0. Last updated: 3.0.1.

ISO639-2B (iso6392B). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'B' specifies the bibliographic code (B code). Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

ISO639-2T (iso6392T). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'T' specifies the terminological code (T code). Status: active. First released: 2.0.0. Last updated: 3.0.1.

ISO639-3 (iso6393). A set of international standards that lists short codes for language names. ISO 639-3 extends the ISO 639-2 alpha-3 codes with an aim to cover all known natural languages. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

ISO639-6 (iso6396). A set of international standards that lists short codes for language names. ISO 639-6 builds off ISO639-3 with the use of four-letter codes, and allowing users to differenciate between variants of languages and language families, such as histroical vs. revived versions of languages. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

ISO 3166-1 alpha-2 country code (isoCode). The ISO 3166-1 alpha-2 code, a two-letter country code which is also used to create the ISO 3166-2 country subdivision code and the Internet country code top-level domain. Status: active. First released: 2.1.0. Last updated: 3.0.0.

ISO 3166-1 alpha-3 country code (isoCodeX). The ISO 3166-1 alpha-3 code, a three-letter country code which may allow a better visual association between the code and the country names than the 3166-1 alpha-2 code. Status: active. First released: 2.1.0. Last updated: 2.1.0.

ISO 3166-2 code for country sub-domain (isoZone). The ISO 3166-2 codes for the names of the principal subdivisions (e.g., provinces, states, departments, regions) of all countries coded in ISO 3166-1. Status: active. First released: 2.1.0. Last updated: 3.0.0.

Method step parent ID (stepProvenanceID). A method step that served as a basis for another method step. This may be due to version changes, or a referencing a method set that was later adapted. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

Organization ID (organizationID). A unique identifier for the organization to which the reporter is affiliated. Status: active. First released: 1.1.0. Last updated: 3.0.1.

Language family (langFam). Specifies the language family of a given language for translation and language tracking purposes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Language name (langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

National language script (langScript). The language(s) and script(s) used for the country's capital endonyms. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Parent dataset ID (parDatasetID). The datasetID that is a parent to another datasetID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Last name of contact (lastName). Specifies the last name of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Link (li). Link to an external reference that describes the geometry of the polygon. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Parent sample ID (parent). If this sample has been pooled into one big sample for analysis this indicates the sample of the larger pooled sample. Status: depreciated. First released: 1.1.0. Last updated: 2.0.0.

Access to local ha (localHA). If this is 'no', the, data will not be available to local health authorities. If missing, data will be available to local health authorities. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Manufacturer (manufacturer). Manufacturer of an instrument. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Parent Site ID (parSiteID). The siteID that is a parent to another siteID; usually the sub-site will be contained in the parentSite. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment name (wide table) (compartmentName). The compartment referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Measure license (measureLic). Specifies the access and use licensing for a given single measurement. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment input (wide table) (compartmentInput). The partID for the compartment being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

State, Province, or Region (stateProvReg). The state, province, or region where a site or organization is located; part of the address. Status: active. First released: 1.0.0. Last updated: 3.0.1.

Summary (summ). Short description of the assay and how it is different from the other assay methods. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Specimen name (wide table) (specimenName). The specimen referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Specimen input (wide table) (specimenInput). The partID for the specimen being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Model (model). Model number or version of the instrument. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Pipeline ID (pipelineID). A primary key linked to a single measure (may be used multiple times), it is the shorthand for the data transformation pipeline used. Serves as a data pipeline identifier. Status: active. First released: 3.0.0. Last updated: 3.0.0.

English name for countries (nameEngl). English-language name of a given country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Official state name (nameOfficial). Official english-language name of a given state. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Native Name (natName). The native name of the language, i.e. what the language is called by its speakers. Status: active. First released: 2.0.0. Last updated: 3.0.1.

National Center for Biotechnology Information (ncbi). NCBI header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NCBI - notes (ncbiNotes). NCBI notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NORMAN (norman). NORMAN header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NORMAN - notes (normanNotes). Norman notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol step version (stepVer). Specifies the version of a given protocol step. Status: active. First released: 1.0.0. Last updated: 2.0.0.

ISO 3166-1 numeric country code (numCode). The ISO 3166-1 numeric code, a three-digit country code which is identical to that developed and maintained by the United Nations Statistics Division, with the advantage of script (writing system) independence, and hence useful for people or systems using non-Latin scripts. Status: active. First released: 2.1.0. Last updated: 2.1.0.

National Wastewater Surveillance System (nwss). NWSS header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NWSS - notes (nwssNotes). NWSS notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NWSS - process (nwssProcess). NWSS process Status: active. First released: 2.0.0. Last updated: 2.0.0.

Calculation Type (calcType). A field to explain the purpose/nature of a single calculation/data treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polgygon ID Subject (polygonIDSubject). The polygon ID subject in a polygon relationship. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Organization level (orgLevel). The geographic level of an organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organization sector (orgSector). The sector of an organization Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organization Type (orgType). Specifies the type or purpose of a given organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample origin (origin). An attribute of a sample specifying the origin. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polygon ID (polygonID). Unique identifier for the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Access to other prov depricated (otherProvDep). If this is 'no', this data will not be available to other data providers not listed before. If missing, data will be available to other data providers not listed before Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Polygon ID Object (polygonIDObject). The polygon ID Object in a polygon relationship. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polygon relationship ID (polygonRelID). Unique identifier for each row in the polygon relationships table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Contact email (email). Contact e-mail address, for the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Primary reporting authority ID (repOrg1). The primary or most responsible authority for rountine surveillance reports or findings, or where the site is located. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Fraction name (wide table) (fractionName). The fraction analyzed referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Fraction input (wide table) (fractionInput). The partID for the fraction being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Postal or Zip Code (pCode). The zip code or postal code for a given address, specifying a specifc geographic area. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Access to phac (phac). If this is 'no', the data will not be available to employees of the Public Health Agency of Canada - PHAC. If missing, data will be available to employees of the Public Health Agency of Canada - PHAC. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Public health action type (actionType). The type of public health action being taken. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHAGE (phage). PHAGE header Status: active. First released: 2.0.0. Last updated: 2.0.0.

PHAGE - notes (phageNotes). PHAGE notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

Country national phone prefix (phone). International dialing code for the country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Standard for Data Adjustment (standard). A field where one can categorically record the standard to which something is being standardized (ie. PMMoV, Crassphage, Flow, etc.) or smoothed (ie. bayesian smoothing, central average smoothing, 7-days, time, etc.). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polygon License (poLic). The license for the availability of the polygon shapefile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Original Data Format (originalFormat). The original structure or model used to record and store the data. This helps indicate if data have been transformed or mapped into the ODM structure. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Protocol ID (protocolID). A unique identifier for a given protocol. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol ID container (protocolIDContainer). Unique identifier for the protocol and the steps and other protocols that make it up. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol ID object (protocolIDObj). The object of the relationship between one protocol and another protocol or step, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Pooled (pooled). Is this a pooled sample, and therefore composed of multiple child samples obtained at different sites Status: active. First released: 1.0.0. Last updated: 2.0.0.

Type of date for case reporting depreciated (popDateTypeDep). Type of date used for confirmed cases. Typically, report or episode are reported. Onset and test date is not usually reported within aggregate data. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Protocol ID subject (protocolIDSub). The subject of the relationship between one protocol and another protocol or step, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol Step ID (stepID). The unique identifier for a specific protocol step. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol step source ID (sourceStep). Specifies the protocol step which serves as a basis for a given protocol step. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Public Health Action Group ID (actionGrpID). ID used for linking multiple public health actions together for a single action. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public health action (action). The specific public health action or designation being taken or applied. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Access to prov ha (provHA). If this is 'no', this data will not be available to provincial health authorities. If missing, data will be available to provincial health authorities. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Pretreatment description - depreciated (ptDescDep). If preTreatment then describe the treatment that was performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Access to public (public). If this is 'no', this data will not be available to the public. If missing, data will be available to the public. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Purpose (purpose). The reason the measure or sample was taken. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality flag (qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample or measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Public Health Action ID (phActionID). Unique identifier for public health actions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Date sample recieved (recDate). The date the sample was received at the laboratory for analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality report ID (qualityReportID). A unique identifier for a given quality report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Relationship between entities (relationshipID). Attribute for specifying the relationship between a sample subject and object. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Public health threat targeted by action (threatTarget). The pathogen or variant for which the designation or action is being taken. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public health action datetime (actionDT). The date and Time of the public health action. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Reporter ID depreciated (reporterIDDep). Unique identifier for the person or organization that is reporting the data. Status: depreciated. First released: 1.1.0. Last updated: 2.0.0.

Health Region for a Site (healthRegion). A free-text variable for listing the health region for a given site. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Reportable (reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied. Status: active. First released: 2.0.0. Last updated: 2.1.0.

Report date (reportDate). The date a measure was reported. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Measure name (wide table) (measureName). The measure referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Measure input (wide table) (measureInput). The partID for the measure being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Replicate Type (repType). Attirbute of a sample, specifying whether the sample is unique, or a replicate. And if it is a replicate, what type of replicate is it? Status: active. First released: 2.0.0. Last updated: 2.0.0.

Contact phone (coPhone). Contact phone number, for the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample ID (sampleID). Unique identifier for a sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Sample material (saMaterial). Type of sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample ID object (sampleIDObject). Populated by `sampleID` - this specifies the object of a sample relationship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample ID subject (sampleIDSubject). Populated by `sampleID` - this specifies the subject of a sample relationship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Secondary reporting authority ID (repOrg2). The secondary, additional or alternative authority for rountine surveillance reports or findings, or where the site is located. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Set ID (setID). The unique identifier of a value set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Latitude (geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721) Status: active. First released: 1.0.0. Last updated: 2.0.0.

Access to self (self). If this is 'no', this data will not be shown on the portal when this reporter logs in. If missing, data will be available to this reporter. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Date sample was sent (sentDate). Date that the sample was sent from the collection site to the lab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site ID (siteID). Unique identifier for the location where a sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Site ID default (siteDef). Used as default when a new sample is created by this reporter. See ID in Site table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Severity indicator (severity). An indicator of the severity or seriousness of a quality flag. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sewer network file link depreciated (sewerNetworkFileBLOB). Link to a file that has any detailed information about the sewer network associated with the site (any format). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Site measure ID (siteMeasureID). Unique identifier for wide table only. Use when all measures are performed on a single sample. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Measure relevance start date (relDateStart). The start date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Longitude (geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000) Status: active. First released: 1.0.0. Last updated: 2.0.0.

Source Protocol ID (sourceProtocol). A protocol that served as a basis for another protocol. This may be due to version changes, or a referencing a protocol that was later adapted. Status: active. First released: 2.0.0. Last updated: 2.0.0.

European Petroleum Survey Group Coordinates (geoEPSG). The unique EPSG code specifying a given geospatial area. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sewer network file link depreciated 2 (snfl). Link to a file that has any detailed information about the sewer network associated with the site (any format). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Method name (wide table) (methodName). The method referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sequence Order (order). The order a single calculation/data treatment takes within the full container pipeline/workflow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Role of contact (role). Specifies the organizational role of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol version (protocolVersion). Specifies the version of a method set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sovereign status of a country (sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Specimen (specimen). The substance or thing upon which the observation was made. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Method input (wide table) (methodInput). The partID for the method being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Unit name (wide table) (unitName). The unit referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Equation (equation). The equation used in the calculation/data treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Country (country). The country where a site or organization is located; part of the address. Status: active. First released: 1.0.0. Last updated: 3.0.1.

Step ID Object (stepIDObj). The object of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Step ID Subject (stepIDSub). The subject of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Synthetic ID for the protocolRelationships table (protocolRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the protocolRelationships table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Value (value). Value of a measure, observation or attribute. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sewer network file blob (storTempDef). A file blob that has any detailed information about the sewer network associated with the site (any format). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Synthetic ID for the sampleRelationships table (sampleRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the sampleRelationships table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Unit (unit). The units of a measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Level of Aggregation of a Sampling Site (siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type of region is represented by the base sewershed. This can be used to pool together or average results across similar sewersheds, and avoid trying to average different scales of sewershed together without a correction for size. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Measure relevance end date (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Country code top-level domain (tld). The internet top-level domain generally used or reserved for a country, sovereign state, or dependent

territory identified with a country code. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Synthetic ID for the translations table (translationID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the translations table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Source Code (sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Type other depreciate2 (tyOtDep2). Description of the site when the site is not listed. See siteType. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Treatment ID (treatmentID). A unique identifier for a single calculation/data treatment, a single data treatment identifier. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Last edited (lastEdited). The date the entry was last updated. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Unit input (wide table) (unitInput). The partID for the unit being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Aggregation name (wide table) (aggregationName). The aggregation referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

U site measure ID (uSiteMeasureID). Unique identifier for each measurement for a site. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

Coordinated universal time (UTC) zone (utc). UTC – Time zone. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Coordinated universal time (UTC) zone in daylight savings (utcDST). Time zone during Daylight Saving Time. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Value Treatment (valTreat). A field which specifies what kinds of data treatments or the nature of the measurement value. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Notes (notes). A note used to describe details that are not captured in other attributes Status: active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 category (version1Category). ODM V1 category Status: active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 location (version1Location). ODM V1 location Status: active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 table (version1Table). ODM V1 table Status: active. First released: 2.0.0. Last updated: 2.0.0.

ODM version 1 to 2 changes (version1to2Changes). Changes for part between ODM v1 and V2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

ODM V1 variable (version1Variable). ODM V1 variable Status: active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation input (wide table) (aggregationInput). The partID for the aggregation being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Index (index). Index number in case the measurement was taken multiple times. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Attribute name (wide table) (attributeName). The attribute referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Attribute input (wide table) (attributeInput). The partID for the attribute being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

World Sphere (W-SPHERE) (wSphere). World Sphere header Status: active. First released: 2.0.0. Last updated: 2.0.0.

World Sphere (W-SPHERE) notes (wSphereNotes). W-Shere notes Status: active. First released: 1.0.0. Last updated: 2.0.0.

English name of country sub-domains (zoneName). The english-language name for a given country sub-domain. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Data Type column (Reported) (dataType). The recorded data type for every part in the part table. This is the attribute in the parts table, not to be confused with dataTypes, the part type. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Part type column (Reported) (partType). The recorded part type for every part in the part table. This is the attribute in the parts table, not to be confused with partTypes, the part type. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Wide name measurement and linkage tag (tag). A tag used in wide names to clarify relationship and linkage in the flattened, single table format. Status: active. First released: 3.0.0. Last updated: 3.0.1.

Bacterial testing method set

(bactMethSet). The set capturing containing all of the valid methods for the bacterial testing method.

Bacterial culture (bacCul). Growing a bacterial culture to test for bacterial presence. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial gradient test (agt). A gradient strip test is performed according to the manufacturer's instructions: a short plastic or paper strip impregnated with antibiotic is placed on inoculated agar. On the standardised 100 mm Petri dish, two strips may be placed, while on the larger 150 mm Petri dish, up to six antibiotics may be tested simultaneously. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gram stain (gramSt). After the sample is taken, the Gram stain is colored purple. Then, a solvent is added to the stain. When the solvent combines with bacteria in a sample, the bacteria will either stay purple or turn pink or red. If the bacteria remain purple, they are Gram-positive. If the bacteria turn pink or red, they are Gram-negative. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Growth in enrichment broth (growBroth). The selective cultivation of microorganisms in a nutrient-rich liquid medium to increase their concentration before analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Boolean value set

(booleanSet). Set that contains the valid possible values for a boolean measure (TRUE or FALSE).

TRUE (TRUE). Boolean data type = TRUE Status: active. First released: 1.0.0. Last updated: 2.3.0.

FALSE (FALSE). Boolean data type = FALSE Status: active. First released: 1.0.0. Last updated: 2.3.0.

Calculation type set

(calcTypeSet). The set of valid inputs for the calculation type field.

Normalization Calculation Type (normalization). A transformation of data to have a mean of zero and a standard deviation of one, commonly used to compare values across different datasets or units. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Standardization Calculation Type (standardization). A method used to scale data to a common range or distribution, often to enable fair comparisons across different variables, time periods, or locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Smoothing Calculation Type (smoothing). A technique used to reduce short-term fluctuations in data to better reveal underlying trends or patterns, such as using moving averages or splines. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Predictive Modeling Calculation Type (predictiveModels). A statistical or machine learning approach used to estimate future values or outcomes based on historical data patterns. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Categories

(categories). A discrete list of values that can be reported for a measure, method or attribute. A use-case example of categories would be how they are used to record the site where a measure is taken (partID =

geoType). For the geoType attribute there are different type of sites where samples can be taken: a wastwater treatment plant, airplane holding tank, wastwater pumping station, etc. Each of these site types is recorded as a category that can be identified in categorySetID = sTypeCatSets

16S Ribosomal Gene Sequencing (16rgs). An amplicon sequencing assay in which the amplicon is derived from universal primers used to amplify the 16S ribosomal RNA gene from isolate bacterial genomic DNA or metagenomic DNA from a microbioal community. Resulting sequences are compared to reference 16S sequence databases to identify or classify bacteria present within a given sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Atline Analyzer (aas). Atline analyzer with sampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

ABRicate Software (abricate). Software tool for screening bacterial genomes against multiple resistance databases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ABySS (abyss). A sequencing software that is a scalable de novo assembler for large genomes, designed for distributed computing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Academic institution (academ). The category of organization type used for academic institutions or research groups. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Accel-NGS 2S Plus DNA Library Kit (accelNGS2Splus). Accel-NGS 2S Plus DNA Library Kit by Swift Biosciences. A library prep kit designed for efficient library prep from fragmented or damaged DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Active (active). Indicator that a part is in current use. Status: active. First released: 2.0.0. Last updated: 2.0.0.

AdapterRemoval (adapterRemoval). A sequencing data processing application that removes adapters and filters reads based on quality and length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CARD Resistance Gene Identifier (RGI) (cardRGI). Software tool that is a part of the Comprehensive Antibiotic Resistance Database (CARD) used for annotation and prediction of AMR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Administrative regions (admRegLevel). Administrative regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

Aeration tank (aerTank). A chamber in wastewater treatment where air is introduced to promote microbial breakdown of organic pollutants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Academic Free License v3.0 (afl30). The licensing for the measure or data set is managed under the Academic Free License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Afternoon (aft). Sample was collected in the afternoon, sometime after lunch. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AfterQC (afterQC). An automated QC pipeline tool for FASTQ data, combining quality assessment and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Air filter (afu). Air filter as part of filtration or circulating unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

GNU Affero General Public License v3.0 (agpl30). The licensing for the measure or data set is managed under the GNU Affero General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Agricultural activity (agri). Agricultural activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial gradient test (agt). A gradient strip test is performed according to the manufacturer's instructions: a short plastic or paper strip impregnated with antibiotic is placed on inoculated agar. On the standardised 100 mm Petri dish, two strips may be placed, while on the larger 150 mm Petri dish, up to six antibiotics may be tested simultaneously. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Airplane (airpln). Airplane sample shed category type Status: active. First released: 1.0.0. Last updated: 2.0.0.

Airport (airport). Airport sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

AliView (aliView). Sequencing software that is a user-friendly alignment editor with consensus sequence options. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AllPaths-LG (allpathsLG). A sequencing software that was designed for high-quality assemblies using large, paired-end Illumina data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Aloh3 precipitation (aloh3). Aloh3 precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Amicon ultrafiltration (amiconUf). Amicon ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

Amicon filter, extract with MP96 (amiMP96). Nucleaic acid extraction, usually used for the liquid fraction of a wastewater sample, using amicon filtration and using an MP96 for final extraction. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Amplicon sequencing (amp). Specifies the amplicon strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Antimicrobial resistance (AMR) classification (amrClass). A public health action type wherein threat level classification has been done on a

strain of antimicrobial resistant (AMR) microbes, and communicated to the public. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AMRFinderPlus Software (amrFinderPlus). Software tool that was developed by NCBI to detect AMR genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

annealing/extension (anneal). Describes the annealing and/or extension cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Apache license 2.0 (apache20). The licensing for the measure or data set is managed under the Apache license 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Apollo PrepX Library Preparation Kits (apolloPrepX). Apollo PrepX Library Preparation Kit by Takara Bio. An automated library preparation kit for Illumina sequencing on Apollo systems. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ARACHNE (arachne). A sequencing software that is an early assembler optimized for large, complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antibiotic Resistance Genes Database (ARDB) (ardb). An archive for antibiotic resistance genes and associated information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Area proportional sample (areaPr). An area proportional sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ARG-ANNOT Annotation Tool (argAnnotSoft). Software annotation tool for antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ARIBA (ariba). ARIBA. Focus: Genotyping, MLST, and serotyping from raw sequencing reads. Applications: Salmonella, Escherichia coli, Klebsiella pneumoniae, and more. Features: Works with custom databases for

serotyping and resistance gene identification. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V1 Primer Set (articV1). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 1.0.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V2 Primer Set (articV2). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 2.0.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Use of the articV3 primer (articV3). Initial implementation of an ARTIC bioinformatics platform for nanopore sequencing of nCoV2019 novel coronavirus; Artic Foundation v3 primer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Use of the articV4 primer (articV4). Artic V4 sequencing primer for VOCs and VOIs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Artic V4.1 Primer Set (articV41). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 4.1.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5 Primer Set (articV500). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.0.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.1 Primer Set (articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2with the attributes of version 5.1.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.2 Primer Set, 1200bp (articV520bp1200). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.2 Primer Set, 400bp (articV520bp400). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.3.2 Primer Set (articV532). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.3.2 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artistic license 2.0 (artistic20). The licensing for the measure or data set is managed under the Artistic license 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Amies Transport Medium (atm). A buffer solution/medium that maintains viability of bacteria in wastewater and environmental samples during transport. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Atropos (atropos). A QC pipeline tool for sequencing data that performs adapter trimming and quality filtering with built-in QC reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Automatic composite sampling (autoComp). A composite sampler which is automated to collect and store multiple wastewater samples across multiple time points. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Autosamplers (autoInst). Autosampler instruments, used to automatically collect flow- or time-proportional samples over a period (e.g., ISCO autosamplers). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Automatic sequential sampling (autoSeq). A composite sampler which is automated to collect and combine multiple samples of equal volume taken at a set time interval. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bacterial culture (bacCul). Growing a bacterial culture to test for bacterial presence. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BacMet Database (bacMet). Database of antibacterial biocide and metal resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bacteroides 16S forward primer (HF183) (ABI) (bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S probe (BacP234) (ABI) (bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S reverse primer (BacR287) (ABI) (bact16sABIRev). Bacteroides 16S reverse primer (BacR287) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bag Mediated Filtration (bagFilt). Sample was collected using bag-mediated filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BamQC (from Qualimap) (bamQC). A QC pipeline tool for sequencing data that focuses on quality control for mapped data in BAM format, reporting alignment quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

bamUtil Dedup (bamUtil). A deduplication method that removes duplicate reads directly from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bar screen (barScreen). A bar screen is a mechanical device used to remove large solid debris from wastewater or sewage as it enters a treatment plant. It consists of a series of parallel bars or rods, spaced at specific intervals, that allow water to pass through while capturing larger objects. This process prevents damage to downstream equipment and ensures efficient treatment. Bar screens are typically installed at the inlet of wastewater treatment facilities and can be cleaned manually or mechanically, depending on the design and operational requirements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BayesHammer (from SPAdes) (bayesHammer). A sequencing data processing application that does error correction tool specifically for Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bayesian Smoothing applied (bayesSmooth). This data treatment smooths the measurement value using bayesian smoothing techniques. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBDuk (from BBTools) (bbduk). A QC pipeline tool for sequencing data that is a part of the BBMap suite, performs filtering and trimming, and generates QC statistics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap (bbmap). BBMap. A general-purpose read mapper. High-sensitivity aligner for DNA and RNA reads. Best for: Error-prone reads from platforms like Nanopore or PacBio. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap Reformat (bbmapReform). A dehosting software that filters out host sequences by aligning to reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap Suite (bbmapSuite). A sequencing data processing application library that includes tools like BBDuk for quality trimming, adapter removal, and quality filtering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bead beating, extract with MP96 (bbMP96). Nucleaic acid extraction, usually used for solid fraction of a wastewater sample, using bead beating and using an MP96 for final extraction. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Bcftools (bcfTools). Sequencing software that works with SAMtools to call variants and produce consensus sequences from alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

bcov culture spike target (bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

bcov spike target (unspecified) (bcovGen). The bovine coronavirus (unspecified) is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

bcov vaccine spike target (bcovVac). The bovine coronavirus vaccine is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Bayesian Evolutionary Analysis by Sampling Trees (BEAST) Software (beast). A lineage or clade analysis software tool for estimating evolutionary relationships and divergence times in a Bayesian framework. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Beef extract flocculation (beeExtractFloc). Beef extract flocculation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Is Before (before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

BIGSdb (Bacterial Isolate Genome Sequence Database) (bigsdb). BIGSdb (Bacterial Isolate Genome Sequence Database). A flexible platform that supports serotyping alongside sequence typing and other typing

schemes. Can be customized for various bacterial species, including Neisseria meningitidis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fragment analyzers or bioanalyzers (bioanalys). Fragment analyzer or bioanalyzer instruments, used to assess fragment size distribution in libraries. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BioEdit (bioEdit). Sequencing software that offers sequence alignment and visualization, used to manually generate consensus sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bioo Scientific NEXTflex Rapid DNA-Seq Kit (biooSci). Bioo Scientific NEXTflex Rapid DNA-Seq Kit by PerkinElmer. A rapid and flexible library prep kit for DNA sequencing on Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Digital droplet emulsification PCR (bioRadDdpcr). Describes a PCR analysis done using BioRad's digital droplet emulsification PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Biological replicate (bioRep). A biological replicate not otherwise specified - these are parallel measurements of biologically distinct samples that capture random biological variation, which can be a subject of study or a source of noise itself. Biological replicates are important because they address how widely your experimental results can be generalized. They indicate if an experimental effect is sustainable under a different set of biological variables. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BLASR (Basic Local Alignment with Successive Refinement) (blasr). BLASR (Basic Local Alignment with Successive Refinement). A long-read specific mapper. Optimized for PacBio data. Best for: High-quality long-read alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BMTagger (bmtagger). A dehosting software developed by NCBI for identifying and removing host sequences based on local alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Border closure (borderClos). A measure shutting entry points to limit cross-border movement and disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Body of water (bow). An outdoor accumuation of water either on the surface or beneath the ground, no other additional details specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bowtie2 (bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that maps reads against a host reference genome to remove aligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Host Subtraction with Bowtie2 & SAMtools (bowtie2XSam). A combined workflow for dehosting where reads mapped to the host are removed from downstream analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Buffered Peptone Water (bpw). A buffer solution/medium used for bacterial enrichment, can also serve as a temporary preservative. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bracken (bracken). A QC pipeline tool for sequencing data and taxonomic profiling that can also be used to identify contamination and assess data quality in metagenomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

brsv culture spike target (brsvCul). Cultured bovine respiratory syncytial virus (BRSV) is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

brsv vaccine spike target (brsvVac). The bovine respiratory syncytial virus (BRSV) vaccine is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

BSD Zero-Clause license (bsd0). The licensing for the measure or data set is managed under the BSD Zero-Clause license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 2-clause "Simplified" license (bsd2Clause). The licensing for the measure or data set is managed under the BSD 2-clause "Simplified" license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 3-clause "New" or "Revised" license (bsd3Clause). The licensing for the measure or data set is managed under the BSD 3-clause "New" or "Revised" license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 3-clause Clear license (bsd3ClauseClear). The licensing for the measure or data set is managed under the BSD 3-clause Clear license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 4-clause "Original" or "Old" license (bsd4Clause). The licensing for the measure or data set is managed under the BSD 4-clause "Original" or "Old" license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Boost Software License 1.0 (bsl10). The licensing for the measure or data set is managed under the Boost Software License 1.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Branch sewer pipleline (bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municpal sewer lines, allowing drainage into the main sewer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Building cleanout (buildCO). Specifies a site type that is a capped pipe that connects to a building's main sewer line. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Building-level Surveillance (builLev). Surveillance is done only at the level of a single building. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bus (bus). A large motor vehicle carrying passengers by road, typically one serving the public on a fixed route and for a fare. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Bus Station (busStat). A terminal where buses arrive and depart. Status: active. First released: 2.2.3. Last updated: 2.2.3.

BWA (Burrows-Wheeler Aligner) (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA for Host Filtering (bwaHost). A dehosting software that maps reads to a host genome, filtering mapped reads from analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA-MEM with Duplicate Marking (bwaMEM). A deduplication method that is used with SAMtools or Picard to mark duplicates during read mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Canal (canal). Artificial watercourse with no flow or a controlled flow used for navigation, drainage or irrigation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Canu (canu). A sequencing software that is a de novo assembler specifically optimized for long-read data from PacBio and Oxford Nanopore. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CapsuleFinder (capFin). CapsuleFinder Used for typing capsular polysaccharides in a variety of bacteria, especially Escherichia coli and Klebsiella species. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Comprehensive Antibiotic Resistance Database (CARD) (cardDtbase). Database that provides high-quality reference sequences for resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Case report date (caRepDate). Date that the numbers were reported publicly. Typically, reported data and this measure is most commonly reported and used. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Central average smoothing applied (caSmooth). This data treatment smooths the measurement value using central average smoothing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cary-Blair Transport Medium (cbtm). A buffer solution/medium commonly used for bacterial preservation in stool and wastewater samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Creative Commons Zero v1.0 Universal (cc010). The licensing for the measure or data set is managed under the Creative Commons Zero v1.0 Universal. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Creative Commons Attribution 4.0 (ccby40). The licensing for the measure or data set is managed under the Creative Commons Attribution 4.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

CC BY-NC 4.0 license (ccbync40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial international license. Status: active. First released: 2.2.3. Last updated: 2.2.3.

CC BY-NC-SA 4.0 license (ccbyncsa40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial, and sharealike international license. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Creative Commons Attribution ShareAlike 4.0 (ccbysa40). The licensing for the measure or data set is managed under the Creative

Commons Attribution ShareAlike 4.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Long-term acute care hospital (ccc). Acute care hospitals, or complex contuing care, that provide care for patients with average length of stay longer than 25 days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Child day care (cdc). Child day care facility. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sarbeco_E forward primer (IDT) (cdcCovEIDTFor). Sarbeco_E forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E probe (IDT) (cdcCovEIDTProbe). Sarbeco_E probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E reverse primer (IDT) (cdcCovEIDTRev). Sarbeco_E reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 forward primer (IDT) (cdcCovN1IDTFor). 2019-nCoV_N1 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 probe (IDT) (cdcCovN1IDTProbe). 2019-nCoV_N1 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 reverse primer (IDT) (cdcCovN1IDTRev). 2019-nCoV_N1 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 forward primer (IDT) (cdcCovN2IDTFor). 2019-nCoV_N2 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 probe (IDT) (cdcCovN2IDTProbe). 2019-nCoV_N2 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 reverse primer (IDT) (cdcCovN2IDTRev). 2019-nCoV_N2 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 forward primer (IDT) (cdcCovN3IDTFor). 2019-nCoV_N3 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 probe (IDT) (cdcCovN3IDTProbe). 2019-nCoV_N3 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 reverse primer (IDT) (cdcCovN3IDTRev). 2019-nCoV_N3 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

CD-HIT (cdHIT). A sequencing data processing application that clusters and removes duplicate sequences, useful for dereplication. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CeCILL Free Software License Agreement v2.1 (cecill21). The licensing for the measure or data set is managed under the CeCILL Free Software License Agreement v2.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Celera Assembler (celera). A sequencing software that was initially developed for the Human Genome Project, still used in some workflows for large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population census (census). Government or other agency census for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Centrifugation (cent). Describes solid separation from a wastewater sample via centrifugation. Likely connected to other method steps prior to analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Centricon ultrafiltration (centriconUf). Centricon ultrafiltration. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Centrifuges (centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ceres nanotrap (ceres). Ceres nanotrap. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Cesspit (cesspit). Cesspit, cesspool and soak pit in some contexts are terms with various meanings: they are used to describe either an underground holding tank (sealed at the bottom) or a soak pit (not sealed at the bottom). A cesspit can be used for the temporary collection and storage of feces, excreta, or fecal sludge as part of an on-site sanitation system and has some similarities with septic tanks or with soak pits. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Chemical contaminant surveillance (chemSurv). Purpose of sampling/measure is to test for the presence of certain chemicals or chemical contaminants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Chemagic viral dna/rna 300 kit (chemVir). Nucleic acid extraction performed using the chemagic viral dna/rna 300 kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ChewBBACA (chewBBACA). ChewBBACA. Focus: Core genome MLST (cgMLST) with optional serotyping analysis. Applications: Broad-spectrum bacterial pathogens. Features: Efficient with large datasets and highly customizable. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Child relationship (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Composite Key (cK). Composite key for a table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Clarified sample (clari). Clarified sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

CLARK (clark). A dehosting software that classifies reads taxonomically, which helps filter out host reads in metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CleanPlex DNA Library Prep Kit (cleanPlex). CleanPlex DNA Library Prep Kit by Paragon Genomics. A library target enrichment kit optimized for high sensitivity and low input. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ClermonTyping (clermonTyp). ClermonTyping. Focus: MLST and phylogenetic typing for Escherichia coli. Applications: Ideal for epidemiological studies. Features: Combines MLST and phylogroup-specific information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Clinic (clinic). A medical clinic, may be used to provide treatment, remedial work, and/or instruction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ClonalFrameML Software (clonalFrameML). A lineage or clade analysis software tool for reconstructing phylogenetic relationships considering recombination, used in bacterial lineage analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cloudy (cloudy). Qualitative category for the weather measure, specifying an overcast day with no rain. Status: active. First released: 2.0.0. Last updated: 2.0.0.

BBMap's Clumpify (clumpify). A deduplication method that groups identical sequences, often used to deduplicate reads efficiently. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Clustal Omega (clustalO). Sequencing software that is widely used for multiple sequence alignment and producing consensus sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Co-located relationship (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Commercial facility - not specified (commFacOth). Specifies a site type which is a commercial facility/worksite that is not otherwise captured or described in the geotype set. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Community-level Surveillance (communitLev). Surveillance is done at the level of an entire community. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Communitor (communitor). A mechanical device that grinds large solid waste in wastewater into smaller particles to prevent clogging. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Composite sample - archival (comp). A composite sample, usually generated by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Composite grab sample of 3 (comp3). A grab-composite sample composed of 3 separate grab samples. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Composite grab sample of 3 depreciate (comp3dep). A grab-composite sample composed of 3 separate grab samples. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Composite 3hr grab sample (comp3h). A 3-hour composite with 3 grab samples each taken once per hour, generally manually performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Composite 3hr grab sample depreciate (comp3hdep). A 3-hour composite with 3 grab samples each taken once per hour, generally manually performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Composite 8hr grab sample depreciated (comp8h). An 8-hour composite with 8 grab samples each taken once per hour, generally manually performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Composite 8hr grab sample deprecated (comp8hDep). A 8-hour composite with 8 grab samples each taken once per hour, generally manually performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Composting toilet (compToi). A self-contained toilet system wherein human waste is designed to be composted. Usually with the addition of secondary materials, like sawdust. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Is concurrent to (concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Cone-shaped sampling (cone). Intrument type is a grab sample that has a controlled valve that opens to take a sample from a specific depth, then closes to bring the sample out. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Contamination (contam). The presence of a constituent, impurity, or some other undesirable element that spoils, corrupts, infects, makes unfit, or makes inferior a material, physical body, natural environment, place of human occupancy, or other material entity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Control measure implementation (contMeasImp). A public health action type wherein authorities have begun implementing infection control measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Control sample (control). Denotes a relationship to a primary sample where the object sample serves as a control to the subject sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Core sampling (core). Intrument type is a grab sampler that captures a vertical section of the substrate matrix of fecal sludge. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Correctional facility (corFcil). Correctional facility Status: active. First released: 1.0.0. Last updated: 2.0.0.

COSCa ball (cosca). COSCa passive sampling device. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population count (count). A count of residents for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

A-Tier Region-level Aggregation at Site (aRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an "A-Tier" region and refers to large, dense urban areas made up of multiple overlapping cities/boroughs. This would be a greater metropolitan area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

B-Tier Region-level Aggregation at Site (bRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an "B-Tier" region, and thus a region within a greater metropolitan area and larger than a single municipality, but smaller than the entire metropolitan area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Countries or sovereign states (countryLevel). Countries or sovereign states Status: active. First released: 2.0.0. Last updated: 3.0.0.

Districts, counties, regions (countyLevel). Districts, counties, regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

Covaris truXTRAC FFPE DNA Library Kit (covarisTruXTRAC). Covaris truXTRAC FFPE DNA Library Kit. A specialized library prep kit for extracting and preparing DNA from FFPE tissue. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Critical priority pathogen (cpp). A microorganism with resistance to multiple drugs and a high threat to human health. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Crassphage Standarized (crassStand). This data treatment standardizes the measurement value to concentration levels of crassphage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CTFinder (ctFinder). CTFinder. Designed for Clostridioides difficile serotyping and subtyping. Identifies capsular polysaccharide synthesis gene clusters to assign serogroups. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cufflinks (with TopHat integration) (cufflinks). Cufflinks (with TopHat integration). A specialized read mapper. Combines mapping with transcriptome assembly and quantification. Best for: RNA-seq studies with integrated analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cutadapt (cutadapt). A sequencing data processing application that does adapter removal and trimming tool for high-throughput sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DADA2 (dada2). A sequencing data processing application that is primarily used in amplicon sequencing for error correction and generating amplicon sequence variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data collection sector or organization (dataColl). Describes organization who collect compile, analyze, and or manage data as their central focus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

7-day smoothing of values (day7Smooth). This data treatment smooths the measurement value across 7-days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DNA Data Bank of Japan (DDBJ) (ddbj). DNA Data Bank of Japan (DDBJ) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Digital Droplet PCR (ddPCR) (ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

DeconSeq (deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DecontaMiner (decontaMiner). A QC pipeline tool for sequencing data for contamination detection and removal in NGS datasets, especially useful in clinical samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Decreased surveillance (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DeepARG Software (deepARG). Software tool that predicts AMR genes using deep learning on metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

denaturation (denat). Describes the denaturation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Depreciated (depreciated). Indicator to say that a part is no longer in current use in the model. See partID = status Status: active. First released: 2.0.0. Last updated: 2.0.0.

Derived data (derived). Derived data, data that has undergone agregation, standardization, adjustment, or any cleaning prior to reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Derived sample (derivedSamp). A sample that is derived or made from another sample or material. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Desk or counter (desk). Desk, table, countertop or other flat working surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dewatered solids (deso). Dewatered solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

De-escalated variant (dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Development (development). Indicator that a part is under development use. See partID = status Status: active. First released: 2.0.0. Last updated: 2.0.0.

DISCOVAR de novo (discovar). A sequencing software that is an assembler optimized for Illumina data in whole-genome sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DNA Template (dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nextera DNA Flex/DNA Prep Library Prep Kit (dnaPrep). Nextera DNA Flex Library Prep Kit, now called DNA Prep, by Illumina. A flexible, transposase-based library prep kit for a wide range of DNA input

amounts, suitable for microbial and human DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DNA/RNA Shield (dnaRNAshield). A stabilizing solution for nucleic acids in samples, including wastewater, protecting against degradation at room temperature. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Domestic travel hub surveillance (domSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to domestic travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Higher education domitory or residential building (dorm). Higher education domitory or residential building Status: active. First released: 2.0.0. Last updated: 2.0.0.

Digital PCR (dPCR) (dpcr). Describes a PCR analysis done using digital PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Digital PCR (dPCR) intruments (dPCRinst). Digital PCR instruments, enables absolute quantification without the need for standard curves (e.g., Bio-Rad QX200). Status: active. First released: 3.0.0. Last updated: 3.0.0.

DDBJ sequence Read Archive (DRA) (dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sewer (drain) (drain). A pipe that carries water or sewage away from a place, or an opening in a surface that leads to said pipe. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Drug surveillance (drugSurv). Purpose of sampling/measure is to surveil drug use in a population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

EAGER (eager). A QC pipeline tool for sequencing data for ancient DNA, providing quality filtering, contamination estimates, and other QC metrics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

EasySeq NGS Targeted Capture Kit (easySeqNGS). EasySeq NGS Targeted Capture Kit by Nimagen. A library preparation kit and targeted capture in one, ideal for small panels. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Educational Community License v2.0 (ecl20). The licensing for the measure or data set is managed under the Educational Community License v2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Eden V1 Primer Set (edenV1). An amplicon strategy which was developed by John-Sebastian Eden with primers for SARS-CoV-2 and attributes of version 1.0.0 which produces amplicons approximately 2500bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Educational facility (edFac). A school or other educational facility not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Education (education). A measure or sample taken for education or training. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater Effluent - non-specified (effluNS). Sample material is wastewater effluent - whether primary, secondary or other is unspecified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Eluate/Resuspended filter material retained (eluate). The eluate fraction, or material resuspended from filtration, is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Elution buffer (elutionBuff). Elution buffer is used to resuspend material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Emboss Cons (embossCons). Sequencing software that is part of the EMBOSS suite, generates consensus sequences from multiple alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Emergency targetted surveillance program (emergSurv). A targeted surveillance strategy which is considered important and/or urgent. Status: active. First released: 3.0.0. Last updated: 3.0.0.

European Nucleotide Archive (ENA) (ena). European Nucleotide Archive (ENA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

ENA Format (enaForm). Dataset was originally recorded and/or stored in ENA format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Enterobase archives (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Temperature and pH probes (enviroInst). Local probe insturments for temperature or pH; allow monitoring of environmental conditions at sites, for example. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Episode date (epiDate). Episode date is the earliest of onset, test or reported date. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Eclipse Public License 1.0 (epl10). The licensing for the measure or data set is managed under the Eclipse Public License 1.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Eclipse Public License 2.0 (epl20). The licensing for the measure or data set is managed under the Eclipse Public License 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

exclusions based sample preparation (ESP) (esp). exclusions based sample preparation (ESP) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Estimated data (estimate). Estimated data, data that should be understood to be an estimation, possiblynot taken directly from sample measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Estuary, natural water body (estuary). Estuary, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

European Union Public License 1.1 (eupl11). The licensing for the measure or data set is managed under the European Union Public License 1.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

European Union Public License 1.2 (eupl12). The licensing for the measure or data set is managed under the European Union Public License 1.2. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Evening (eve). Sample was collected in the evening, late in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

4s method (extract4s). Nucleic acid extraction performed using the 4s method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Fecal matter (faeces). Fecal matter. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Fast-flowing (faFlow). A quality of a body of water wherein there is a fast flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Farm (farm). An aggricultural area, builing, or tract of land. Used for the cultivation of crops or grazing of livestock, including any buildings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FastMLST (fastMLST). FastMLST. Focus: Lightweight MLST and serotyping from assembled genomes or raw reads. Applications: Broad bacterial species. Features: Quick and simple, designed for routine use. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTP (fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FastQC (fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTQ Screen (fastqScreen). A dehosting software that checks reads against multiple reference genomes, including host genomes, to remove contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FastUniq (fastUniq). A deduplication method that is specifically designed to remove duplicates in paired-end sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTX Toolkit (fastXTools). A sequencing data processing application that provides various functions for FASTQ processing, including quality filtering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fecal-contamination (fecContam). A contamination quality in which fecal matter is a key component of the contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Field sample (field). Specifies a sample taken from the field; directly collected from an area for testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Field sample replicate (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Filtration (filt). Describes solid separation from a wastewater sample via filtration. Proceeds further concentration or analysis of the liquid filtrate. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Filtration units (filtInst). Filtration instruments; remove large particulates or concentrate targets (e.g., tangential flow filtration). Status: active. First released: 3.0.0. Last updated: 3.0.0.

First Nation (fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Foreign key (fK). Foreign key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Flocculation (floc). The process of aggregating suspended particles into larger clusters (flocs) using coagulants to aid in sedimentation or filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Floor (floor). Floor of a building or room. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Flow proportional 24hr sample depreciated (flow24hDep). A flow proportional 24-hour composite sample generally collected by an autosampler. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Flow meters (flowInst). Flow meter instruements; used to measure wastewater flow rates to enable standardization of sample data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flow proportional sample (flowPr). A flow proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Flow Standarized (flowStand). This data treatment standardizes the measurement value to flow rates. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fluidigm digital PCR (fluiDpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Flye (flye). A sequencing software that is an assembler for long-read data, particularly effective on nanopore sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Country-level Aggregation at Site (countLevel). Specifies that a sewershed/site represents an entire nation or country. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Foggy (foggy). Qualitative category for the weather measure, specifying a foggy or hazy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Fqtrim (fqtrim). A sequencing data processing fast tool for adapter removal, quality trimming, and quality control. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FRCbam (frcBam). A QC pipeline tool for sequencing data that assesses read quality and genome assembly quality metrics for high-throughput data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Freyja Script (freyja). Freyja Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gaussian distribution stanrdized/Normalized (gauss). Standardize the data to a gaussian/normal distribution, such that the data have a mean of zero and a standard deviation of one. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GEM Mapper (gemMapper). GEM Mapper. A specialized read mapper. High-speed and accurate alignment tool for short reads. Best for: Genomic applications with short reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GenBank Archives (genBank). GenBank Archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Geneious (geneious). Sequencing software that is popular for sequence assembly, alignment, and consensus sequence generation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GenoTyphi (genoTyphi). GenoTyphi. Focus: Specific MLST and serotyping for Salmonella Typhi. Applications: Outbreak investigations and epidemiology. Features: Highly specialized for typhoidal Salmonella. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GNU Free Documentation License v1.3 (gfdl13). The licensing for the measure or data set is managed under the GNU Free Documentation License v1.3. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Global Initiative on Sharing All Influenza Data (GISAID) archives (gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GitHub (github). GitHub external data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

10% Glycerol Solution (glycerol10). 10% Glycerol Solution - Common cryoprotectant for bacterial and viral storage in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GMAP (gmap). GMAP. A specialized read mapper. A long-read aligner for genomic mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Government agency (govt). The category of organization type used for government agencies, programs, or crown-owned bodies. Status: active. First released: 2.0.0. Last updated: 2.0.0.

GNU General Public License v2.0 (gpl20). The licensing for the measure or data set is managed under the GNU General Public License v2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU General Public License v3.0 (gpl30). The licensing for the measure or data set is managed under the GNU General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Grab samplers (grabInst). Grab sampler instruments; manually collect a single sample at a point in time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gram stain (gramSt). After the sample is taken, the Gram stain is colored purple. Then, a solvent is added to the stain. When the solvent combines with bacteria in a sample, the bacteria will either stay purple or turn pink or red. If the bacteria remain purple, they are Gram-positive. If the bacteria turn pink or red, they are Gram-negative. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GraphMap (graphmap). GraphMap. A long-read specific mapper. Long-read aligner optimized for highly error-prone reads. Best for: De novo assemblies using long-read data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gravity settling (graSet). Describes solid separation from a wastewater sample where the sample material is allowed to settle by gravity, and then separated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Grab sample (grb). A single large representative grab sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Grit chamber (gritCham). A sedimentation basin in wastewater treatment that removes heavy, inorganic particles (e.g., sand, gravel) before biological treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gromstole 1.0 Script (gromstole). Gromstole 1.0 Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Growth in enrichment broth (growBroth). The selective cultivation of microorganisms in a nutrient-rich liquid medium to increase their concentration before analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ground water (grWa). Underground water which is located in pore spaces found in rock or unconsolidated deposits such as soil, clay, or gravel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Genome Sequence Archive (GSA) (gsa). Genome Sequence Archive (GSA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

GSNAP (gsnap). GSNAP. A specialized read mapper. A splice-aware aligner for RNA-seq reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Guanidine Thiocyanate (gt). A buffer solution/medium that serves as a strong preservative for viral RNA, commonly used in molecular biology for RNA preservation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

First Nation Territory/Métis Settlement-level Aggregation at Site (fnmiLevel). Specifies that a sewershed/site represents the entirety of a First Nations territory or reservation, or a Métis settlement. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hand hygiene advisory (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hank's Balanced Salt Solution (HBSS) (hbss). Hank's Balanced Salt Solution (HBSS) - Nutrient-rich buffer that maintains cell and microbial integrity in samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Healthcare activity (hcAct). Healthcare activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Healthcare facility (hcf). A building for the provision of healthcare, not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Header (header). Header for a table. Also known as a table variable or entiy relationship 'attribute'. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Health administration or planning agency (healthAdm). Health adminstrative or planning organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Heat inactivated sars-cov-2 virus spike target (heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

hep g armored rna spike target (hepGRnaMat). Hepatitis G armored RNA is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Fraction Analyzed (hFr). An indicator in wide-names to show that information on the fraction analyzed in found under a separate header. Status: active. First released: 2.2.0. Last updated: 2.2.0.

High severity (high). Indicates a very sever quality issue, likely meaning the data should not be reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

HISAT2 (hisat2). HISAT2. A general-purpose read mapper. Successor to TopHat, optimized for RNA-seq data with splicing awareness. Best for: Large-scale RNA-seq experiments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sewer Network Health Region (hlthReg). Health region served by the sewer network Status: active. First released: 1.0.0. Last updated: 2.0.0.

Hand Measurement (hma). Handheld measurement analyzer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Hollow fiber dead end ultrafiltration (hollowFiberUF). Hollow fiber dead end ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

Stay-at-home order (homeOrder). A directive requiring people to remain at home except for essential activities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Horizontal grab sampling (horGrb). Intrument type is a grab sampler in which the container for the sample is mounted on the end of a rod, which is suitable for collecting discharge from a pipe or truck. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hospital (hosptl). Hospital Status: active. First released: 1.0.0. Last updated: 2.0.0.

Holding tank wastewater depreciated (hoTaWa). Wastewater from a holding tank, such as from an airplane or ship Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

High priority pathogen (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Holding tank wastewater (htSam). Wastewater sampled from a holding tank, such as from an airplane or ship Status: active. First released: 2.0.0. Last updated: 2.0.0.

Holding tank (htSite). Holding tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

Animal husbandry (husb). Animal husbandry occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hybrid Selection Method (hySel). Selection by hybridization in array or solution for genomic target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

IDBA-UD (idbaUD). A sequencing software that is an iIterative assembler optimized for metagenomics and complex genomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Illumina DNA Prep with Enrichment (illuminaDNAprep). Illumina DNA Prep with Enrichment by Illumina. A library prep kit that integrates DNA library prep with enrichment for target regions, ideal for targeted sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Increased surveillance (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Industrial plant (indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occaisonally services, and making them into products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Industrial activity (indus). Industrial activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Influent pump station (infPump). A facility that ransports raw wastewater from collection systems to treatment plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Innovaprep ultrafiltration (innovaprepUF). Innovaprep ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

Input (input). Input for a table. Indicates if a part can be used in a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

International Nucleotide Sequence Database Collaboration (INSDC) Archives (insdc). International Nucleotide Sequence Database Collaboration (INSDC) Archives - often includes ENA, NCBI, or DDBJ inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Institution-level Surveillance (instituLev). Surveillance is done at the level of an entire insitution. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Other instrument (instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Internal reference (internalRef). Reference an internal (i.e. private) database within the user's own organization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

International travel hub surveillance (internatSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to international travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

IQ-TREE Software (iqTree). A lineage or clade analysis software tool for constructing phylogenetic trees with clade support. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ISC (isc). The licensing for the measure or data set is managed under the ISC license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

iVar (iVar). A sequencing data processing application that is designed for viral amplicon data, removes primers and can trim low-quality bases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

KAPA HyperPrep Kit (kapaHyperPrep). KAPA HyperPrep Kit by Roche. An optimized library prep kit for high-quality libraries from low-input or degraded DNA, commonly used for Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Kaptive (kaptive). Kaptive. Identifies capsular (K) serotypes in Klebsiella pneumoniae and related species using whole-genome sequence data. Useful for studying capsule diversity and epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

KneadData (kneadData). A sequencing data processing pipeline for quality control, including trimming and host decontamination (uses Trimmomatic and Bowtie2). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Kraken2 (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Laboratory (lab). Laboratory for environmental testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory duplicate (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Lagoon system (lagoon). Lagoon system for extensive wastewater treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

Lake, natural water body (lake). Lake, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Land-based Transit Hub (landTH). A transport hub is a place where passengers and cargo are exchanged between land-based vehicles and/or between land-based transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

LAST (Large-Scale Alignment and Search Tool) (last). LAST (Large-Scale Alignment and Search Tool). A long-read specific mapper. Flexible tool for aligning long and error-prone reads. Best for: Comparative genomics with long reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Latrine (latrine). A toilet or outhouse, especially a communal one in a camp or barracks. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Laboratory control sample duplicate (lcsd). Known amounts of an analyte or representative compounds are added to a second "clean" matrix (lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

<10 people (less10). Fewer than 10 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

10 - 100 people (less100). Between 10 and 100 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

10,000 - 100,000 people (less100k). Between 10,000 and 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

1,000 - 10,000 people (less10k). Between 1,000 and 10,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

100 - 1,000 people (less1k). Between 100 and 1,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

100,000 - 1,000,000 people (less1mil). Between 100,000 and 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GNU Lesser General Public License v2.1 (lgpl21). The licensing for the measure or data set is managed under the GNU Lesser General Public License v2.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU Lesser General Public License v3.0 (lgpl30). The licensing for the measure or data set is managed under the GNU Lesser General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Library preparation instruments (libPrepInst). Instruments for the preparation of sequencing libraries, e.g., automation platforms like the Illumina NeoPrep. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ligase-Dependent Library Prep Kits (ligaseDep). Ligase-Dependent Library Prep Kits by Lucigen/Epicentre. A library prep kit suitable for long-read applications and used with Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

LINEAGE Software (lineage). LINEAGE - Tool for bacterial lineage analysis, often applied to genome sequences in epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liquid fraction (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Liquid/Supernatant retained (liquid). The liquid or supernatant is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Liquid (liquidMat). Material is liquid, ie. is a state of matter with a definite volume but no fixed shape, adapting to the shape of their container. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lockdown (lockdown). Broad restrictions on movement and activities within a region to control disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Longitudinal, repeat sampling surveillance program (longSurv). A surveillance strategy in which an individual or site is selected to undergo repeat sampling over a defined period of time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Low severity (low). A marker for low severity Status: active. First released: 2.0.0. Last updated: 2.0.0.

LaTeX Project Public License v1.3c (lppl13c). The licensing for the measure or data set is managed under the LaTeX Project Public License v1.3c. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Lactated Ringer's Solution (lrs). A buffer solution/medium sometimes used in combination with other preservatives to stabilize microbial samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Long-term care facility (ltcf). A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Long-term care - assisted living or retirement home (ltcfAl). A residential facility that provides assistance with daily care but generally

does not provide skilled nursing care. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other long-term care (ltcfO). Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or assisted living facilities. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Life technologies digital PCR (ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

luminultra wastewater extraction kit (luminWWExtract). luminultra wastewater extraction kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

Lysis buffer (lysi). Lysis buffer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

MAFFT (mafft). Sequencing software that performs multiple sequence alignment, commonly used in consensus sequence generation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Magnetic nanobead binding (magBead). The use of tiny, magnetized beads to selectively capture and isolate biological molecules (e.g., DNA, proteins) in a magnetic field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Magnetic separation racks (magInst). Magnetic separation rack instrument; may be used with magnetic beads for nucleic acid extraction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Shopping mall (mall). A large commercial complex with multiple retail stores, services, and restaurants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Manual Composite Sample (manComp). Specifies a composite sample where the sub-samples were collected manually. Status: active. First released: 2.2.0. Last updated: 2.2.0.

MapSplice (mapSplice). MapSplice. A specialized read mapper. Designed specifically for spliced alignment of RNA-seq reads. Best for: Transcriptomics with a focus on detecting splice junctions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

mash Software (mash). A lineage or clade analysis software tool for the clustering-based method of lineage and clade analysis, comparing large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mask mandate (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mask recommendation (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Maryland Super Read Celera Assembler (MaSuRCA) (masurca). A sequencing software that is a hybrid assembler that can integrate both short and long reads for high-quality assemblies, and large, complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mate pair layout (mateLay). Specifies the mate pair layout for a sequencing method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Meat processing plant (meatPl). A processing plant for slaughtering, processing, packaging, labelling, handling, and storing of food animal carcasses, parts of carcasses, and meat products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Molecular Evolutionary Genetics Analysis (MEGA) (mega). Sequencing software that provides tools for sequence alignment and consensus

sequence extraction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MEGAHIT (megahit). A sequencing software that is a fast and memory-efficient assembler for large metagenomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MEGARes database (megares). A comprehensive database of antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

membrane filtration with addition of mgcl3 (memMgCl3). membrane filtration with addition of mgcl3 Status: active. First released: 2.2.0. Last updated: 2.2.0.

MetAMOS (metAMOS). A sequencing software that is an automated pipeline for metagenomic assembly and annotation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MetaPhlAn Software (metaPhIAn). Software tool that profiles microbial communities and can provide resistance gene insights. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Membrane filtration with acidification and mgcl2 (mfAcidmgcl2). Membrane filtration with acidification and mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with acidification and mgcl2, membrane recombined with separated solids (mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with addition of mgcl2 (mfMgcl2). Membrane filtration with addition of mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with mgcl2 and separated solids (mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with

separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with no amendment (mfNoAmend). Membrane filtration with no amendment Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with no amendment, membrane recombined with separated solids (mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with sample acidification (mfSampleAcid). Membrane filtration with sample acidification Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with sample acidification, membrane recombined with separated solids (mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

MGIEasy DNA Library Prep Kit (mgiEasy). MGIEasy DNA Library Prep Kit by MGI/BGI. A library prep kit designed for MGI sequencing platforms, offering flexibility in sample input. Status: active. First released: 3.0.0. Last updated: 3.0.0.

murine hepatitis virus (MHV) spike target (mhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mid-level severity (mid). A marker for med-level severity, where there are some concerns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Midnight and BC-CDC V1 Primer Set (midnightBCCDCv1). An amplicon strategy which is for SARS-CoV-2 and based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 1.0.0

which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V2 Primer Set (midnightBCCDCv2). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V3 Primer Set (midnightBCCDCv3). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 3.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V4 Primer Set (midnightBCCDCv4). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 4.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V1 Primer Set (midnightV1). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V2 Primer Set (midnightV2). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V3 Primer Set (midnightV3). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Miniasm (miniasm). A sequencing software that is a lightweight assembler for long reads, typically followed by polishing steps. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Minimap2 (minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MIT (mit). The licensing for the measure or data set is managed under the MIT license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

MIT No Attribution (mit0). The licensing for the measure or data set is managed under the MIT no attribution license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

MitoZ Deduplication (mitoZ). A deduplication method that is used primarily for mitochondrial genomes but can handle deduplication by read clustering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mixed/homogenized sample (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

MLST (Center for Genomic Epidemiology) (mlst). MLST (Center for Genomic Epidemiology). Focus: Classical MLST and optional serotype determination. Applications: Compatible with curated schemes for various pathogens. Features: Web-based and command-line versions available. Status: active. First released: 3.0.0. Last updated: 3.0.0.

monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) (monarchRNA). monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Moore swab passive sample (moorSw). Moore swab passive sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

1,000,000+ people (more1mil). More than 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Morning (morn). Sample was collected at some point in the morning, early in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mozilla Public License 2.0 (mpl20). The licensing for the measure or data set is managed under the Mozilla Public License 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Medium priority pathogen (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MrBayes Software (mrBayes). A lineage or clade analysis software tool for bayesian inference of phylogeny, used for inferring clade relationships with high accuracy. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ms2 coliphage spike target (ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Matrix spike duplicate (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Microsoft Public License (mspl). The licensing for the measure or data set is managed under the Microsoft Public License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Moore swab passive sample depreciated (mspsDep). Moore swab passive sample. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Major sewer pipeline (mSwrPpl). Major sewer pipeline Status: active. First released: 1.0.0. Last updated: 2.0.0.

murine coronavirus spike target (muCoMat). Murine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Multiple fraction (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Mulan Permissive Software License, Version 2 (mulanPSL20). The licensing for the measure or data set is managed under version 2 of the Mulan Permissive Software License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Multi-Community-level Surveillance (multiComLev). The scope of the surveillance covers multiple communities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Multiple Purpose (multiple). A measure or sample taken for multiple purposes, not easily captured by the other purpose categories. Status: active. First released: 2.0.0. Last updated: 2.0.0.

MultiQC (multiQC). A QC pipeline tool for sequencing data that aggregates QC results from multiple sources (e.g., FastQC, SAMtools) into a single report, useful in large pipelines. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Municipalities or communes (municipalLevel). Municipalities or communes Status: active. First released: 2.0.0. Last updated: 3.0.0.

Municipality (municp). A complete municipality, this specifies an entire metropolitan area, either a city, town, etc. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Municipality-level Aggregation at Site (muniLevel). Specifies that a sewershed/site represents an entire municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mykrobe (mykrobe). Mykrobe. Focus: Rapid detection of resistance, MLST, and serotyping. Applications: Mycobacterium tuberculosis and other pathogens. Features: Fast processing and species-specific database compatibility. Status: active. First released: 3.0.0. Last updated: 3.0.0.

No amplification control (nac). Denotes a no amplification control replicate sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NanoPlot (nanoPlot). A QC pipeline tool for sequencing data that does visualizations for quality assessment of long-read data, particularly from Oxford Nanopore. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NCBI Format (ncbiForm). Dataset was originally recorded and/or stored in NCBI format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NCBI's Pathogen Detection Isolates Browser (ncbiPDIB). Database that tracks AMR in pathogens and provides resistance profiles for pathogens worldwide. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ncov-tools (ncovtools). Tools and plots for perfoming QC on coronavirus sequencing results. Status: active. First released: 3.0.0. Last updated: 3.0.0.

University of Illinois/NCSA Open Source License (ncsa). The licensing for the measure or data set is managed under the University of Illinois/NCSA Open Source License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

National Database of Antibiotic Resistant Organisms (NDARO) (ndaro). A database maintained by the USCDC with genomic data on AMR organisms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NEBNext Ultra II DNA Library Prep Kit (nebnextUltraII). NEBNext Ultra II DNA Library Prep Kit by New England Biolabs. A high-efficiency library prep kit for low DNA input, ideal for whole-genome and target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V1a Long Primer Set (nebVarSkipV1aLong). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a long. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V1a short Primer Set (nebVarSkipV1aShort). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a short. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V2a Primer Set (nebVarSkipV2a). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2a. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V2b Primer Set (nebVarSkipV2b). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with

the attributes of version 2b. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Negative experimental control (negCon). A sample or experimental condition where the expected outcome should not occur, intended to check the original sample matrix for contamination, false positives, or unintended effects. An example would be testing for viral RNA or DNA in a sample known to be free of that virus. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Neighbourhood (neigh). A municipal neighbourhood, this specifies a sub-section of a larger municipality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Local administrative units or neighborhoods (neighborLevel). Local administrative units or neighborhoods Status: active. First released: 2.0.0. Last updated: 3.0.0.

Neighbourhood-level Aggregation at Site (neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a municipaility. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nextera XT DNA Library Preparation Kit (nexteraXT). Nextera XT DNA Library Preparation Kit by Illumina. A fast and efficient library prep kit for small genomes and amplicons, uses transposase-based fragmentation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nextstrain Software (nextstrain). A lineage or clade analysis software tool for real-time tracking of pathogen evolution, with tools for clade and lineage analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NGMLR (Next-Generation Mapping and Long-Read Alignment) (ngmlr). NGMLR (Next-Generation Mapping and Long-Read Alignment). A long-read specific mapper. Specialized for long-read platforms like PacBio and Nanopore. Best for: Structural variant analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Next-Generation Sequencing (NGS) platforms or intruments (ngsInst). Next generation sequencer instruments and platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Night (night). Sample was collected at night, between sunset and sunrise. Status: active. First released: 3.0.0. Last updated: 3.0.0.

No liquid concentration, liquid recombined with separated solids (noliquid). No liquid concentration, liquid recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

No sample storage medium used (none). No sample storage medium used Status: active. First released: 3.0.0. Last updated: 3.0.0.

No rain (noRain). Qualitative category for the weather measure, specifying no rainfall for a given day. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Purpose is normalization (norm). The purpose of a measure or sample is for normalization. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Normalization Calculation Type (normalization). A transformation of data to have a mean of zero and a standard deviation of one, commonly used to compare values across different datasets or units. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Norman Format (normanForm). Dataset was originally recorded and/or stored in Norman format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

No Seperation or Concentration (noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Novoalign (novoalign). Novoalign. A specialized read mapper. Commercial aligner known for high accuracy. Best for: Applications requiring

precise alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NovoPlasty (novoPlasty). A sequencing software that is an assembler tailored for organellar genomes (mitochondrial and chloroplast). Status: active. First released: 3.0.0. Last updated: 3.0.0.

MinusRT (nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Non-template control (ntc). Denotes a non-template control sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

No target present (ntp). Denotes a sample replicate/control with no target present. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nuclisens automated magnetic bead extraction kit (nucAuto). Nucleic acid extraction performed using the nuclisens automated magnetic bead extraction kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

nucleomag (ref. 744220.4) using kingfisher automated instrument (nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument Status: active. First released: 2.2.0. Last updated: 2.2.0.

Nuclisens manual magnetic bead extraction kit (nucManu). Nucleic acid extraction performed using the nuclisens manual magnetic bead extraction kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

US-CDC NWSS Format (nwssForm). Dataset was originally recorded and/or stored in the US-CDC's NWSS format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Water (nww). Non-wastewater, coming from any kind of water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

oc43 spike target (oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ocean, natural water body (ocean). Ocean, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Other Collection depreciated (oColDep). Other type of collection method. Add description to collectionOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Odour Control Unit (ocu). Odour Control Unit ventilation extends the life of a sewer by reducing the amount of maintenance the pipeline needs, making management of the network much more efficient. The filters used in the Odour Control Unit and ventilation stacks absorb gases such as hydrogen sulphide, which is a common source of odours from sewerage systems. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Office (office). A workplace where administrative, managerial, or clerical tasks are performed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SIL Open Font License 1.1 (ofl11). The licensing for the measure or data set is managed under the SIL Open Font License 1.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Lab Analysis (ola). Offline laboratory analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Onset date (onsDate). Earliest that symptoms were reported for this case. This data is often not known and reported. In lieu, episode is used. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Online Sensor (onse). Online sensor Status: active. First released: 1.0.0. Last updated: 2.0.0.

Open license not otherwise described (open). The licensing for the measure or data set is managed under an open license not otherwise described. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Optical calibrator sample (opt). Denotes a sample control or replicate used for optical calibration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surface water (opWa). An outdoor accumuation of water either on the surface of the earth, no other additional details specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Other residential building (orb). Individual residential buildings or institutions not captured in other categories Status: active. First released: 2.0.0. Last updated: 2.0.0.

OrthoFinder Software (orthoFinder). OrthoFinder - For orthogroup identification and phylogenetic tree building, often useful in evolutionary clade studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Open Science Foundation (OSF) (osf). Open Science Foundation project/data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Open Software License 3.0 (osl30). The licensing for the measure or data set is managed under the Open Software License 3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Other Collection depreciated (otco). Other type of collection method. Add description to collectionOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Other (other). Other Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

Other (or proprietary) Format (otherForm). Dataset was originally recorded and/or stored in a format not otherwise described. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Other Site - sample depreciated (otsisaDep). Other type of site. Add description to typeOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Other Site - Site depreciated (otsisiDep). Other site type. Add description to typeOther Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Outbreak declaration (outb). Public health action type used to indicate outbreak status. Given that when outbreaks occur, full data on case counts may not be available or completely accurate, using this measure indicates that case counts may be approximate. Status: active. First released: 2.0.0. Last updated: 3.0.0.

End of Outbreak (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Outbreak - on-going (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Declared outbreak or Outbreak start (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

polymerase activation (pAct). Describes the polymerase activation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Paired Layout (pairLay). Specifies the paired layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

Pangolin Software (pangolinSoft). A lineage or clade analysis software tool used for lineage assignment in SARS-CoV-2 and other viral genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Parapoxvirus Orf Virus Spike Target (parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Passive Sample - General (passiveGen). Used to specify a passive sampling method not otherwise specified was used to collect the sample. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Pathogenwatch (pathogenwatch). Pathogenwatch. Focus: Integrates MLST, serotyping, and resistance typing with a user-friendly interface. Applications: Primarily used for Salmonella and Escherichia coli. Features: Combines typing results with interactive visualization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PATRIC/RAST Database (patricRast). Database that hosts resistance gene annotations within their microbial genome data resources. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PBPfinder (pbfinder). PBPfinder. Used for typing and serotyping of Streptococcus pneumoniae through analysis of penicillin-binding proteins and capsular genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Phosphate Buffered Saline (PBS) (pbs). An isotonic solution for general sample preservation, used when immediate freezing is available. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Primary Clarifier Effluent depreciated (pceDep). Effluent obtained after primary clarifiers. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

PCR Sequencing Selection Method (pcrSeq). Specifies the PCR selection method for sequencing, ie. that a pre-determined primer was used. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Primary Clarifier Sludge depreciated (pcs). Sludge produced by primary clarifiers. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Primary clarifier effluent (pEfflu). Effluent obtained after primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Polyethyleneglycol (PEG) precipitation (peg). Peg precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

PEHaplo (pehaplo). A sequencing software that is an assembler that considers heterozygosity in diploid genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PGAP (Prokaryotic Genome Annotation Pipeline) (pgap). PGAP (Prokaryotic Genome Annotation Pipeline). Focus: Annotation pipeline that integrates MLST and antigen typing. Applications: Broad bacterial pathogens. Features: Provided by NCBI, designed for high-throughput workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHA4GE Format (pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public health advisory (phAdvise). A public health action type wherein a public health advisory is deseminated to the public. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Phandango (phandango). Phandango. A visualization tool that integrates serotype predictions with phylogenetic analyses for population studies. Often used alongside other serotyping tools. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Pharmaceutical manufacturing plant (pharmPl). An industrial building in which pharamceutical drugs are synthesised and processed on an industrial scale. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public health emergency (outbreak) (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Phenol chloroform (phenCl). Nucleic acid extraction performed using phenol chloroform. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PHES-ODM Version 1 Format (phesODMFormV1). Dataset was originally recorded and/or stored in PHES-ODM version 1 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHES-ODM Version 2 Format (phesODMFormV2). Dataset was originally recorded and/or stored in PHES-ODM version 2 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHES-ODM Version 3 Format (phesODMFormV3). Dataset was originally recorded and/or stored in PHES-ODM version 3 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

phi6 spike target (phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PhyloPhlAn Software (phyloPhIAn). A lineage or clade analysis software tool, specialized in high-resolution phylogenetic analysis, typically used for microbial clade analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PhyloSuite Software (phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PhyML Software (phyML). A lineage or clade analysis software tool that builds phylogenetic trees using maximum likelihood methods, with clade confidence assessments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Picard MarkDuplicates (picard). A deduplication method within the Picard suite that marks duplicate reads in BAM files based on mapped location. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PIQMIe (piqmie). A comprehensive QC and contamination assessment pipeline for metagenomic datasets and sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PiSeqQC (piSeqQC). A QC pipeline tool for sequencing data for microbiome and metagenomic sequencing data, including quality filtering and contaminant removal. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Primary key (pK). Primary key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Platanus (platanus). A sequencing software that is an assembler, optimized for large, diploid genome assemblies, particularly plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Plumbing drain (pluDra). An artificial channel which transports unwanted water or waste liquids away from their source, either to a more useful area, a receptacle, or into sewers or stormwater mains as waste discharge to be released or processed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PMMoV Standarized (pmmovStand). This data treatment standardizes the measurement value to concentration levels of pepper mild mottle virus (PMMoV). Status: active. First released: 3.0.0. Last updated: 3.0.0.

PMMV forward primer (ABI) (pmmvABIFor). PMMV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

PMMV probe (ABI) (pmmvABIProbe). PMMV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

PMMV reverse primer (ABI) (pmmvABIRev). PMMV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Post-Grit depreciated (pogr). Raw wastewater after a treatment plant's headworks. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Policy and political sector or organization (policy). Describes organizations whose core focus is on policy or political activity. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Time Proportional 24hr sample (tp24s). A time proportional 24-hour composite sample generally collected by an autosampler. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Porechop (porechop). A sequencing data processing application that is specifically designed for adapter trimming in Oxford Nanopore Technologies data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Port or Harbour (port). A harbor is any sheltered body of water where boats or ships may moor or anchor. A port is an installation that has been built around a harbor with facilities for loading and unloading such vessels. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Positive experimental control (posCon). A sample or experimental condition where the expected outcome is known to occur, intended to confirm that the experimental setup is working properly. An example would be a wastewater sample spiked with a known quantity of SARS-CoV-2 virus. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PostgreSQL License (postgreSQL). The licensing for the measure or data set is managed under the PostgreSQL License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Precipitation (from solution) (prec). The formation of a solid from a dissolved substance in a solution, typically induced by chemical reactions or changes in temperature/pH. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Predicted data (predicted). Predicted data, data generated by predictove models or algorithims, not taken directly from sample measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Predictive Modeling Calculation Type (predictiveModels). A statistical or machine learning approach used to estimate future values or outcomes based on historical data patterns. Status: active. First released: 3.0.0. Last updated: 3.0.0.

preQC (from Meraculous) (preQC). A QC pipeline tool for sequencing data that evaluates data quality before assembly, particularly for large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Primary clarifer (primClar). A large settling tank that removes solids and floating materials from wastewater before secondary treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PRINSEQ (prinseq). A QC pipeline tool for sequencing data for assessing and filtering sequences based on complexity, quality scores, and GC content. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Prinseq-lite (prinseqLite). A sequencing data processing application that filters sequences based on complexity and removes low-quality reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Private sector (priv). The category of organization type used for private sector or non-profit groups that are not otherwise captured by the academic category. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Private data - not for disemination (private). The measure or data set is private data - not for disemination. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Environmental survey or profiling (profil). Purpose of sampling/measure is to record characteristics and profile a given environment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Prokka (with serotyping integration) (prokka). Prokka (with serotyping integration) While primarily an annotation tool, Prokka outputs can be paired with databases for identifying serotypes of certain bacterial pathogens. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Prokka + Roary Pipeline (Nextflow) (prokkaRoary). Prokka + Roary Pipeline. Focus: Genome annotation (Prokka) with MLST and serotyping integration via Roary. Applications: Broad compatibility with bacterial pathogens. Features: Facilitates core-genome MLST and accessory gene analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

promega automated tna kit (promAuto). Nucleic acid extraction performed using the promega automated tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega wastewater large volume tna capture kit - depreciated (promegaLVTNA). promega wastewater large volume tna capture kit Status: depreciated. First released: 2.2.0. Last updated: 3.0.1.

promega ht tna kit (promHt). Nucleic acid extraction performed using the promega ht tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega manual tna kit (promManu). Nucleic acid extraction performed using the promega manual tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega wastewater large volume tna capture kit (promWW). Nucleic acid extraction performed using the promega wastewater large volume tna capture kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Provisional report (provisional). A provisional or interm report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Province-level Aggregation at Site (provLevel). Specifies that a sewershed/site represents a sub-national state, province, or region. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Primary clarifier sludge (pSludge). Sludge produced by primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Pumping station (pStat). Pumping station - these stations transport sewage or various types of water from one place to another, to facilitate its movement toward treatment plants. Sometimes also referred to as "lift stations". Status: active. First released: 1.0.0. Last updated: 2.0.0.

Post-grit (pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but priort to

a primary clarifier) Status: active. First released: 1.0.0. Last updated: 2.0.0.

Public Administration (pubAdm). An organisation type that describes governmental organizations that manage or administer programs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public Authority (pubAuth). An organization type describing a public agency with authority over a given domain. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public health agency (pubHealth). Public health agency. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PubMLST (pubMLST). PubMLST. Focus: Web-based platform for MLST and serotyping analyses. Applications: Neisseria, Campylobacter, Salmonella, and more. Features: Combines curated databases with user-uploaded sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Puro virus spike target (puroMat). Puro Virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Peptone Water with Glycerol (pwWg). A buffer solution/medium used in environmental sampling, especially for preserving microorganisms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

QC3 (qc3). A comprehensive QC pipeline for NGS sequencing data that provides summary statistics on sequence quality and contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

qiagen allprep dna/rna kit (qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen digital PCR (qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen ez1 virus mini kit v2.0 (qgEz1). Nucleic acid extraction performed using the qiagen ez1 virus mini kit v2.0. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep powerfecal dna/rna kit (qgPwrFecal). Nucleic acid extraction performed using the qiagen allprep powerfecal dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep powerviral dna/rna kit (qgPwrViral). Nucleic acid extraction performed using the qiagen allprep powerviral dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen powerwater kit (qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen qiaamp buffers with epoch columns (qgQiAmp). Nucleic acid extraction performed using the qiagen qiaamp buffers with epoch columns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen rneasy kit (qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen rneasy powermicrobiome kit (qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep dna/rna kit depreciated (qiAllprep). qiagen allprep dna/rna kit Status: depreciated. First released: 2.2.0. Last updated: 3.0.1.

qiagen qiaamp dsp viral rna mini kit (qiampDSP). qiagen qiaamp dsp viral rna mini kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

QIAseq FX DNA Library Kit (qiaSeqFX). QIAseq FX DNA Library Kit by Qiagen. Alibrary prep kit that uses enzymatic fragmentation, suitable for a variety of applications, including whole-genome sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Quantitative Real-Time PCR (qpcr). Real-time PCR, also called 'quantAggScale' PCR Status: active. First released: 2.0.0. Last updated: 2.0.0.

qPCR instruments (quantitative PCR) (qPCRinst). A quantitative PCR instrument, to detect and quantify specific DNA/RNA targets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

qProfiler2 (qProfiler2). A QC pipeline tool for sequencing data that produces reports with detailed QC metrics for aligned and unaligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Quality control (qualityControl). A measure or sample taken for the purpose of quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quarantine recommendation (quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Raindance digital PCR (rainDpcr). Describes a PCR analysis done using Raindance's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Rainy (rainy). Qualitative category for the weather measure, specifying a rainy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Random sampling surveillance program (randomSurv). A surveillance sampling strategy in which baseline is established at the beginning of a

study or project by the selection of sample units via random sampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Random sequencing selection method (ranSeq). Specifies the random selection method for sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raw data (raw). Raw data, without adjustment or additional treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Raw wastewater (raws). Raw wastes water sample Status: active. First released: 1.0.0. Last updated: 2.0.0.

Raw sewage at site (rawWW). Wastewater without any form of treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

Raw sewage downstream from a site (rawWWdown). Downstream from a site. See partType = rawWWup. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raw sewage upstream from a site (rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjuctiion with downstream sample. For example, if the site is a long-term care home, but ther is not access to the building or property cleanout. Use two sameple, one sample upstream and one sample downstream. Status: active. First released: 2.0.0. Last updated: 2.0.0.

RaxML Software (raxML). A lineage or clade analysis software tool, popular for rapid maximum likelihood-based phylogenetic tree building with clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Redundans (redundans). A sequencing software that is a genome assembler that reduces redundancy, useful for fragmented assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Refugee camp (refCamp). A temporary, often makeshift shelter for persons displaced by war, political oppression, or for religious beliefs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Regular Pathogen Surveillance (regular). A measure or sample taken for surveillance or epidemiology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Relationship Not Reported (relNR). A relationship ID used in relationship tables across the ODM when two entities are related or connected in some way, but the actual nature of that relationship is not clear or reported. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Representative grab sample (repGrab). A single large representative grab sample. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Resistant strain identified (rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Reservoir (res). An artificial body of water, often contained by a dam, constructed for the purpose of water storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Resuspend COSCa filter collection (resCosca). Nucleic acid extraction via resuspension of a sample collected using the COSCa ball method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Research sector or organization (research). Describes organizations whose focus is on research generation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Research purposes (researchPurp). Purpose of sampling/measure is for research. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ResFinder Database (resFinderDtbase). nomenclaturre from the National Center for Biotechnology Information Status: active. First released: 3.0.0. Last updated: 3.0.0.

ResFinder Tool (resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Restaurant (restaurant). A commercial establishment that prepares and serves food and beverages to customers. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Retention pond (retPond). Retention pond Status: active. First released: 1.0.0. Last updated: 2.0.0.

Review of records (rev). A review of records for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

River, natural water body (river). River, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

RNA Template (rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

rRNA Depletion Method (rnaDepl). Removal of background RNA for the purposes of enriching the genomic target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

RNAlater (rnaLater). A buffer solution/medium the stabilizes RNA and DNA in samples, effective for preserving nucleic acids in wastewater. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Road (road). A paved or unpaved pathway designed for vehicular and pedestrian travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Roadside (roadside). The area adjacent to a road, including sidewalks, shoulders, or drainage ditches. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Routine surveillance (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Raw post-pasteurized wastewater (rppw). Raw wastewater sample post-pasteurization Status: active. First released: 1.0.0. Last updated: 2.0.0.

reverse transcription (rt). Describes the reverse transcription cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

RT-qPCR intruments (rtqPCRinst). Real-time quantitative PCR instruments, used when detecting RNA viruses (an additional a reverse transcription step). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Rural (rural). Rural populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

SalmonellaTypeFinder (salTypeFin). SalmonellaTypeFinder A specialized tool for predicting Salmonella serotypes based on genomic data, similar to SeqSero. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sample concentrate (samConc). Sample concentrate. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sampling Event (sampleEvent). In settings where a person goes out and collects multiple samples, but more accurate location data is not recorded, this is used to group samples from that outing, or 'sampling event'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SAMtools rmdup (samRmdup). A deduplication method that identifies and removes PCR duplicates based on alignment data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SAMtools (samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Secondary clarifier effluent depreciated (sce). Effluent obtained after secondary clarifiers. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

School (school). A school serving students in the kindergarten to 12th grade range Status: active. First released: 1.0.0. Last updated: 2.0.0.

School closure (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

sciencell viral rna isolation kit (sciencellRNA). sciencell viral rna isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

Secondary clarifier sludge depreciated (scsDep). Sludge produced by secondary clarifiers. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Sludge dryer (sDryer). A facility or equipment used to reduce moisture content in wastewater sludge for easier handling and disposal. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sterile Distilled Water with Sodium Thiosulfate (sDWwST). Sterile Distilled Water with Sodium Thiosulfate - Used to neutralize chlorine for microbiological analysis in wastewater samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sea, natural water body (sea). Sea, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Secondary clarifer (secClar). A tank in wastewater treatment that removes biological solids (e.g., microbial flocs) after aeration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

See unit (value) (seeUnitVal). A value for maximum or minimum value in the dictionary, use when the maximum or minimum value is determined by the unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Secondary clarifier effluent (sEfflu). Effluent obtained after secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Semi-solid (semSol). A state of matter consisting of molecules in a non-rigid structure that can retain its shape and volume but that is not resistant to such change. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Septic tank wastewater (septage). Wastewater from within a septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

Septic tank (septTnk). Septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

SeqKit rmdup (seqKitRmdup). A deduplication method that works within SeqKit for duplicate removal in FASTA/FASTQ files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqKit stats (seqKitStats). Part of SeqKit, a QC pipeline tool for sequencing data that providing a summary of sequence metrics like length, GC content, and quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqMan Pro (Lasergene) (seqManPro). Sequencing software that is for de novo sequence assembly and consensus calling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqSero2 (seqSero2). SeqSero2. Specifically designed for Salmonella serotyping using raw sequence reads, assemblies, or even complete genomes. Provides results based on antigenic formulas or serotype names. Status: active. First released: 3.0.0. Last updated: 3.0.0.

seqtk (seqtk). A lightweight sequencing data toolkit for FASTQ and FASTA manipulation, including trimming and subsampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqTyping (seqTyping). SeqTyping. Focus: Simultaneous MLST and serotyping for Escherichia coli and Salmonella. Applications: Integrated with bacterial genome typing databases. Features: Compatible with short-read sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

serial dillution (serDil). Describes a serial dilution process for standard curve generation for PCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Serial dilution (serialDilution). The serial dilution method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

SerotypeFinder (serotypeFin). SerotypeFinder. A web-based tool that predicts serotypes for Escherichia coli and other bacteria by detecting genes encoding O-antigens and H-antigens. Developed by the Center for Genomic Epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sewer Sediments Depreciated (seseDep). Sediments obtained in sewer. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Shasta (shasta). A sequencing software that is a fast assembler optimized for nanopore long-read data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ship (ship). A cruise ship or other ship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ShortBRED Software (shortBRED). Software tool that screens for known AMR genes in shotgun metagenomic sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sickle (sickle). A sequencing data processing application that is a quality-based trimming tool for Illumina data with single-end and paired-end support. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Single Layout (sinLay). Specifies the single layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

Singleplex, probe-based, one-step RT-qPCR (sinProbeOne). Describes a PCR method that is singleplex, probe-based, and one-step RT-qPCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Salmonella In Silico Typing Resource (SISTR) (sistr). Salmonella In Silico Typing Resource (SISTR). Used for in silico serotyping of Salmonella enterica based on whole-genome sequencing. Combines genomic data with the traditional White-Kauffmann-Le Minor serotyping scheme. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Skewer (skewer). A sequencing data processing application that is a fast tool for adapter trimming and quality trimming in Illumina data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Skimmed milk flocculation (skimMilkFloc). Skimmed milk flocculation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Slow-flowing (slFlow). A quality of a body of water wherein there is a slow flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater Sludge - non-specified (sludgeNS). Sample material is wastewater sludge - whether primary, secondary or other is unspecified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Slurry (slur). An quality in which the fluid like material is more viscous due to the suspension of insoluble solid particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SMALT (smalt). SMALT. A highly parallelized mapper. High-speed aligner for genomic DNA reads. Best for: Applications requiring flexibility

with non-standard parameters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SMARTer ThruPLEX Plasma-seq Kit (smarterThruPLEX). SMARTer ThruPLEX Plasma-seq Kit by Takara Bio. A library prep kit optimized for low-input DNA, including cell-free DNA for liquid biopsy studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Skim Milk–Glycerol Medium (smgm). A buffer solution/medium that protects bacteria in environmental samples, preventing freeze-thaw damage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Smoothing Calculation Type (smoothing). A technique used to reduce short-term fluctuations in data to better reveal underlying trends or patterns, such as using moving averages or splines. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Snap (snap). Snap. A highly parallelized mapper. Ultrafast, designed for genomic and RNA-seq applications. Best for: Large-scale sequencing projects. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SNAPP Software (snapp). A lineage or clade analysis software tool in BEAST for species delimitation and clade analysis in population genomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Snowy (snowy). Qualitative category for the weather measure, specifying a snowy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Soap2 (soap2). Soap2. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Soap3 (soap3). Soap3. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SOAPdenovo (soapDenovo). A sequencing software that is an assembler for short-read data, suited to large and complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Social distancing measures (socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Solid fraction (general) (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Solid Fraction (Dry) (solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Solids/Pellet retained (solid). The solids or pellet is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Solid (solidMat). The state in which a substance has no tendency to flow under moderate stress; resists forces (such as compression) that tend to deform it; and retains a definite size and shape. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Solid fraction (Wet) (solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. Status: active. First released: 2.3.0. Last updated: 2.3.0.

SortMeRNA (sortMeRNA). A sequencing data processing application that is used for ribosomal RNA filtering in metatranscriptomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SPAdes (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Specifies (specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Spectrophotometers or fluorometers (spectroFluoro). Spetrometer and fluorometer instruments; may be used to assess concentration and purity (e.g., NanoDrop™, Qubit™). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sucrose Phosphate Glutamate (SPG) Buffer (spg). A buffer solution/medium that stabilizes viruses, including in wastewater samples, by preventing RNA degradation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Spike matrix and recovery (spike). The spike matrix and recovery method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Spring (spr). A surface landform which provides an egress for groundwater or steam to flow out of the ground. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequence Read Archive (SRA) (sra). Sequence Read Archive (SRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

SRST2 Software (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SSAKE (ssake). A sequencing software that is a simple de novo assembler for highly overlapping short reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Streptococcus Serotyping Tool (SSI) (SSI). Streptococcus Serotyping Tool (SSI) A web-based platform for serotyping Streptococcus pneumoniae based on capsular polysaccharide synthesis loci. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Secondary clarifier sludge (sSludge). Sludge produced by secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Social services shelter (sss). Other type of social services shelter Status: active. First released: 2.0.0. Last updated: 2.0.0.

Stabilization pond (stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment to reduce the organic content and remove pathogens from wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Stagnant (stag). A quality of a body of water wherein it has no current or flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Statistical Analysis of Metagenomic Profiles (STAMP) Software (stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Standardization Calculation Type (standardization). A method used to scale data to a common range or distribution, often to enable fair comparisons across different variables, time periods, or locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

STAR (Spliced Transcripts Alignment to a Reference) (star). STAR (Spliced Transcripts Alignment to a Reference). A general-purpose read mapper. Fast aligner designed for RNA-seq, supports spliced alignment. Best for: Transcriptome data analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

StarAMR Software (starAMR). Software tool that is used to detect AMR genes in genome assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Departments, states, or provinces (stateProvLevel). Departments, states, or provinces Status: active. First released: 2.0.0. Last updated: 3.0.0.

Standard sample (std). Denotes a standard sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Stormy Weather (stormy). Stormy weather Status: active. First released: 3.0.0. Last updated: 3.0.0.

Stream (str). A watercourse which is linear and flows across the solid portion of a planetary surface. Status: active. First released: 3.0.0. Last updated: 3.0.0.

StrainPhlAn Software (strainPhlAb). A lineage or clade analysis software tool within MetaPhlAn for strain-level lineage analysis from metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sodium Thiosulfate Solution (sts). A buffer solution/medium that neutralizes residual chlorine in wastewater samples, ensuring microbial viability. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Subread (subread). Subread. A general-purpose read mapper. Includes the subread-align algorithm for mapping DNA and RNA reads. Best for: High-throughput data with a balance of speed and accuracy. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Subsample (General) (subSamp). A general replicate type for a subsample not otherwise defined. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Suburban (suburban). Suburban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sunny (sunny). Qualitative category for the weather measure, specifying a clear and sunny day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

SureSelect XT HS2 DNA Library Preparation Kit (sureSelectXThs2). SureSelect XT HS2 DNA Library Preparation Kit by Agilent. A high-sensitivity library prep kit with target capture capabilities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Other surface (surface). Surface other than floor or desk. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface swab (surfSw). Surface swab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surveillance alert (survAlert). A public health action type wherein authorities have made a decision about surveillance and communicated the alert. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sewage truck (swgTrck). Sewage truck Status: active. First released: 1.0.0. Last updated: 2.0.0.

Swift 2S Turbo DNA Library Kit (swift2STurbo). Swift 2S Turbo DNA Library Kit by Swift Biosciences. A fast library prep kit workflow with robust performance for low-input DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sewer sediment (swrSed). Sediments obtained in sewer Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sewer catchment area (swrSet). Sewer catchment area. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Synthetic sample (synthetic). A synthetic or artificially generated sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Targeted surveillance program (targetSurv). A surveillance sampling strategy in which an aspired outcome is explicitly stated. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Targetted surveillance initiated (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Taxonium Software (taxonium). Taxonium - A scalable tool for viewing and analyzing large phylogenetic trees, including clade annotations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Technical replicate (techRep). A sample that comes from the same biological or environmental source (e.g., the same extracted DNA, the same RNA aliquot, or the same water sample). Helps detect inconsistencies due to pipetting errors, instrument fluctuations, or reagent inconsistencies, rather than biological variation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Airport terminal (terminal). Airport terminal sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

Test date (tesDate). Date that the covid-19 test was performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Protocol testing (testing). A measure or sample taken to test a new method. These measures are typically used for internal lab uses and not reported to external partners. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Thermal cyclers (thermCyc). A thermal cycler instrument, used to perform temperature-controlled reactions for PCR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

thermo magmax microbiome ultra nucleic acid isolation kit (thermMag). Nucleic acid extraction performed using the thermo magmax microbiome ultra nucleic acid isolation kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

thermo magmax viral/pathogen nucleic acid isolation kit (thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

Threat designation (threatDes). A public health action type wherein a threat level is determined and communicated by authorities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ThruPLEX DNA-seq Kit (thruPLEX). ThruPLEX DNA-seq Kit by Takara Bio. A low-input library prep kit with fast, three-step protocol. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Transport hub - General (tHub). A tansport hub not otherwise specified. i.e. a place where passengers and cargo are exchanged between vehicles or/and between transport modes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Time proportional sample (timePr). A time proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Time standardized (timeStand). This data treatment standardizes the measurement value against time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TopHat (tophat). TopHat. A general-purpose read mapper. An older RNA-seq aligner, splicing-aware. Replaced by HISAT2 in most workflows. Best for: Historical RNA-seq studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Traditional Serotyping methods (tradSero). Traditional Serotyping methods used for serotyping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Train (train). A series of railroad cars moved as a unit by a locomotive or by integral motors. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Transportation vehicle - general (transp). A vehicle, i.e. a mobile machine, transporting people or cargo, of a type not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Passive (trap) sampling (trap). A composite sampler that passively collects a sample without use of electricity or a battery. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel ban (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel hub surveillance - general (travelSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel warning (travWa). A notice advising against travel to certain areas due to health risks. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Treated (treat). A quality which denotes an altered state of an item resulting from purposeful interventions or processes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TreeTime Software (treeTime). A lineage or clade analysis software tool for phylodynamic analysis, often for molecular clock dating and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TrimGalore! (trimGalore). A QC pipeline tool for sequencing data that integrates Cutadapt and FastQC to assess sequence quality and remove adapters in one step. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Trimmomatic (trimmomatic). A sequencing data processing application that trims adapters and low-quality bases from Illumina sequencing reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Trinity (trinity). A sequencing software that is an assembler designed specifically for RNA-seq data, creating transcriptome assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TE Buffer (Tris-EDTA) (trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater Triturator (triturator). The location where wastewater transportation vehicles unload wastewater. Status: active. First released: 2.2.3. Last updated: 2.2.3.

trizol, zymo mag beads w/ zymo clean and concentrator (trizol). Nucleic acid extraction performed using the trizol, zymo mag beads w/ zymo clean and concentrator method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

trizol, garnet bead beating, alcohol precipitation (trizolEtOH). trizol, garnet bead beating, alcohol precipitation Status: active. First released: 2.2.0. Last updated: 2.2.0.

trizol and RNA purification kit (trizolRNA). trizol and RNA purification kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

Train Station (trStat). A place on a railroad line where trains regularly stop so that passengers can get on or off. Status: active. First released: 2.2.3. Last updated: 2.2.3.

TruSeq DNA PCR-Free Library Prep Kit (truSeqDNA). TruSeq DNA PCR-Free Library Prep Kit by Illumina. A high-quality library prep kit without PCR amplification, reducing bias. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Tryptic Soy Broth (TSB) (tsb). Tryptic Soy Broth (TSB) - A nutrient-rich medium for bacterial survival, sometimes used for short-term storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

University campus (uCampus). Universityor college campus - comprising an entire campus or part of a campus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Ugene (uGene). Sequencing software that offers alignment and consensus sequence generation features. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ultracentrifuges (ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

UMI-tools (umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Unicycler (unicycler). A sequencing software that is a hybrid assembler for bacterial genomes, combining short and long reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Unique sample (unique). A unique sample, not duplicated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unknown sample (unkn). Denotes an unknown sample replicate type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

The Unlicense (unlicense). The licensing for the measure or data set is managed under The Unlicense. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Ultracentrifugation (untracent). Ultracentrifugation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Untreated (untreat). A quality which denotes an absence of purposeful intervention or processes on an item. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Upstream sites (upstream). A general site type for upstream wastewater sampling sites. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Urban (urban). Urban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ultrafast Sample placement on Existing tRees (UShER) Software (usher). A lineage or clade analysis software tool that adds new genomes to an existing phylogenetic tree, widely used for SARS-CoV-2 clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Utilities sector or organization (utilities). Describes organization that manage or provide utilities services, whether water, gas, heat, etc. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Universal Transport Medium (UTM) (utm). Universal Transport Medium (UTM) - Used for microbial preservation in various environmental samples, including wastewater. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Vacuum sludge sampling (vac). Intrument type is a grab sampler that takes a sample at a designated depth with minimal disturbance to surrounding layers. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Validation study (validationStudy). A meaure or sample taken for a validation study. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Change to Vaccine Schedule (vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Velvet (velvet). A sequencing software that is a de novo assembler optimized for short-read data, often used in microbial genomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Vertical grab sampling (vertGrb). Intrument type is a grab sampler in which the container for the sample is mounted on the end of a rod, which is suitable for collecting waste from a tank. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Viral passage experiment (viralPass). A research sampling strategy in which samples are selected in order to perform a viral passage experiment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Variant of concern (voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for

assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Variant of interest (voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Volume proportional sample (volPr). A volume proportional sample generally collected by an autosampler. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Vesicular stomatitis virus (VSV) target (vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

VSV forward primer (ABI) (vsvABIFor). VSV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

VSV probe (ABI) (vsvABIProbe). VSV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

VSV reverse primer (ABI) (vsvABIRev). VSV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Viral Transport Medium (VTM) (vtm). A buffer solution/medium the preserves viral samples during transport, commonly used for wastewater viral studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

variant under monitoring (vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

water concentrating buffer (R2042-1) (watConcBuff). water concentrating buffer (R2042-1) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Water depreciated (water). Non-wastewater, coming from any kind of water body. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

Water-based Transit Hub (waterTH). A transport hub is a place where passengers and cargo are exchanged between water-based vehicles and/or between water-based transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Well (well). A cylindrical hole, pit, or tunnel drilled or dug down to a depth from which water, oil, or gas can be pumped or brought to the surface. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Whole genome sequencing (wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unique Molecular Identifier (UMI) Tagging (umiTag). A deduplication method that adds unique tags to individual DNA fragments, allowing identification and removal of duplicate reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Whole Metagenome Sequencing (wms). A DNA sequencing assay that intends to provide information on the DNA sequences of multiple genomes (a metagenome) from different organisms present in the same input sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

wSphere Format (wSphereForm). Dataset was originally recorded and/or stored in wSphere format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater Treatment Agency (wta). An organization type that includes those organizations who manage wastewater treatment programs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

WTDBG (aka wtdbg2) (wtdbg2). A sequencing software that is an assembler for long-read data that generates contigs rapidly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Do What The F*ck You Want To Public License (wtfpl). The licensing for the measure or data set is managed under the Do What The F*ck You Want To Public License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Wastewater Treatment Plant Operator (wtpo). An organization type that includes those organizations who run and operate wastewater treatment facilities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Whole Virome Sequencing (wvs). A whole metagenome sequencing assay that intends to provide information on multiple genome sequences from different viruses present in the same input sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater aerobic digestion (wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater anaerobic digestion (wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

wastewater comminution process (wwCominuated). wastewater comminution process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge removal (wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge dewatering (wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge drying (wwDry). Wastewater sludge drying occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater filtration (wwFilt). Wastewater filtration occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater grit removal (wwGrit). Wastewater grit removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater microbial treatment (wwMic). Wastewater microbial treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewtaer primary sedimentation (wwPriSed). Wastewtaer primary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater screening process (wwScreen). Wastewater screening process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater secondary sedimentation (wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater treatment plant (wwtp). A general site type for wastewater treatment plants. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Wastewater treatment efficiency assessment (wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Back-up wastewater treatment site (wwtpBack). Indicates a wastewater treatment plant where multiple labs are or were sampling, and where secondary samples are being taken taken. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Industrial wastewater treatment plant (wwtpInd). Industrial wastewater treatment plant Status: active. First released: 1.0.0. Last updated: 2.0.0.

Municipal wastewater treatment plant for combined sewage (wwtpMuC). Municipal wastewater treatment plant for combined sewage Status: active. First released: 1.0.0. Last updated: 2.0.0.

Municipal wastewater treatment plant for sanitary sewage only (wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater treatment (wwTrt). Wastewater treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Zenodo (zenodo). Zenodo open data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

zLib License (zlib). The licensing for the measure or data set is managed under the zLib License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

zymo quick-rna viral kit #r1035 (zymo1035). zymo quick-rna viral kit #r1035 Status: active. First released: 2.2.0. Last updated: 2.2.0.

zymo quick-rna viral 96 kit #r1041 (zymo1041). zymo quick-rna viral 96 kit #r1041 Status: active. First released: 2.2.0. Last updated: 2.2.0.

zymo environ water rna kit (cat. r2042) (zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit (cat. r2042). Status: active. First released: 2.0.0. Last updated: 2.0.0.

zymo quick-rna fungal/bacterial miniprep #r2014 (zymoQuick). Nucleic acid extraction performed using the zymo quick-rna fungal/bacterial miniprep #r2014 kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

zymo environ water rna kit (cat. r2042) - depreciated (zymoWatRNA). zymo environ water rna kit (cat. r2042) Status: depreciated. First released: 2.2.0. Last updated: 3.0.1.

FALSE (FALSE). Boolean data type = FALSE Status: active. First released: 1.0.0. Last updated: 2.3.0.

TRUE (TRUE). Boolean data type = TRUE Status: active. First released: 1.0.0. Last updated: 2.3.0.

Overlapping relationship (overlap). Locations/polygon have overlapping portions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Neighbouring relationship (neighbour). Locations/polygon are neighbouring eachother. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Region (region). Specifies a region that combines multiple urban areas, and/or large rural areas. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Hotel or motel (hotel). A building which 1) contains multiple dwellings of pre-furnished accomodation and 2) is rented for lodging on a short term and/or longer-term basis. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Calibration purpose (cali). Purpose of calibrating a machine, method, or other. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Lineage- or Clade-analysis Software Set

(cladeAnSet). Valid category set for lineage or clade analysis software types.

Pangolin Software (pangolinSoft). A lineage or clade analysis software tool used for lineage assignment in SARS-CoV-2 and other viral genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nextstrain Software (nextstrain). A lineage or clade analysis software tool for real-time tracking of pathogen evolution, with tools for clade and lineage analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

IQ-TREE Software (iqTree). A lineage or clade analysis software tool for constructing phylogenetic trees with clade support. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bayesian Evolutionary Analysis by Sampling Trees (BEAST) Software (beast). A lineage or clade analysis software tool for estimating evolutionary relationships and divergence times in a Bayesian framework. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PhyloSuite Software (phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

RaxML Software (raxML). A lineage or clade analysis software tool, popular for rapid maximum likelihood-based phylogenetic tree building with clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PhyML Software (phyML). A lineage or clade analysis software tool that builds phylogenetic trees using maximum likelihood methods, with clade confidence assessments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Statistical Analysis of Metagenomic Profiles (STAMP) Software (stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ClonalFrameML Software (clonalFrameML). A lineage or clade analysis software tool for reconstructing phylogenetic relationships considering recombination, used in bacterial lineage analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TreeTime Software (treeTime). A lineage or clade analysis software tool for phylodynamic analysis, often for molecular clock dating and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SNAPP Software (snapp). A lineage or clade analysis software tool in BEAST for species delimitation and clade analysis in population genomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

mash Software (mash). A lineage or clade analysis software tool for the clustering-based method of lineage and clade analysis, comparing large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

StrainPhlAn Software (strainPhIAb). A lineage or clade analysis software tool within MetaPhlAn for strain-level lineage analysis from metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ultrafast Sample placement on Existing tRees (UShER) Software (usher). A lineage or clade analysis software tool that adds new genomes to an existing phylogenetic tree, widely used for SARS-CoV-2 clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MrBayes Software (mrBayes). A lineage or clade analysis software tool for bayesian inference of phylogeny, used for inferring clade relationships with high accuracy. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PhyloPhlAn Software (phyloPhIAn). A lineage or clade analysis software tool, specialized in high-resolution phylogenetic analysis, typically used for microbial clade analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

OrthoFinder Software (orthoFinder). OrthoFinder - For orthogroup identification and phylogenetic tree building, often useful in evolutionary clade studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Taxonium Software (taxonium). Taxonium - A scalable tool for viewing and analyzing large phylogenetic trees, including clade annotations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

LINEAGE Software (lineage). LINEAGE - Tool for bacterial lineage analysis, often applied to genome sequences in epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Classes

(classes). A class is a collection of one or more related measures or methods within a group. A group can have one more more classes to describe different parts or the class.

Alleles class (allele). Measures and methods related to alleles. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Bacteria and Fungus Class (bactFung). Measures and methods relating to bacteria. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Capacity class (capacity). Measures and methods relating to capacity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Conductivity class (conductivity). Measures and methods related to conductivity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Database and Data Repository Class (database). Measures and methods related to databases and data repositories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dilution Class (dilution). Measures and methods relating to dilutions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Diseases (human) class (disease). Measure and methods related to disease or infection in humans. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Flow class (flowClass). Measures and methods related to flow. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Gas class (gas). Measures and methods relating to gas and gases. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Humidity class (humid). Measures and methods related to humidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dictionary tables (lookup). Tables to describe and support the ODM dictionary. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Mutations class (mutation). Measures and methods related to mutations. Status: depreciated. First released: 2.0.0. Last updated: 2.3.0.

Mutation panels class (mutationPanel). Measures and methods related to a panel or list of more than one mutation from the same sequence read. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Class not applicable (naClass). Class is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organism (organism). Organism class Status: active. First released: 2.2.0. Last updated: 2.2.0.

Outbreak class (outbreak). Measures and methods relating to public health outbreaks. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

qPCR Class (pcr). Measures and methods relating to qPCR. Status: active. First released: 2.0.0. Last updated: 2.0.0.

pH class (pHClass). Measures and methods relating to pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Physical class (physical). Measures and methods related to generic physical properties. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population Class (popClass). Measures and methods relating to population (ie. Measures of population, location). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Precipitation class (precipitation). Measures and methods related to precipitation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Program decription tables (programDescr). Tables used to describe surveillance and testing programs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Proteins class (protein). Measures and methods related to proteins. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Results tables (results). Tables used to record samples, measures and quality reports. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Genetic sequences class (sequence). Measures and methods related to genetic sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Software Class (software). Measures and methods related to software. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Speed class (speed). Measures and methods relating to speed. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard concentrations class (standardConc). Measures and methods relating to standard conentrations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard curve class (standardCurve). Measures and methods relating to generating or recording a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Temperature class (temperature). Measures and methods related to temperatures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Time class (timeClass). Measures and methods relating to time. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Turburdity class (turbidity). Measures and methods relating to water and wastewater turbidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Variants class (variant). Measures and methods relating to variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Weather class (weather). Measures and methods relating to weather. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Collection Approximate Time Period Set

(collAppxSet). The category set of valid inputs for the collGenT attribute field.

Morning (morn). Sample was collected at some point in the morning, early in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Afternoon (aft). Sample was collected in the afternoon, sometime after lunch. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Evening (eve). Sample was collected in the evening, late in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Night (night). Sample was collected at night, between sunset and sunrise. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sample collection set

(collectSet). Methods for collection samples. Sample collection methods include water, air, and surface. See the attribute `Compartment set` of the sample collection method.

Area proportional sample (areaPr). An area proportional sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

COSCa ball (cosca). COSCa passive sampling device. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Flow proportional sample (flowPr). A flow proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Grab sample (grb). A single large representative grab sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Moore swab passive sample (moorSw). Moore swab passive sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Surface swab (surfSw). Surface swab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Time proportional sample (timePr). A time proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Volume proportional sample (volPr). A volume proportional sample generally collected by an autosampler. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Composite sample - archival (comp). A composite sample, usually generated by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Manual Composite Sample (manComp). Specifies a composite sample where the sub-samples were collected manually. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Passive Sample - General (passiveGen). Used to specify a passive sampling method not otherwise specified was used to collect the sample. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Core sampling (core). Intrument type is a grab sampler that captures a vertical section of the substrate matrix of fecal sludge. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Vacuum sludge sampling (vac). Intrument type is a grab sampler that takes a sample at a designated depth with minimal disturbance to surrounding layers. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cone-shaped sampling (cone). Intrument type is a grab sample that has a controlled valve that opens to take a sample from a specific depth, then closes to bring the sample out. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Horizontal grab sampling (horGrb). Intrument type is a grab sampler in which the container for the sample is mounted on the end of a rod, which is suitable for collecting discharge from a pipe or truck. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Vertical grab sampling (vertGrb). Intrument type is a grab sampler in which the container for the sample is mounted on the end of a rod, which is suitable for collecting waste from a tank. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Passive (trap) sampling (trap). A composite sampler that passively collects a sample without use of electricity or a battery. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Automatic composite sampling (autoComp). A composite sampler which is automated to collect and store multiple wastewater samples across multiple time points. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Automatic sequential sampling (autoSeq). A composite sampler which is automated to collect and combine multiple samples of equal volume taken at a set time interval. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bag Mediated Filtration (bagFilt). Sample was collected using bag-mediated filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Compartments

(compartments). The substance from which a sample was taken. For example, wastewater has component of "water". Compartments are attributes of measures, methods, units, and aggregations.

Air compartment (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Compartment (hCo). A indicator for wide-names that the compartment information is stored in a separate column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human compartment (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment not applicable (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Water compartment (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Compartment sets

(compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured in people (humans), water, surface, or air.

Air compartment set

(airCompartmentSet)A compartment set for measures and methods in the air compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Air compartment (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Air and surface compartment set

(airSurfaceCompartmentSet)A compartment set for measures and methods in the air or surface compartments. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Air compartment (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Air and water compartment set

(airWaterCompartmentSet)A compartment set for measures and methods in the air or water compartments. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Air compartment (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Any compartment set

(anyCompartmentSet)A compartment set for measures and methods in any compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Air compartment (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Human compartment (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Water compartment (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Human compartment set

(humanCompartmentSet)A compartment set for measures and methods in the human compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Human compartment (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment set not applicable

(naCompartmentSet)Compartment not applicable. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Compartment not applicable (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment set

(surfaceCompartmentSet)A compartment set for measures and methods in the surface compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Surface compartment (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface and water compartment set

(surfaceWaterCompartmentSet)A compartment set for measures and methods in the surface or water compartments. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Surface compartment (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Water compartment (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Water compartment set

(waterCompartmentSet)A compartment set for measures and methods in the water compartment. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

Water compartment (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Compartment set for wide names

(wideCompartmentSet)Compartment set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 3.0.0.

Air compartment (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Compartment (hCo). A indicator for wide-names that the compartment information is stored in a separate column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Compartment not applicable (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Water compartment (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Compartment sets

(compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured in people (humans), water, surface, or air.

Air compartment set (airCompartmentSet). A compartment set for measures and methods in the air compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Air and surface compartment set (airSurfaceCompartmentSet). A compartment set for measures and methods in the air or surface compartments. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Air and water compartment set (airWaterCompartmentSet). A compartment set for measures and methods in the air or water compartments. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Any compartment set (anyCompartmentSet). A compartment set for measures and methods in any compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Human compartment set (humanCompartmentSet). A compartment set for measures and methods in the human compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment set not applicable (naCompartmentSet). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface compartment set (surfaceCompartmentSet). A compartment set for measures and methods in the surface compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Surface and water compartment set (surfaceWaterCompartmentSet). A compartment set for measures and methods in the surface or water compartments. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Water compartment set (waterCompartmentSet). A compartment set for measures and methods in the water compartment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Compartment set for wide names (wideCompartmentSet). Compartment set for wide names. Status: active. First released: 2.2.0. Last updated: 3.0.0.

Consensus Sequence Software Set

(conSeqSoftSet). The valid set of consensus sequencing software categories.

Geneious (geneious). Sequencing software that is popular for sequence assembly, alignment, and consensus sequence generation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MAFFT (mafft). Sequencing software that performs multiple sequence alignment, commonly used in consensus sequence generation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Clustal Omega (clustalO). Sequencing software that is widely used for multiple sequence alignment and producing consensus sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Molecular Evolutionary Genetics Analysis (MEGA) (mega). Sequencing software that provides tools for sequence alignment and consensus sequence extraction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SAMtools (samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BioEdit (bioEdit). Sequencing software that offers sequence alignment and visualization, used to manually generate consensus sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bcftools (bcfTools). Sequencing software that works with SAMtools to call variants and produce consensus sequences from alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Emboss Cons (embossCons). Sequencing software that is part of the EMBOSS suite, generates consensus sequences from multiple alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AliView (aliView). Sequencing software that is a user-friendly alignment editor with consensus sequence options. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqMan Pro (Lasergene) (seqManPro). Sequencing software that is for de novo sequence assembly and consensus calling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ugene (uGene). Sequencing software that offers alignment and consensus sequence generation features. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SPAdes (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA (Burrows-Wheeler Aligner) (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Control Measure Implementation Value Set

(contMeasImpSet). A set of valid categories for the public health action field, where the action type is 'control measure implementation'.

Stay-at-home order (homeOrder). A directive requiring people to remain at home except for essential activities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Border closure (borderClos). A measure shutting entry points to limit cross-border movement and disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

School closure (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lockdown (lockdown). Broad restrictions on movement and activities within a region to control disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mask mandate (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Social distancing measures (socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data Repository Set

(dataRepoSet). The mma set for all valid input categories for the dataRepo field.

International Nucleotide Sequence Database Collaboration (INSDC) Archives (insdc). International Nucleotide Sequence Database Collaboration (INSDC) Archives - often includes ENA, NCBI, or DDBJ inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GenBank Archives (genBank). GenBank Archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequence Read Archive (SRA) (sra). Sequence Read Archive (SRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Global Initiative on Sharing All Influenza Data (GISAID) archives (gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

European Nucleotide Archive (ENA) (ena). European Nucleotide Archive (ENA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

DDBJ sequence Read Archive (DRA) (dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Genome Sequence Archive (GSA) (gsa). Genome Sequence Archive (GSA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Enterobase archives (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GitHub (github). GitHub external data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Open Science Foundation (OSF) (osf). Open Science Foundation project/data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Internal reference (internalRef). Reference an internal (i.e. private) database within the user's own organization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DNA Data Bank of Japan (DDBJ) (ddbj). DNA Data Bank of Japan (DDBJ) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Zenodo (zenodo). Zenodo open data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Comprehensive Antibiotic Resistance Database (CARD) (cardDtbase). Database that provides high-quality reference sequences for resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ResFinder Database (resFinderDtbase). nomenclaturre from the National Center for Biotechnology Information Status: active. First released: 3.0.0. Last updated: 3.0.0.

MEGARes database (megares). A comprehensive database of antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

National Database of Antibiotic Resistant Organisms (NDARO) (ndaro). A database maintained by the USCDC with genomic data on AMR organisms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antibiotic Resistance Genes Database (ARDB) (ardb). An archive for antibiotic resistance genes and associated information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PATRIC/RAST Database (patricRast). Database that hosts resistance gene annotations within their microbial genome data resources. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BacMet Database (bacMet). Database of antibacterial biocide and metal resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NCBI's Pathogen Detection Isolates Browser (ncbiPDIB). Database that tracks AMR in pathogens and provides resistance profiles for pathogens worldwide. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data types part type

(dataTypes). The data type for a part. Data types used in the ODM include: varchar, booleen, float, category, date, time, datetime, url, email. dataType corresponds the the entry or cell within a data table, most commonly within a report table. If the data entry has a unit, then the dataType corresponds to the unit and the dataType refers to 'unit'. If the data entry is a category, then the dataType refers to 'category'. All categories are varchar. Otherwise the dataType is identifed within the part entry. TBA: dataType for dictionary.

Binary Large Object (BLOB) data type (blob). The data type for Binary Large Object (BLOB) data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Boolean data type (boolean). The data type for boolean/binary data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Categorical data type (categorical). The data type for categorical data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Date data type (date). The data type for date data (does not include time). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Datetime data type (datetime). The data type for date and time data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Float data type (float). The data type for float data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Integer data type (integer). The data type for integers. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See unit (data type) (seeUnitData). The data type entry when the data type for a given entry is specified by the unit used. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Variable character data type (varchar). The data type for variable character data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Deduplication Method Set

(dedupSet). The valid set of deduplication method categorical inputs.

Unique Molecular Identifier (UMI) Tagging (umiTag). A deduplication method that adds unique tags to individual DNA fragments, allowing identification and removal of duplicate reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Picard MarkDuplicates (picard). A deduplication method within the Picard suite that marks duplicate reads in BAM files based on mapped location. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SAMtools rmdup (samRmdup). A deduplication method that identifies and removes PCR duplicates based on alignment data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap's Clumpify (clumpify). A deduplication method that groups identical sequences, often used to deduplicate reads efficiently. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FastUniq (fastUniq). A deduplication method that is specifically designed to remove duplicates in paired-end sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA-MEM with Duplicate Marking (bwaMEM). A deduplication method that is used with SAMtools or Picard to mark duplicates during read mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

UMI-tools (umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

bamUtil Dedup (bamUtil). A deduplication method that removes duplicate reads directly from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqKit rmdup (seqKitRmdup). A deduplication method that works within SeqKit for duplicate removal in FASTA/FASTQ files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MitoZ Deduplication (mitoZ). A deduplication method that is used primarily for mitochondrial genomes but can handle deduplication by read clustering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dehosting Method Set

(dehostSet). The valid set of dehosting method categorical inputs.

Kraken2 (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bowtie2 (bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that maps reads against a host reference genome to remove aligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BMTagger (bmtagger). A dehosting software developed by NCBI for identifying and removing host sequences based on local alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DeconSeq (deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap Reformat (bbmapReform). A dehosting software that filters out host sequences by aligning to reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTQ Screen (fastqScreen). A dehosting software that checks reads against multiple reference genomes, including host genomes, to remove contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MetaPhlAn Software (metaPhIAn). Software tool that profiles microbial communities and can provide resistance gene insights. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA for Host Filtering (bwaHost). A dehosting software that maps reads to a host genome, filtering mapped reads from analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Host Subtraction with Bowtie2 & SAMtools (bowtie2XSam). A combined workflow for dehosting where reads mapped to the host are removed from downstream analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CLARK (clark). A dehosting software that classifies reads taxonomically, which helps filter out host reads in metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Additional dictionary sheets

(dictionarySupport). Additional sheets for the Excel version of the ODM dictionary. Sheets or tabs for the ODM Excel dictionary include: all ERD tables (look-up tables and data entry tables) and additional supportig tables.

Airport lists worksheet (airportLists). Parts lists used to generate airport and airplane data entry templates. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Airport Surveillance Template (airportTemplate). The input template for airport and airplane surveillance in the EU. Status: active. First released: 2.0.0. Last updated: 2.1.0.

List worksheet (lists). Parts lists for template dropdowns and other documentation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Summary worksheet (summary). Summary sheet of the dictionary.xlxs file. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Domains

(domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature).

All domains (allDo). Domain that specifies that it could apply to al domains; biological, chemical, and physical. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Biologic (bio). A living organism or biological substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Chemical (che). A chemical compound. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Domain not applicable (naDomain). Not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Physical property (phy). A physical property or object not characterized by life or chemistry. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Exceptions Part Type

(exceptions). An exception part type for use in creating wide names that do not follow the general structure.

Nucleic Acid Extraction set

(extractSet). set used for storing all the valid category values for the nucleic acid extraction method.

4s method (extract4s). Nucleic acid extraction performed using the 4s method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Amicon filter, extract with MP96 (amiMP96). Nucleaic acid extraction, usually used for the liquid fraction of a wastewater sample, using amicon filtration and using an MP96 for final extraction. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Bead beating, extract with MP96 (bbMP96). Nucleaic acid extraction, usually used for solid fraction of a wastewater sample, using bead beating and using an MP96 for final extraction. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Chemagic viral dna/rna 300 kit (chemVir). Nucleic acid extraction performed using the chemagic viral dna/rna 300 kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nuclisens automated magnetic bead extraction kit (nucAuto). Nucleic acid extraction performed using the nuclisens automated magnetic bead extraction kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nuclisens manual magnetic bead extraction kit (nucManu). Nucleic acid extraction performed using the nuclisens manual magnetic bead extraction kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Phenol chloroform (phenCl). Nucleic acid extraction performed using phenol chloroform. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega automated tna kit (promAuto). Nucleic acid extraction performed using the promega automated tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega ht tna kit (promHt). Nucleic acid extraction performed using the promega ht tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega manual tna kit (promManu). Nucleic acid extraction performed using the promega manual tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

promega wastewater large volume tna capture kit (promWW). Nucleic acid extraction performed using the promega wastewater large volume tna capture kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep dna/rna kit (qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen ez1 virus mini kit v2.0 (qgEz1). Nucleic acid extraction performed using the qiagen ez1 virus mini kit v2.0. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep powerfecal dna/rna kit (qgPwrFecal). Nucleic acid extraction performed using the qiagen allprep powerfecal dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen allprep powerviral dna/rna kit (qgPwrViral). Nucleic acid extraction performed using the qiagen allprep powerviral dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen powerwater kit (qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen qiaamp buffers with epoch columns (qgQiAmp). Nucleic acid extraction performed using the qiagen qiaamp buffers with epoch columns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen rneasy kit (qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen rneasy powermicrobiome kit (qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Resuspend COSCa filter collection (resCosca). Nucleic acid extraction via resuspension of a sample collected using the COSCa ball method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

thermo magmax microbiome ultra nucleic acid isolation kit (thermMag). Nucleic acid extraction performed using the thermo magmax microbiome ultra nucleic acid isolation kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

trizol, zymo mag beads w/ zymo clean and concentrator (trizol). Nucleic acid extraction performed using the trizol, zymo mag beads w/ zymo clean and concentrator method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

zymo environ water rna kit (cat. r2042) (zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit (cat. r2042). Status: active. First released: 2.0.0. Last updated: 2.0.0.

zymo quick-rna fungal/bacterial miniprep #r2014 (zymoQuick). Nucleic acid extraction performed using the zymo quick-rna fungal/bacterial miniprep #r2014 kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

exclusions based sample preparation (ESP) (esp). exclusions based sample preparation (ESP) Status: active. First released: 2.2.0. Last updated: 2.2.0.

luminultra wastewater extraction kit (luminWWExtract). luminultra wastewater extraction kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) (monarchRNA). monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) Status: active. First released: 2.2.0. Last updated: 2.2.0.

nucleomag (ref. 744220.4) using kingfisher automated instrument (nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument Status: active. First released: 2.2.0. Last updated: 2.2.0.

qiagen qiaamp dsp viral rna mini kit (qiampDSP). qiagen qiaamp dsp viral rna mini kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

sciencell viral rna isolation kit (sciencellRNA). sciencell viral rna isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

thermo magmax viral/pathogen nucleic acid isolation kit (thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

trizol and RNA purification kit (trizolRNA). trizol and RNA purification kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

trizol, garnet bead beating, alcohol precipitation (trizolEtOH). trizol, garnet bead beating, alcohol precipitation Status: active. First released: 2.2.0. Last updated: 2.2.0.

zymo quick-rna viral 96 kit #r1041 (zymo1041). zymo quick-rna viral 96 kit #r1041 Status: active. First released: 2.2.0. Last updated: 2.2.0.

zymo quick-rna viral kit #r1035 (zymo1035). zymo quick-rna viral kit #r1035 Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample fraction set

(fractionSet). set for the fraction of the sample (solid, liquid, etc.).

Liquid fraction (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Mixed/homogenized sample (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Solid fraction (general) (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not applicable (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Solid fraction (Wet) (solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Solid Fraction (Dry) (solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Multiple fraction (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Geographic set

(geoTypeSet). set for different type of geographic components.

Sewer Network Health Region (hlthReg). Health region served by the sewer network Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sewer catchment area (swrSet). Sewer catchment area. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Groups

(groups). A collection of related measures. Used primary to group measurements and methods, this helps pare down the drop down list for a given measurement or methods.

Acinetobacter Group (acinetobacterGrp). A group of measures/methods related to acinebacter bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Adenovirus Group (adenovirusGrp). A group of measures/methods related to Adenoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Anti-microbial resistance Group (amrGrp). The group for measures and methods pertaining to anti-microbial resistant microbes (general). Status: active. First released: 2.1.0. Last updated: 2.1.0.

Anaplasma Group (anaplasmaGrp). A group of measures/methods related to anaplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Astrovirus Group (astrovirusGrp). A group of measures/methods related to astroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Babesia or Nuttallia Group (babesiaGrp). A group of measures/methods related to babesia parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides Group (bacteroidesGrp). A group of measures/methods related to bacteroides bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Miscellaneous bacteria group (bactMisc). A group of measures/methods related to miscellaneous bacteria. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Beta Coronavirus Group (betaCoronaGrp). A group of measures/methods related to beta coronaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Beta-Lactamase Anti-microbial resistance Group (bLacAMRGrp). The group for measures and methods pertaining to beta-lactamase-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Borrelia burgdorferi or Lyme Disease Group (borreliaGrp). A group of measures/methods related to Borrelia burgdorferi or Lyme Disease. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Brucella Group (brucellaGrp). A group of measures/methods related to brucella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Campylobacter Group (campGrp). A group of measures/methods related to campylobacter bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Candida auris Group (cAurisGrp). A group of measures/methods related to Candida auris. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Chikungunya Group (chikungunyaGrp). A group of measures/methods related to chikungunya virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Chlamydia Group (chlamydiaGrp). A group of measures/methods related to chlamydia bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Clostridium Group (clostridiumGrp). A group of measures/methods related to clostridium bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Colistin Anti-microbial resistance group (colAMRGrp). The group for measures and methods pertaining to colistin-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Collection group (colGrp). A group of measurement-like attributes related to sample collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Cryptosporidium Group (cryptosporidiumGrp). A group of measures/methods related to cryptosporidium parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 Delta Variant Group (deltaGrp). A group of measures/methods related to the SARS-CoV-2 Delta Variant. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Diphtheria Group (diptheriaGrp). A group of measures/methods related to the diptheria bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Escherichia coli group (ecoliGrp). A group of measures/methods related to Escherichia coli bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Enterovirus Group (enterovirusGrp). A group of measures/methods related to enteroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Flavivirus (West Nile, Dengue, Zika) Group (flavivirusGrp). A group of measures/methods related to flaviviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

FLiRT/SLip Variant Group (flirtSLipGrp). The group for measures and methods pertaining to the FLiRT and SLip variants of SARS-CoV-2. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Influenza A Virus Group (fluAGrp). A group of measures/methods related to Influenza A viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Influenza B Virus Group (fluBGrp). A group of measures/methods related to Influenza B viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Influenza Virus General Group (fluGrp). A group of measures/methods related to general influenza viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Gonococcus Group (gonococcusGrp). A group of measures/methods related to gonococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Haemophilus Group (haemophilusGrp). A group of measures/methods related to haemophilus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis Group (hepGrp). A group of measures/methods related to hepatitis viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Herpes Virus Group (herpesGrp). A group of measures/methods related to herpes viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

HIV Group (hivGrp). A group of measures/methods related to Human Immunodeficiency Virus (HIV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rhinovirus Group (hrvGrp). A group of measures/methods related to rhinoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Integrase Anti-microbial resistance Group (intAMRGrp). The group for measures and methods pertaining to integrase-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Klebsiella Group (klebsiellaGrp). A group of measures/methods related to klbsiella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Legionella Group (legionellaGrp). A group of measures/methods related to legionella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Lentivirus Group (lentiGrp). A group of measures/methods related to lentiviruses, including viral vectors such as the Puro virus vector. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Listeria Group (listeriaGrp). A group of measures/methods related to listeria bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Plasmodium or Malaria Group (malariaGrp). A group of measures/methods related to plasmodium parasites or malaria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Measurement group (measGrp). A group of measures that cannot be otherwise categorized. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measles Group (measlesGrp). A group of measures/methods related to the measles virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Metabolite Group (metaboliteGrp). A group of measures/methods related to metabolites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Miscellaneous attribute group (miscAttr). A group of miscellaneous measurement-like attributes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Miscellaneous measure group (miscMeas). A group of measures that cannot be otherwise categorized. Status: active. First released: 2.0.0. Last updated: 2.0.0.

MPox Clade I Group (mpoxCldIGrp). A group of measures/methods related to Mpox Clade I (formerly "Monkey Pox"). Status: active. First released: 2.2.0. Last updated: 2.2.0.

MPox Clade II Group (mpoxCldIIGrp). A group of measures/methods related to Mpox Clade II (formerly "Monkey Pox"). Status: active. First released: 2.2.0. Last updated: 2.2.0.

MPox Group (mpoxGrp). A group of measures/methods related to Mpox (formerly "Monkey Pox"). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Metapneumovirus Group (mpvGrp). A group of measures/methods related to metapneumoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mumps Group (mumpsGrp). A group of measures/methods related to the mumps virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mycoplasma Group (mycoplasmaGrp). A group of measures/methods related to mycoplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Group not applicable (naGroup). Used when there is no group; ie. group is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 Nimbus Variant Group (nimbusGrp). A group of measures/methods related to the SARS-CoV-2 Nimbus Variant. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Norovirus GI Group (noroGIGrp). A group of measures/methods related to norovirus GI. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Norovirus GII Group (noroGIIGrp). A group of measures/methods related to norovirus GII. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Norovirus Group (noroGrp). A group of measures/methods related to noroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 Omicron Variant Group (omicronGrp). A group of measures/methods related to the SARS-CoV-2 Omicron Variant. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Orthopox Virus Group (orthoGrp). A group of measures/methods related to orthopox viruses (excluding variolla viruses). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Papilomavirus Group (papilomavirusGrp). A group of measures/methods related to papilomaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Parainfluenza Group (parafluGrp). A group of measures/methods related to parainfluenza viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteriophage Group (phageGrp). A group of measures/methods related to bacteriophages. Status: active. First released: 2.2.0. Last updated: 2.2.0.

PMMoV Group (pmmovGrp). A group of measures/methods related to the Pepper Mild Mottle Virus (PMMoV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Poliovirus Group (polioGrp). A group of measures/methods related to polioviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population group (popGrp). A group of measures/methods related to population-level factors. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Processing group (procGrp). A group of measures/methods related to processing samples for analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Pseudomonas Group (pseudomonasGrp). A group of measures/methods related to pseudomonas bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rickettsia Group (rickettsiaGrp). A group of measures/methods related to ricketsia parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rotavirus Group (rotavirusGrp). A group of measures/methods related to rotaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Respiratory syncytial virus (RSV) Group (rsvGrp). Human Respiratory Syncytial virus (RSV). Status: active. First released: 2.0.0. Last updated: 2.1.2.

Rubella Group (rubellaGrp). A group of measures/methods related to the rubella virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Salmonella Group (salmonellaGrp). A group of measures/methods related to salmonella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sapovirus Group (sapovirusGrp). A group of measures/methods related to sapoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 (sarsCov2). A group of measures/methods related to the SARS-CoV-2 virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Shigella Group (shigellaGrp). A group of measures/methods related to shigella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Site features group (siteFeat). A group of environmental measures/methods and those pertaining to the features of a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Staphylococcus Group (staphGrp). A group of measures/methods related to staphylococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Streptococcus Group (strepGrp). A group of measures/methods related to streptococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Tetracycline Anti-microbial resistance Group (tetAMRGrp). The group for measures and methods pertaining to tetracycline-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Treponema Group (treponemaGrp). A group of measures/methods related to treponema bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Trichomonas Group (trichomonasGrp). A group of measures/methods related to trichomonas bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Tuberculosis Group (tuberculosisGrp). A group of measures/methods related to tuberculosis. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Francisella tularensis (tularemia) Group (tularemiaGrp). A group of measures/methods related to Francisella tularensis. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Ureaplasma Group (ureaplasmaGrp). A group of measures/methods related to ureaplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Vancomycin Anti-microbial resistance Group (vanAMRGrp). The group for measures and methods pertaining to vancomycin-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Varicella Group (varicellaGrp). A group of measures/methods related to varicella viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Vibrio Group (vibrioGrp). A group of measures/methods related to vibrio bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Miscellaneous viruses group (virusMisc). A group of measures/methods related to miscellaneous viruses. Status: depreciated. First released: 1.0.0. Last updated: 2.2.0.

Vesicular Stomatitis Virus (VSV) Group (vsvGrp). A group of measures/methods related to Vesicular Stomatitis Virus (VSV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Water Quality Group (waterQualityGrp). A group of measures/methods related to water quality. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Yersinia Group (yersiniaGrp). A group of measures/methods related to yersinia bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Orthoebolavirus Group (ebolaGrp). A group of measures/methods related to Orthoebolaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Orthohantavirus Group (hantaGrp). A group of measures/methods related to Orthohantaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichivirus (AiV) Group (Aichivirus A) (aichivAGrp). A group of measures/methods related to human aichiviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Kobuvirus Group (kobuGrp). A group of measures/methods related to kobuviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Bocaparvovirus Group (bocaparvGrp). A group of measures/methods related to bocaparvoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Circovirus Group (circoGrp). A group of measures/methods related to circoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Cosavirus Group (cosaVGrp). A group of measures/methods related to cosaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Deltaretrovirus Group (deltaretroGrp). A group of measures/methods related to deltaretroviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Eastern equine encephalitis virus group (eeevGrp). A group of measures/methods related to eastern equine encephalitis viruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Erythroparvovirus Group (erythroparvoGrp). A group of measures/methods related to erythroparvoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Giardia Group (giardiaGrp). A group of measures/methods related to Giardia. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Gammaretrovirus Group (gammaretroGrp). A group of measures/methods related to gammaretroviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Lymphocryptovirus Group (lymphocryptoGrp). A group of measures/methods related to lymphocryptoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus Group (mastadenoGrp). A group of measures/methods related to human mastadenoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Parechovirus group (parechoGrp). A group of measures/methods related to parechoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Picobirnavirus Group (picobirnaGrp). A group of measures/methods related to picobirnaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Polyomavirus Group (polyomaGrp). A group of measures/methods related to polyomaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Roseolovirus (Human Herpesvirus-6) Group (hhvGrp). A group of measures/methods related to roseoloviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Salivirus Group (saliGrp). A group of measures/methods related to salivirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold Virus Group (saffoldGrp). A group of measures/methods related to saffold virus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Tanapox Group (tanapoxGrp). A group of measures/methods related to tanapox viruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Torque Teno Virus Group (ttvGrp). A group of measures/methods related to torque teno viruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Genomic Target Enrichment Methods Set

(gteSet). The set for valid inputs for the Genomic Target Enrichment method.

Hybrid Selection Method (hySel). Selection by hybridization in array or solution for genomic target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

rRNA Depletion Method (rnaDepl). Removal of background RNA for the purposes of enriching the genomic target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Inhibition set

(inhibitionSet). Category set for inhibition methods.

Serial dilution (serialDilution). The serial dilution method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Spike matrix and recovery (spike). The spike matrix and recovery method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Instrument set

(insTypeSet). List of instruments that are used for measures and methods

Atline Analyzer (aas). Atline analyzer with sampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Hand Measurement (hma). Handheld measurement analyzer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Other instrument (instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Lab Analysis (ola). Offline laboratory analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Online Sensor (onse). Online sensor Status: active. First released: 1.0.0. Last updated: 2.0.0.

qPCR instruments (quantitative PCR) (qPCRinst). A quantitative PCR instrument, to detect and quantify specific DNA/RNA targets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

RT-qPCR intruments (rtqPCRinst). Real-time quantitative PCR instruments, used when detecting RNA viruses (an additional a reverse transcription step). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Digital PCR (dPCR) intruments (dPCRinst). Digital PCR instruments, enables absolute quantification without the need for standard curves

(e.g., Bio-Rad QX200). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Thermal cyclers (thermCyc). A thermal cycler instrument, used to perform temperature-controlled reactions for PCR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Next-Generation Sequencing (NGS) platforms or intruments (ngsInst). Next generation sequencer instruments and platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Library preparation instruments (libPrepInst). Instruments for the preparation of sequencing libraries, e.g., automation platforms like the Illumina NeoPrep. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fragment analyzers or bioanalyzers (bioanalys). Fragment analyzer or bioanalyzer instruments, used to assess fragment size distribution in libraries. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Spectrophotometers or fluorometers (spectroFluoro). Spetrometer and fluorometer instruments; may be used to assess concentration and purity (e.g., NanoDrop™, Qubit™). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Centrifuges (centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Filtration units (filtInst). Filtration instruments; remove large particulates or concentrate targets (e.g., tangential flow filtration). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ultracentrifuges (ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Magnetic separation racks (magInst). Magnetic separation rack instrument; may be used with magnetic beads for nucleic acid extraction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Autosamplers (autoInst). Autosampler instruments, used to automatically collect flow- or time-proportional samples over a period (e.g., ISCO autosamplers). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Grab samplers (grabInst). Grab sampler instruments; manually collect a single sample at a point in time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flow meters (flowInst). Flow meter instruements; used to measure wastewater flow rates to enable standardization of sample data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Temperature and pH probes (enviroInst). Local probe insturments for temperature or pH; allow monitoring of environmental conditions at sites, for example. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Library Preparation Kit Set

(libraryKitSet). The valid set of categorical values for sequencing library preparation kits.

Nextera XT DNA Library Preparation Kit (nexteraXT). Nextera XT DNA Library Preparation Kit by Illumina. A fast and efficient library prep kit for small genomes and amplicons, uses transposase-based fragmentation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nextera DNA Flex/DNA Prep Library Prep Kit (dnaPrep). Nextera DNA Flex Library Prep Kit, now called DNA Prep, by Illumina. A flexible, transposase-based library prep kit for a wide range of DNA input

amounts, suitable for microbial and human DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NEBNext Ultra II DNA Library Prep Kit (nebnextUltraII). NEBNext Ultra II DNA Library Prep Kit by New England Biolabs. A high-efficiency library prep kit for low DNA input, ideal for whole-genome and target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

KAPA HyperPrep Kit (kapaHyperPrep). KAPA HyperPrep Kit by Roche. An optimized library prep kit for high-quality libraries from low-input or degraded DNA, commonly used for Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Swift 2S Turbo DNA Library Kit (swift2STurbo). Swift 2S Turbo DNA Library Kit by Swift Biosciences. A fast library prep kit workflow with robust performance for low-input DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

QIAseq FX DNA Library Kit (qiaSeqFX). QIAseq FX DNA Library Kit by Qiagen. Alibrary prep kit that uses enzymatic fragmentation, suitable for a variety of applications, including whole-genome sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Illumina DNA Prep with Enrichment (illuminaDNAprep). Illumina DNA Prep with Enrichment by Illumina. A library prep kit that integrates DNA library prep with enrichment for target regions, ideal for targeted sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SureSelect XT HS2 DNA Library Preparation Kit (sureSelectXThs2). SureSelect XT HS2 DNA Library Preparation Kit by Agilent. A high-sensitivity library prep kit with target capture capabilities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Accel-NGS 2S Plus DNA Library Kit (accelNGS2Splus). Accel-NGS 2S Plus DNA Library Kit by Swift Biosciences. A library prep kit designed

for efficient library prep from fragmented or damaged DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ligase-Dependent Library Prep Kits (ligaseDep). Ligase-Dependent Library Prep Kits by Lucigen/Epicentre. A library prep kit suitable for long-read applications and used with Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ThruPLEX DNA-seq Kit (thruPLEX). ThruPLEX DNA-seq Kit by Takara Bio. A low-input library prep kit with fast, three-step protocol. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MGIEasy DNA Library Prep Kit (mgiEasy). MGIEasy DNA Library Prep Kit by MGI/BGI. A library prep kit designed for MGI sequencing platforms, offering flexibility in sample input. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TruSeq DNA PCR-Free Library Prep Kit (truSeqDNA). TruSeq DNA PCR-Free Library Prep Kit by Illumina. A high-quality library prep kit without PCR amplification, reducing bias. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SMARTer ThruPLEX Plasma-seq Kit (smarterThruPLEX). SMARTer ThruPLEX Plasma-seq Kit by Takara Bio. A library prep kit optimized for low-input DNA, including cell-free DNA for liquid biopsy studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bioo Scientific NEXTflex Rapid DNA-Seq Kit (biooSci). Bioo Scientific NEXTflex Rapid DNA-Seq Kit by PerkinElmer. A rapid and flexible library prep kit for DNA sequencing on Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Covaris truXTRAC FFPE DNA Library Kit (covarisTruXTRAC). Covaris truXTRAC FFPE DNA Library Kit. A specialized library prep kit for extracting and preparing DNA from FFPE tissue. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CleanPlex DNA Library Prep Kit (cleanPlex). CleanPlex DNA Library Prep Kit by Paragon Genomics. A library target enrichment kit optimized for high sensitivity and low input. Status: active. First released: 3.0.0. Last updated: 3.0.0.

EasySeq NGS Targeted Capture Kit (easySeqNGS). EasySeq NGS Targeted Capture Kit by Nimagen. A library preparation kit and targeted capture in one, ideal for small panels. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Apollo PrepX Library Preparation Kits (apolloPrepX). Apollo PrepX Library Preparation Kit by Takara Bio. An automated library preparation kit for Illumina sequencing on Apollo systems. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data license set

(licSet). The set to describe valid categorical values for the licensing fields for measures or datasets.

Academic Free License v3.0 (afl30). The licensing for the measure or data set is managed under the Academic Free License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Apache license 2.0 (apache20). The licensing for the measure or data set is managed under the Apache license 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Artistic license 2.0 (artistic20). The licensing for the measure or data set is managed under the Artistic license 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Boost Software License 1.0 (bsl10). The licensing for the measure or data set is managed under the Boost Software License 1.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 2-clause "Simplified" license (bsd2Clause). The licensing for the measure or data set is managed under the BSD 2-clause "Simplified" license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 3-clause "New" or "Revised" license (bsd3Clause). The licensing for the measure or data set is managed under the BSD 3-clause "New" or "Revised" license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 3-clause Clear license (bsd3ClauseClear). The licensing for the measure or data set is managed under the BSD 3-clause Clear license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD 4-clause "Original" or "Old" license (bsd4Clause). The licensing for the measure or data set is managed under the BSD 4-clause "Original" or "Old" license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

BSD Zero-Clause license (bsd0). The licensing for the measure or data set is managed under the BSD Zero-Clause license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

CeCILL Free Software License Agreement v2.1 (cecill21). The licensing for the measure or data set is managed under the CeCILL Free Software License Agreement v2.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Creative Commons Zero v1.0 Universal (cc010). The licensing for the measure or data set is managed under the Creative Commons Zero v1.0 Universal. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Creative Commons Attribution 4.0 (ccby40). The licensing for the measure or data set is managed under the Creative Commons Attribution 4.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Creative Commons Attribution ShareAlike 4.0 (ccbysa40). The licensing for the measure or data set is managed under the Creative Commons Attribution ShareAlike 4.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Do What The F*ck You Want To Public License (wtfpl). The licensing for the measure or data set is managed under the Do What The F*ck You Want To Public License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Educational Community License v2.0 (ecl20). The licensing for the measure or data set is managed under the Educational Community License v2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Eclipse Public License 1.0 (epl10). The licensing for the measure or data set is managed under the Eclipse Public License 1.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Eclipse Public License 2.0 (epl20). The licensing for the measure or data set is managed under the Eclipse Public License 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

European Union Public License 1.1 (eupl11). The licensing for the measure or data set is managed under the European Union Public License 1.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

European Union Public License 1.2 (eupl12). The licensing for the measure or data set is managed under the European Union Public License 1.2. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU Affero General Public License v3.0 (agpl30). The licensing for the measure or data set is managed under the GNU Affero General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU Free Documentation License v1.3 (gfdl13). The licensing for the measure or data set is managed under the GNU Free Documentation License v1.3. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU General Public License v2.0 (gpl20). The licensing for the measure or data set is managed under the GNU General Public License v2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU General Public License v3.0 (gpl30). The licensing for the measure or data set is managed under the GNU General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mulan Permissive Software License, Version 2 (mulanPSL20). The licensing for the measure or data set is managed under version 2 of the Mulan Permissive Software License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU Lesser General Public License v2.1 (lgpl21). The licensing for the measure or data set is managed under the GNU Lesser General Public License v2.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

GNU Lesser General Public License v3.0 (lgpl30). The licensing for the measure or data set is managed under the GNU Lesser General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

ISC (isc). The licensing for the measure or data set is managed under the ISC license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

LaTeX Project Public License v1.3c (lppl13c). The licensing for the measure or data set is managed under the LaTeX Project Public License v1.3c. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Microsoft Public License (mspl). The licensing for the measure or data set is managed under the Microsoft Public License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

MIT No Attribution (mit0). The licensing for the measure or data set is managed under the MIT no attribution license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

MIT (mit). The licensing for the measure or data set is managed under the MIT license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mozilla Public License 2.0 (mpl20). The licensing for the measure or data set is managed under the Mozilla Public License 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Open Software License 3.0 (osl30). The licensing for the measure or data set is managed under the Open Software License 3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

PostgreSQL License (postgreSQL). The licensing for the measure or data set is managed under the PostgreSQL License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

SIL Open Font License 1.1 (ofl11). The licensing for the measure or data set is managed under the SIL Open Font License 1.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

University of Illinois/NCSA Open Source License (ncsa). The licensing for the measure or data set is managed under the University of Illinois/NCSA Open Source License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

The Unlicense (unlicense). The licensing for the measure or data set is managed under The Unlicense. Status: active. First released: 2.2.0. Last updated: 2.2.0.

zLib License (zlib). The licensing for the measure or data set is managed under the zLib License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Open license not otherwise described (open). The licensing for the measure or data set is managed under an open license not otherwise described. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Private data - not for disemination (private). The measure or data set is private data - not for disemination. Status: active. First released: 2.2.0. Last updated: 2.2.0.

CC BY-NC-SA 4.0 license (ccbyncsa40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial, and sharealike international license. Status: active. First released: 2.2.3. Last updated: 2.2.3.

CC BY-NC 4.0 license (ccbync40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial international license. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Sample Material Characteristics Set

(matCharSet). The set for recording the possible valid values for describing the sample material characteristics.

Stagnant (stag). A quality of a body of water wherein it has no current or flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Slow-flowing (slFlow). A quality of a body of water wherein there is a slow flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fast-flowing (faFlow). A quality of a body of water wherein there is a fast flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liquid (liquidMat). Material is liquid, ie. is a state of matter with a definite volume but no fixed shape, adapting to the shape of their container. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Slurry (slur). An quality in which the fluid like material is more viscous due to the suspension of insoluble solid particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Contamination (contam). The presence of a constituent, impurity, or some other undesirable element that spoils, corrupts, infects, makes unfit, or makes inferior a material, physical body, natural environment, place of

human occupancy, or other material entity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fecal-contamination (fecContam). A contamination quality in which fecal matter is a key component of the contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Semi-solid (semSol). A state of matter consisting of molecules in a non-rigid structure that can retain its shape and volume but that is not resistant to such change. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Solid (solidMat). The state in which a substance has no tendency to flow under moderate stress; resists forces (such as compression) that tend to deform it; and retains a definite size and shape. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Treated (treat). A quality which denotes an altered state of an item resulting from purposeful interventions or processes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Untreated (untreat). A quality which denotes an absence of purposeful intervention or processes on an item. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Measures

(measurements). The attribute to describe a part type of measures. All measures have `partType` = "measure". mes

a1306s delta-variant gene target (a1306s). a1306s delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

a1918v delta-variant gene target (a1918v). a1918v delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

a2710t omicron-variant gene target (a2710t). a2710t omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

a63t omicron-variant gene target (a63t). a63t omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

a67v omicron-variant gene target (a67v). a67v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant a67v del69 and del70 mutations (a67vDel69Del70). Omicron Variant a67v mutation mutation, and del 69 and del70 mutations co-occuring Status: active. First released: 2.2.0. Last updated: 2.2.0.

Absolute humidity (absHum). A measure of the total mass of water vapour present in the air per volume of air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Acinetobacter (acinetobacter). Acinetobacter Status: active. First released: 2.2.0. Last updated: 2.2.0.

Adenovirus (F40/41) (adenovirusF40). Adenovirus (F40/41) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Adenovirus 40 (adv40). Adenovirus serotype 40. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Adenovirus 41 (adv41). Adenovirus serotype 41. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Adenovirus F41 Fibre Gene Target (advF41Fibre). Human Adenovirus Group F41 Fiber gene target Status: active. First released: 2.1.0. Last updated: 2.1.0.

Environmental temperature (airTemp). Environmental temperature. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Alkalinity (alkaline). Measure of alkalinity Status: active. First released: 3.0.0. Last updated: 3.0.0.

Assay Limit of Detection (LOD) (alod). The minimum level of a target consistently detectable (e.g., with 95% probability) using the assay considering only the amplification and quantification steps of RT-qPCR. Status: active. First released: 2.2.0. Last updated: 3.0.0.

The number of ambiguous bases (Ns) normalized (ambigNs). The number of ambiguous bases (Ns) normalized per 100 kilobasepairs (kbp). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Amplicon Size (ampSize). The length of the amplicon generated by PCR amplification. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Anaplasma phagocytophilum (aPhagocytophilum). Anaplasma phagocytophilum Status: active. First released: 2.2.0. Last updated: 2.2.0.

Arrival temperature (arTemp). The temperature of a sample upon arrival at the laboratory for analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Astrovirus (astrovirus). Astrovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

Babesia (babesia). Babesia Status: active. First released: 2.2.0. Last updated: 2.2.0.

Borrelia burgdorferi (bBurgdorferi). Borrelia burgdorferi Status: active. First released: 2.2.0. Last updated: 2.2.0.

bcov (bcov). Measure of the amount of bovine coronavirus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Beta (beta). B.1.351 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Cephamycin Beta-Lactamase-Resistance gene target (blaCMY). Cephamycin Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

CTX-M Beta-Lactamase-Resistance gene target (blaCTXM1). CTX-M Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Impenemase (IMP) Beta-Lactamase-Resistance gene target (blaIMP). Impenemase (IMP) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase-Resistance gene target (blaKPC). Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

New-Delhi Metallo- (NDM) Beta-Lactamase-Resistance gene target (blaNDM). New-Delhi Metallo- (NDM) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

OXA-type Beta-Lactamase-Resistance gene target (blaOXA48). OXA-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

SHV Beta-Lactamase-Resistance gene target (blaSHV). SHV-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

TEM Beta-Lactamase-Resistance gene target (blaTEM). TEM-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase-Resistance-resistance gene target (blaVIM). Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

5-Day carbonaceous biochemical oxygen demand (bod5c). The quantity of oxygen utilized for the biochemical degradation of organic matter under standard laboratory procedures in five (5) days in the presence of a nitrification inhibitor, expressed in milligrams per litre (mg/l). Status: active. First released: 1.1.0. Last updated: 2.0.0.

5-day total biochemical oxygen demand (bod5t). 5 day total biochemical oxygen demand. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Bovine respiratory syncytial virus group (brsv). Bovine respiratory syncytial virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

BRSV-N (brsvN). bovine respiratory syncytial virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

Brucella (brucella). Brucella Status: active. First released: 2.2.0. Last updated: 2.2.0.

C28311T Omicron N1 Point Mutation (c2811t). A measure of the C to T point mutation at position 28311 (C28311T) of the N1 probe, present in all Omicron sub-linages. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Caffeine (caff). Caffeine (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Calprotectin (Calprotectin). Calprotectin is a calcium- and zinc-binding protein of the S-100 protein family which is mainly found within neutrophils and throughout the human body. The presence of calprotectin in faeces is a consequence of neutrophil migration into the gastrointestinal tissue due to an inflammatory process. Status: active. First released: 2.2.0. Last updated: 3.0.0.

Campylobacter (camp). Campylobacter. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Candida auris (cAuris). The yeast species Candida auris, or C. auris. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Carbonaceous Biochemical Oxygen Demand (cbod). A measure of the amount of oxygen required by microorganisms to break down organic carbon-based compounds in water over a specified period, typically five days at 20°C (CBOD). Unlike BOD (Biochemical Oxygen Demand), CBOD excludes oxygen demand from the oxidation of nitrogenous compounds (such as ammonia). It is used to assess organic pollution in wastewater and natural waters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Carbapenemase-encoding genes (cbp). Carbapenemase-encoding genes. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Clostridium difficile (cDiff). Clostridium difficile Status: active. First released: 2.2.0. Last updated: 2.2.0.

Corynebacterium diphtheriae (cDip). Corynebacterium diphtheriae Status: active. First released: 2.2.0. Last updated: 2.2.0.

Centrifugation speed (centSpeed). Centrifugation speed Status: active. First released: 2.2.0. Last updated: 2.2.0.

Chikungunya virus (CHIKV) (chikv). Chikungunya virus (CHIKV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Chlamydia (chlamydia). Chlamydia Status: active. First released: 2.2.0. Last updated: 2.2.0.

Campylobacter jejuni bacteria (cJejuni). Campylobacter jejuni gene target/measurement Status: active. First released: 2.1.0. Last updated: 2.1.0.

Carbon Dioxide (co2). A measure of an amount or concentraion of carbon dioxide. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Chemical Oxygen Demand (cod). Chemical oxygen demand. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Time from collection to storage (col2Frdg). The amount of time between sample collection and the samples placement in stable storage/refrigeration. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Colistin resistance (colis). Colistin-resistant bacteria. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Concentration measure (conc). Measurement of concentration (generalized) - designed for describing protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample volume after concentration (concVol). The total volume of a sample after the concentration step. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Water conductivity (cond). Measurement of conductivity of sample or site. Status: active. First released: 1.0.0. Last updated: 2.0.0.

consensus genome length (conGenLen). The length of the genome defined by the most common nucleotides at each position. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Covid-19 (cov). Covid-19 infection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 measure (cov2Me). Measure the amount of SARS-CoV-2 virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2-B.1.1.7 (covB117). Variant B.1.1.7 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

SARS-CoV-2-B.1.351 (covB135). Variant B.1.351 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

SARS-CoV-2-E (covE). SARS-CoV-2 E gene. Status: active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2 M Gene target (covM). SARS-CoV-2 M gene (orf5) Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2-N1 (covN1). SARS-CoV-2 nucleocapsid gene, allele 1. Status: active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2-N2 (covN2). SARS-CoV-2 nucleocapsid gene, allele 2. Status: active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2-N200 (covN200). SARS-CoV-2 nucleocapsid gene, amino acids 199-202. Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2-N3 (covN3). SARS-CoV-2 nucleocapsid gene, allele 3. Status: active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2-P.1 (covP1). Variant P.1 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

SARS-CoV-2-RdRp (covRdrp). SARS-CoV-2 RdRp gene. Status: active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2 S Gene Target (covS). S sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-COV-2 5' UTR Gene target (covUTR5). SARS-COV-2 5' UTR Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

Clostridium perfringens (cPerfrigens). Clostridium perfringens Status: active. First released: 2.2.0. Last updated: 2.2.0.

crAssphage-N (cra). crAssphage virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

Creatinine (crea). Creatinine (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Cryptosporidium (cryptosporidium). Cryptosporidium Status: active. First released: 2.2.0. Last updated: 2.2.0.

Circulating vaccine-derived poliovirus type 2 (cVDPV2). Circulating vaccine-derived poliovirus type 2 Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of cycles (cyNum). The number of cycles of a PCR machine, or any other cycling process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

D339H Mutation (d339h). The FLiRT/SLip variant mutation D339H. Status: active. First released: 2.2.0. Last updated: 2.2.0.

d377y delta-variant gene target (d377y). d377y delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

d3g omicron-variant gene target (d3g). d3g omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

d63g delta-variant gene target (d63g). d63g delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

d796y omicron-variant gene target (d796y). d796y omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

d950n delta-variant gene target (d950n). d950n delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ddcov_e sars-cov-2 gene target (ddcovE). ddcov_e sars-cov-2 mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ddcov_n sars-cov-2 gene target (ddcovN). ddcov_n sars-cov-2 mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant 142-144 Deletion (del142144). Omicron Variant 142-144 Deletion mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

del143/145 (del143). 143 or 145 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Delta Variant 156-157 Deletion (del156157). Delta Variant 156-157 Deletion mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

del 157/158 (del157). 157 or 158 deletion delta-variant gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

del2084/2084 (del2084). 2084 or 2084 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

del212/212 (del212). 212 or 212 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant 142-14431-33 Deletion (del3133). Omicron Variant 142-14431-33 Deletion mutation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

del3674/3676 (del3674). 3674 or 3676 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

del69/70 (del6970). 69 or 70 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Delta (delta). B.1.617.2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dengue Virus Type 1 (den1). Dengue virus, Type 1, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus Type 2 (den2). Dengue virus, Type 2, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus Type 3 (den3). Dengue virus, Type 3, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus Type 4 (den4). Dengue virus, Type 4, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue (dengue). Dengue virus, general measurement Status: active. First released: 2.2.0. Last updated: 2.2.0.

depth of coverage threshold (depCovThresh). The threshold used as a cut-off for the depth of coverage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Detected Lineage or Clade Name (detLinClade). The measurement for reporting detected lineage or clade information - used as an "other" for measurements not already captured in the ODM structure. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dilution factor (dilFact). Specifies the extent to which a sample or aliquot was diluted prioir to analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Point dillutions (dillute). Exact concentration or dillutions for generating a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dissolved oxygen (dissOxy). Measure of dissolved oxygen in liquid medium Status: active. First released: 3.0.0. Last updated: 3.0.0.

DNA Fragment Length (dnaFragLen). The length of the DNA fragment generated by mechanical shearing or enzymatic digestion for the purposes of library preparation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus E Gene (dnvE). Dengue Type 2-specific gene taget. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus NS5 Gene (dnvNS5). Dengue Type 1-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dengue Virus prM Gene (dnvprM). Dengue Type 3 and 4-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Duration time of a method (duration). The duration of time for a given method as described in protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

e156g delta-variant gene target (e156g). e156g delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

e484a omicron-variant gene target (e484a). e484a omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Enteroaggregative Escherichia coli (EAEC) (eaec). Enteroaggregative Escherichia coli (EAEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Epstein–Barr virus (EBV) (ebv). Epstein–Barr virus (EBV), formerly known as Human gammaherpesvirus 4 Status: active. First released: 2.2.0. Last updated: 2.2.0.

Escherichia coli (ecoli). Concentration of bacteria that are passed through the faecal excrement of humans, livestock and wildlife Status: active. First released: 2.0.0. Last updated: 2.0.0.

Enterohemorrhagic Escherichia coli (EHEC) (ehec). Enterohemorrhagic Escherichia coli (EHEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Enteroinvasive Escherichia coli (EIEC) (eiec). Enteroinvasive Escherichia coli (EIEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Enterovirus (enterovirus). Enterovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rainfall (envRnF). Rainfall, i.e. amount of precipitation in the form of rain. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Ground snow depth (envSnwD). Total depth of snow on the ground. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Snowfall (envSnwF). Snowfall, i.e. amount of precipitation in the form of snow. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Enteropathogenic Escherichia coli (EPEC) (epec). Enteropathogenic Escherichia coli (EPEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sarbecovirus-specific E sars-cov-2 gene target (eSarbec). Sarbecovirus-specific E sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

ESBL-encoding genes (esbl). Extended-spectrum beta-lactamase-encoding genes. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Estimated frequency of reads (estFreqReads). Estimated frequency of reads in a sequencing assay Status: active. First released: 2.0.0. Last updated: 2.0.0.

Enterotoxigenic Escherichia coli (ETEC) (etec). Enterotoxigenic Escherichia coli (ETEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 exoN gene (nsp14) (exoNnsp14). SARS-CoV-2 exoN gene (nsp14) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Extraintestinal pathogenic Escherichia coli (ExPEC) (expec). Extraintestinal pathogenic Escherichia coli (ExPEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Extraction Recovery Percent (extractRecov). The percentage of spiked in or endogenous compound used to assess extraction recovery of nucleic acids. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Extraction volume of sample (exvol). Extraction volume of sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

F456L Mutation (f456l). The FLiRT/SLip variant mutation F456L. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Male-specific (F+) coliphage - general (fColiphage). Male-specific (F+) coliphage - general Status: active. First released: 2.2.0. Last updated: 2.2.0.

F+ DNA coliphage (fDNA). F+ DNA coliphage Status: active. First released: 2.2.0. Last updated: 2.2.0.

Fecal coliform count (fecalCol). Measure of prevalence of fecal coliform bacteria Status: active. First released: 3.0.0. Last updated: 3.0.0.

Final volume (finVol). The final volume of a testing solution or sample. Status: active. First released: 2.2.0. Last updated: 2.2.0.

FLiRT Variants (flirtV). FLiRT is the name given to an entire family of COVID-19 subvariants that are gaining dominance. They've evolved from the JN.1 subvariant. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Flow rate (floRate). Wastewater volumetric flow rate at the sample collection location over the 24-hr period during which the sample was collected. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Flow volume (flowVol). Volume of influent. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Influenza virus measure (flu). General influenza virus measure Status: active. First released: 2.0.0. Last updated: 2.0.0.

Influenza A virus (fluA). Influenza A virus. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Influenza virus A1 (fluA1). Influenza virus A1 type Status: active. First released: 2.0.0. Last updated: 2.0.0.

Influenza virus A1 and A2 combined (fluA1A2c). Measure of influenza virus A1 and A2 combined, usually due to single fluorescence channel. Status: active. First released: 2.0.0. Last updated: 2.0.0.

influenza virus A2 (fluA2). influenza virus A2 type Status: active. First released: 2.0.0. Last updated: 2.0.0.

Influenza virus B (fluB). Influenza virus B type Status: active. First released: 2.0.0. Last updated: 2.0.0.

Influenza A H5 hemagglutinin gene (fluH5hema). Measure of the H5 hemagglutinin gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Influenza A M gene (fluIAVm). A measure of the M gene found in Influenza A viruses (IAV). The virus has segmented RNA genome and 7th segment, M gene, encodes 2 proteins. M1 is a matrix protein and M2 is a membrane protein. The M gene may be involved in determining host tropism. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Influenza A N1 neuraminidase gene (fluN1neur). Measure of the N1 neuraminidase gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. Status: active. First released: 2.2.0. Last updated: 2.2.0.

F-Specific RNA bacteriophages (fRNABact). A measure for amount of F-Specific RNA bacteriophages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

F+ RNA coliphage (fRNAColi). F+ RNA coliphage Status: active. First released: 2.2.0. Last updated: 2.2.0.

F-Specific RNA bacteriophages, G2 (frnaG2). A measure for amount of G2 F-Specific RNA bacteriophages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Field sample temperature (fst). Temperature that the sample is stored at while it is being sampled. This field is mainly relevant for composite samples which are either kept at ambient temperature or refrigerated while being sampled. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Francisella tularensis (fTularensis). Francisella tularensis Status: active. First released: 2.2.0. Last updated: 2.2.0.

g215c delta-variant gene target (g215c). g215c delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

g339d omicron-variant gene target (g339d). g339d omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

g496s omicron-variant gene target (g496s). g496s omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

g662s delta-variant gene target (g662s). g662s delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gamma (gam). P.1 Status: active. First released: 2.0.0. Last updated: 2.0.0.

genome completeness (genComplete). The percentage of expected genes identified in the genome being sequenced. Missing genes indicate missing genomic regions (incompleteness) in the data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

H5N1 avian influenza A virus (IAV) (h5n1). General measurement for the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Haemophilus ducreyi (hDucreyi). Haemophilus ducreyi Status: active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 hel gene (nsp13) (hel). SARS-CoV-2 hel gene (nsp13) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hepatitis A (hepA). Hepatitis A Status: active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis B (hepB). Hepatitis B Status: active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis C (hepC). Hepatitis C Status: active. First released: 2.2.0. Last updated: 2.2.0.

Hepatitis E (hepE). Hepatitis E Status: active. First released: 2.2.0. Last updated: 2.2.0.

hep g armored rna (hepGRna). Measure of the amount Hepatitis G Armored RNA. Status: active. First released: 2.0.0. Last updated: 2.0.0.

HF183 Bacteriodes 16S (hf183). Human-Specific HF183 Bacteriodes 16S rRNA Status: active. First released: 2.2.0. Last updated: 2.2.0.

5-hydroxyindoleacetic acid (5-HIAA) (hiaa5). A serotonin metaboliteused for normalizing wastewater surveillance signal. Analysis of 5-HIAA is done in clinical settings to assess the possibility of carcinoid syndorme in patients, and used in wastewater analysis to estimate human population numbers. Studies have shown that 5-HIAA can be quanitified in samples from WWTPs, and that measured quantities of this molecule have a positive correlation with the population calculated using hydrochemical parameters, and are also correlated well with the census population measures. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Haemophilus influenzae (hInfluenzae). Haemophilus influenzae Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Immunodeficiency Virus (HIV) (hiv). Human Immunodeficiency Virus (HIV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

See Header for Measure (hMe). An indicator to show in a wide-name that measure information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Metapneumovirus (HMPV) (hmpv). Human Metapneumovirus (HMPV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Parainfluenza Virus (HPIV) (hpiv). Human Parainfluenza Virus (HPIV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Papiloma Virus (HPV) (hpv). Human Papiloma Virus (HPV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) (hrv). Human Rhinovirus (HRV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) A (hrvA). Human Rhinovirus (HRV) A Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) B (hrvB). Human Rhinovirus (HRV) B Status: active. First released: 2.2.0. Last updated: 2.2.0.

Human Rhinovirus (HRV) C (hrvC). Human Rhinovirus (HRV) C Status: active. First released: 2.2.0. Last updated: 2.2.0.

Herpes Simplex Virus (hsv). Herpes Simplex Virus Status: active. First released: 2.2.0. Last updated: 2.2.0.

i1566v omicron-variant gene target (i1566v). i1566v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

i3758v omicron-variant gene target (i3758v). i3758v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

i82t delta-variant gene target (i82t). i82t delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ibuprofen (ibu). Ibuprofen (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Industrial input (indusIn). Percentage of total wastewater input coming from industrial sources. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Influent equilibration (influEqui). Binary indicator for whether a site stores influent wastewater prior to treatment to equilibrate flow rates. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Inhibition measure (inhibMe). Parameter to report whether or not inhibition was detected in the sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Omicron Variant ins214epe Insertion (ins214epe). Omicron Variant ins214epe Insertion mutation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Integrase Class I gene target (integraseCl1). Integrase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Combined ip2 and ip4 sars-cov-2 gene target (ip2ip4). Combined ip2 and ip4 sars-cov-2 gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

JN.1.7 Variant (jn17V). The JN.1.7 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

JN.1 Variant (jn1V). The JN.1 variant is a subvariant of Omicron variant BA.2.86, and contains several mutations that are associated with escape from vaccine-mediated immune protection. The source of the FLiRT variants of SARS-CoV-2. Status: active. First released: 2.0.0. Last updated: 2.0.0.

k856r omicron-variant gene target (k856r). k856r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Klebsiella pneumoniae (klebsiellaPneu). Klebsiella pneumoniae Status: active. First released: 2.2.0. Last updated: 2.2.0.

KP.1.1 Variant (kp11V). The KP.1.1 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

KP.1 Variant (kp1V). The KP.1 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

KP.2 Variant (kp2V). The KP.2 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

KP.3.1.1 Variant (kp311V). The KP.3.1.1 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

KP.3 Variant (kp3V). The KP.3 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Omicron Variant l24s mutation (l24s). Omicron Variant l24s mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

l452r delta-variant gene target (l452r). l452r delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

L455S Mutation (l455s). The FLiRT/SLip variant mutation L455S. Status: active. First released: 2.2.0. Last updated: 2.2.0.

l981f omicron-variant gene target (l981f). l981f omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Lachnospiraceae (Lachno3) (lachno3). Human-associated bacteria in the family Lachnospiraceae (Lachno3), often used as microbial source

tracking markers for human fecal pollution tracking in environmental waters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lambda (lamba). C.37 Status: active. First released: 2.0.0. Last updated: 2.0.0.

LB.1 Variant (lb1V). The LB.1 variant of SARS-CoV-2,similar to other FLiRT variants but with an additional mutation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Legionella (legionella). Legionella Status: active. First released: 2.2.0. Last updated: 2.2.0.

Listeria (listeria). Listeria Status: active. First released: 2.2.0. Last updated: 2.2.0.

Limit of Blank (LOB) (lob). The highest concentration of a target analyte (DNA or RNA) that can be expected in a blank sample (a sample with no target DNA/RNA) while still considering the sample as negative. Defines the upper limit of "noise" or background signal that should not be confused with a true positive. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Limit of detection (LOD) (lod). Limit of detection, ie. the minimum level of a genetic target. Status: active. First released: 1.1.0. Last updated: 3.0.0.

Limit of detection (LOD) - sewage (lodSewa). Limit of detection, ie. the minimum level of a genetic target, for sewage samples. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Limit of quantification (LOQ) (loq). Sample limit of quantification (LOQ) is defined as "the concentration of a target that can be quantified with an acceptable level of precision when present in a sample" (Ahmed et al., 2021). Status: active. First released: 1.1.0. Last updated: 3.0.0.

LP.8.1 Variant (lp81V). The LP.8.1 variant of SARS-CoV-2, a Omicron subvariant of JN.1, and FLiRT variant. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Omicron Variant LPPA24S mutation (lppa24s). Omicron Variant LPPA24S mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample Material Characteristics (matChar). A site measurement for describing the qualitative characteristics of the sample material in situ (ie. The material from which the sample is collected. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Concentration Factor (mCF). Concentration Factor (CF) is the degree to which the concentration observed in the final qPCR assay volume has been magnified compared to concentration of the analyte in the original sample (see Box 2.1 Protocol). Status: active. First released: 3.0.0. Last updated: 3.0.0.

MCR-1.1 Colistin-resistence gene target (mcr11). The MCR-1.1 colistin anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Measles (measles). Measles Status: active. First released: 2.2.0. Last updated: 2.2.0.

Other Measure (measOth). Other measure, not otherwise specified in measures. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Other Measure Description (meOthDe). Description of other measure (measOtherDesc). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Effective Sample Size/Volume (mESV). Effective Sample Size/Volume (ESV) is the amount of the original sample size/volume that was actually analyzed in a qPCR reaction (see Box 2.1 Protocol) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mycoplasma genitalus (mGenitalus). Mycoplasma genitalus Status: active. First released: 2.2.0. Last updated: 2.2.0.

Murine Hepatitis Virus (mhv). A measure for amount of murine hepatitis viurs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

minimum post-trimming read length (minPTLength). The threshold used as a cut-off for the minimum length of a read after trimming. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Method Limit of Detection (LOD) (mlod). The minimum level of a target necessary for its consistent detection considering all sample processing steps as in the definition of SLOD), but considering biases attributable to method losses. The MLOD is experimentally determined using a rigorous and iterative testing approach and it is sensitive to the recovery surrogate used and the sample matrix encountered. Status: active. First released: 2.2.0. Last updated: 3.0.0.

Mpox (mpox). The virus known as Mpox, previously also known as Monkey Pox. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Mpox B6R Gene Target (mpxB6R). Human MPox Virus (hMPXV) gene target. Envelope protien gene CDC Assay; selective for MPXV. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Clade I Mpox C3L Gene Target (mpxC3L). Human MPox Virus (hMPXV) Clade I gene target. hMPXV C3L primers and probe detect Clade I viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mpox Clade I (mpxClI). The virus known as Mpox, previously also known as Monkey Pox, Clade I virus type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mpox Clade II (mpxClII). The virus known as Mpox, previously also known as Monkey Pox, Clade II virus type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mpox & Orthopox E9L-NVAR Gene Target (mpxe9lNVAR). Human MPox Virus (hMPXV) gene target for Orthopoxvirus DNA polymerase. CDC Assay detects all hMPXV clades and non-variola Orthopox viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mpox & Orthopox E9L-OPX3 Gene Target (mpxe9lOPX3). Human MPox Virus (hMPXV) gene target using the generic orthopox virus OPX3. Lower sensitivity for MPox. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mpox Clade I F3L Gene Target (mpxF3L). Human MPox Virus (hMPXV) Clade I gene target, F3L Status: active. First released: 2.3.0. Last updated: 2.3.0.

Mpox G2R-G Gene Target (mpxG2RG). Human MPox Virus (hMPXV) gene target using the G2R_G primers and probe which detects all MPox Virus strains . Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mpox G2R-NML Gene Target (mpxG2RNML). Human MPox Virus (hMPXV) gene target using the G2R_NML primers and probe which detects all MPox Virus strains . Status: active. First released: 2.3.0. Last updated: 2.3.0.

Clade II Mpox G2R-WA Gene Target (mpxG2RWA). Human MPox Virus (hMPXV) Clade II gene target, measured with G2R_WA primers and probe to detects Clade II viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mpox GT Molecular Gene Target (mpxGTmol). Human MPox Virus (hMPXV) gene target - this specific measure and gene target are proprietary to GT Molecular Status: active. First released: 2.2.0. Last updated: 2.2.0.

Methicillin-resistant Staphylococcus aureus (MRSA) (mrsa). Methicillin-resistant Staphylococcus aureus (MRSA) Status: active. First released: 2.2.0. Last updated: 2.2.0.

ms2 coliphage (ms2Col). Measure of the amount of ms2 coliphage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Mycobacterium tuberculosis (mTuberculosis). Mycobacterium tuberculosis Status: active. First released: 2.2.0. Last updated: 2.2.0.

Mu (mu). B.1.621 Status: active. First released: 2.0.0. Last updated: 2.0.0.

murine coronavirus (muCo). Measure of the amount of murine coronavirus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Mumps (mumps). Mumps Status: active. First released: 2.2.0. Last updated: 2.2.0.

N sars-cov-2 gene target (n). N sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Combined N1 and N2 sars-cov-2 gene target (n1n2). Combined N1 and N2 sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron Variant n211i mutation (n211i). Omicron Variant n211i mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

N50 (n50). The length of the shortest read that, together with other reads, represents at least 50% of the nucleotides in a set of sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Omicron Variant n679k mutation (n679k). Omicron Variant n679k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant n856k mutation (n856k). Omicron Variant n856k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant n969k mutation (n969k). Omicron Variant n969k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NB.1.8.1 variant (Nimbus) (nb181V). The Nimbus variant of SARS-CoV-2 (NB.1.8.1), descendant of the recombinant variant XDV.1.5.1. Status: active. First released: 3.0.0. Last updated: 3.0.0.

number of base-pairs sequenced (nBPSeq). The number of total base pairs generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

number of contigs (nContig). The number of contigs (contiguous sequences) in a sequence assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Neisseria gonorrhoeae (nGonorrhoeae). Neisseria gonorrhoeae Status: active. First released: 2.2.0. Last updated: 2.2.0.

Ammonia and Ammonium as Nitrogen (nh3nh4). Ammonia and Ammonium combined concentration, as Nitrogen Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ammonium Nitrogen (nH4N). Ammonium nitrogen concentration, as N. Status: active. First released: 1.0.0. Last updated: 2.0.0.

niid_2019-ncov_n sars-cov-2 gene target (niid19). niid_2019-ncov_n sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Norovirus (noro). Norovirus. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Norovirus G1 (noroG1). Norovirus genogroup 1 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Norovirus G2 (noroG2). Norovirus genogroup 2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sarbecovirus-specific N sars-cov-2 gene target (nSarbec). Sarbecovirus-specific N sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 nsp1 Gene target (nsp1). SARS-CoV-2 nsp1 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp10 Gene target (nsp10). SARS-CoV-2 nsp10 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp11 Gene target (nsp11). SARS-CoV-2 nsp11 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp15 Gene target (nsp15). SARS-CoV-2 nsp15 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp16 Gene target (nsp16). SARS-CoV-2 nsp16 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp2 Gene target (nsp2). SARS-CoV-2 nsp2 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp3 Gene target (nsp3). SARS-CoV-2 nsp3 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp4 Gene target (nsp4). SARS-CoV-2 nsp4 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp5 Gene target (nsp5). SARS-CoV-2 nsp5 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp6 Gene target (nsp6). SARS-CoV-2 nsp6 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp7 Gene target (nsp7). SARS-CoV-2 nsp7 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp8 Gene target (nsp8). SARS-CoV-2 nsp8 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 nsp9 Gene target (nsp9). SARS-CoV-2 nsp9 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

number of total reads (nTotRead). The total number of non-unique reads generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Number of NTCs per Run (numNTC). The number of no-template controls included in each PCR instrument run. Status: active. First released: 2.2.0. Last updated: 2.2.0.

number of unique reads (nUniRead). The number of unique reads generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

coronavirus OC43 (oc43). Measure of the amount of coronavirus OC43. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.1 (omicr1). Omicron B.1.1.529 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.2 (omicr2). Omicron BA.2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.2.75 (omicr275). Omicron BA.2.75 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.4 (omicr4). Omicron BA.4 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Omicron BA.5 (omicr5). Omicron BA.5 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Orthophosphates (ophos). Ortho-phosphate concentration. Status: active. First released: 1.0.0. Last updated: 2.0.0.

SARS-CoV-2 orf10 Gene target (orf10). SARS-CoV-2 orf10 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf14 Gene target (orf14). SARS-CoV-2 orf14 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

ORF1a sars-cov-2 gene target (orf1a). ORF1a sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

ORF1ab sars-cov-2 gene target (orf1ab). ORF1ab sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

ORF1b sars-cov-2 gene target (orf1b). ORF1b sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

SARS-CoV-2 orf3a Gene target (orf3a). SARS-CoV-2 orf3a Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf3b Gene target (orf3b). SARS-CoV-2 orf3b Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf6 (ns6) Gene target (orf6). SARS-CoV-2 orf6 (ns6) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf7a Gene target (orf7a). SARS-CoV-2 orf7a Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf7b (ns7b) Gene target (orf7b). SARS-CoV-2 orf7b (ns7b) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf8 (ns8) Gene target (orf8). SARS-CoV-2 orf8 (ns8) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf9b Gene target (orf9b). SARS-CoV-2 orf9b Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

SARS-CoV-2 orf9c Gene target (orf9c). SARS-CoV-2 orf9c Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

Oxidation reduction potential (ORP) (orp). Oxidation-reduction potential (ORP) measures the ability of a lake or river to cleanse itself or

break down waste products, such as contaminants and dead plants and animals. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Variants Other (otherV). Used for reporting variants detected for which a specific measureID doesn't already exist. The ODM team will periodically migrate collected responses in this category into set measureIDs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Delta Variant p100l mutation (p100l). Delta Variant p100l mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant p13l mutation (p13L). Omicron Variant p13l mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

Delta Variant p2046l mutation (p2046l). Delta Variant p2046l mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Delta Variant p2287s mutation (p2287s). Delta Variant p2287s mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Omicron Variant p3395h mutation (p3395h). Omicron Variant p3395h mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Delta Variant p681r (p681r). Delta Variant p681r mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Paraxanthine (PARA) (para). A metabolite of the common central nervous system stimulant caffeine, measred levels of paraxanthine have been found to be less affected by the genetic heterogeneity and population structure than caffeine is, and it may serve as a useful population biomarker in wastewater. Status: active. First released: 2.2.0. Last updated: 2.2.0.

percent read contamination (percContam). The percent of the total number of reads identified as contamination (not belonging to the target organism) in a sequence dataset. Status: active. First released: 3.0.0. Last updated: 3.0.0.

percent Ns across total genome length (percNLength). The percentage of the assembly that consists of ambiguous bases (Ns). Status: active. First released: 3.0.0. Last updated: 3.0.0.

pH (ph). pH measurement Status: active. First released: 1.1.0. Last updated: 2.0.0.

Phagetyping Results (phagetype). The phagetyping results from an organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Pseudomonas virus phi6 (phi6). Measure of the amount of pseudomonas virus phi6. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Total phosphorous (phos). Total phosphorous Status: active. First released: 1.1.0. Last updated: 2.0.0.

Total Phosphates (phostot). Total phosphates Status: active. First released: 1.1.0. Last updated: 2.0.0.

PHRED quality score (phred). PHRED Quality Score For Sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Plasmodium (plasmodium). Plasmodium Status: active. First released: 2.2.0. Last updated: 2.2.0.

Polygon Population (polyPop). An attribute of a polygon, which specifies the population of that polygon. A rough estimate of the number of human residents. Status: active. First released: 2.0.0. Last updated: 2.3.0.

Populated area type (popAreaType). Type of populated area being sample (ie. urban, rural) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population density (popDensity). Measure of population density of a site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population Served (popServ). An measure of a site, which specifies the population of/population served by a given site. Status: active. First released: 2.0.0. Last updated: 2.3.0.

Population Served - Interval (popServRange). Population served by a site, when reported as an interval. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PMMoV-CP (ppmv). Pepper mild mottle virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

Precipitation - general (precip). General measure of precipitation, type not specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Storage temperature prior to concentration (preConcTemp). The temperature at which a sample was stored between collection and concentration. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Storage time prior to concentration (preConcTime). Length of time for which a sample is stored between collection and concentration. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Storage temperature prior to extraction (preExtractTemp). The temperature at which a sample was stored between concentration and extraction. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Storage time prior to extraction (preExtractTime). Length of time for which a sample is stored between concentration and extraction. Status: active. First released: 2.2.0. Last updated: 2.2.0.

presampling activity (presampAct). A measure for recording any relevant activities that occur upstream of the sampling source. For example, recording that the river one is sampling from flows through farmland, or that filtration and/or sedimentation occurred at the wastewater treatment plant before the sample was collected. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Pre-sampling weather (preSampWeath). Weather leading up to, but not including, the day of sampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Pretreatment (pretreat). Was the sample chemically treated in anyway with the addition of stabilizers or other Status: active. First released: 1.0.0. Last updated: 2.0.0.

Pseudomonas (pseudomonas). Pseudomonas Status: active. First released: 2.2.0. Last updated: 2.2.0.

Puro virus (puro). Measure of the amount of puro virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Poliovirus type 2 (pv2). Poliovirus type 2 Status: active. First released: 2.2.0. Last updated: 2.2.0.

q19e omicron-variant gene target (q19e). q19e omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

q493r omicron-variant gene target (q493r). q493r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

q498r omicron-variant gene target (q498r). q498r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

q954h omicron-variant gene target (q954h). q954h omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

r203m delta-variant gene target (r203m). r203m delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

R346T Mutation (r346t). The FLiRT/SLip variant mutation R346T. Status: active. First released: 2.2.0. Last updated: 2.2.0.

dPCR Rain Percentage (rainPerc). The percentage of droplets tha fall between the major positive and negative population in digital droplet PCR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

IP2 rdrp sars-cov-2 gene target (rdrpIP2). IP2 rdrp sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

IP4 rdrp sars-cov-2 gene target (rdrpIP4). IP4 rdrp sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Recombinant Lineage Variant (recomb). A catch-all measure for viruses of non-specified and recombinant lineages, defined as those virsues wherein viruses of two different parent strains coinfect the same host cell and interact during replication to generate virus progeny that have some genes from both parents. Recombination generally occurs between members of the same virus type (e.g., between two influenza viruses or between two herpes simplex viruses). This is particularly common in the evolution of coronaviruses and sarbecoviruses. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Relative humidity (relHum). The unit of relative humidity, or the air-water mixture. The ratio of the partial pressure of water vapor in the mixture to the equilibrium vapor pressure of water over a flat surface. of pure water at a given temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

replicate number (repNum). The replicate number for a Ct or Cq value - used for specifying out a protocol standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Rickettsia (rickettsia). Rickettsia Status: active. First released: 2.2.0. Last updated: 2.2.0.

Ribonuclease P (RNase P) (rnaseP). Ribonuclease P (RNase P) (usually measured as a human fecal indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Rotavirus (rotavirus). Rotavirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

Respiratory syncytial virus A and B combined (rsvAB). Human Respiratory Syncytial Virus Type A (RSV A) and Type B (RSV B). Status: active. First released: 2.1.0. Last updated: 2.1.3.

Respiratory syncytial virus A (rsvAMe). Human Respiratory Syncytial Virus Type A (RSV A). Status: active. First released: 2.1.0. Last updated: 2.1.3.

Respiratory syncytial virus B (rsvB). Human Respiratory Syncytial Virus Type B (RSV B). Status: active. First released: 2.1.0. Last updated: 2.1.3.

Respiratory syncytial virus (rsvMe). Human Respiratory Syncytial virus (RSV), generic measure. Status: active. First released: 2.0.0. Last updated: 2.1.2.

RSV N-gene (rsvN). Human Respiratory syncytial Virus, N-gene region. Status: active. First released: 2.1.3. Last updated: 2.1.3.

Rubella (rubella). Rubella Status: active. First released: 2.2.0. Last updated: 2.2.0.

s2083i omicron-variant gene target (s2083i). s2083i omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

s371l omicron-variant gene target (s371l). s371l omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

s373p omicron-variant gene target (s373p). s373p omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

s375f omicron-variant gene target (s375f). s375f omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

s477n omicron-variant gene target (s477n). s477n omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Salinity (salinity). Measurement of salinity/salt content Status: active. First released: 3.0.0. Last updated: 3.0.0.

Salmonella (salmonella). Salmonella Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample volume (samVol). The volume of a given sample. Status: active. First released: 2.2.0. Last updated: 3.0.0.

Sapovirus (sapovirus). Sapovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

Standard curve frequency (scf). A measurment for specifying the frequecy over which a standard curve (or 'Master Curve') is used. Status: active. First released: 2.0.0. Last updated: 3.0.1.

sequence assembly length (seqAssLen). The length of the genome generated by assembling reads using a scaffold or by reference-based mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Serological Variant (Serovar) (serovar). The serovar of the organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Settled solids (settsol). Amount of settled solids from a wastewater sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sewage equivalent (sewEq). Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sewage travel time (sewTrTi). A measure of sewage travel time, often approximate, from sewage source to the sampling site. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Shaker aggitation speed (shaker). The speed/aggitation level for a shaker plate/shaker platform. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Shigella (shigella). Shigella Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample Limit of Detection (LOD) (slod). The minimum level of a target within a sample that would be consistently detectable considering all sample processing steps, from sample concentration leading up to and including amplification and quantification steps of RT-qPCR. In this Protocol, the SLOD is the concentration factor-adjusted ALOD, which provides a theoretical estimate of the minimum concentration in the original sample that would yield consistent detection of the target, assuming no method losses. Status: active. First released: 2.2.0. Last updated: 3.0.0.

Specific humidity (specHum). Measure for specific humidity, the unit is the ratio of the mass of water vapour and the mass of total air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Spike Concentration (spikeConc). Concentration of the recovery efficiency target in a spike matrix and recovery assay. Status: active. First released: 2.2.0. Last updated: 2.2.0.

SARS-CoV-2 Spike gene (orf2) (spikeGene). SARS-CoV-2 Spike gene (orf2) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Shiga-toxin-producing Escheria coli (STEC) (stec). Shiga-toxin-producing Escheria coli (STEC). Status: active. First released: 2.1.0. Last updated: 2.1.0.

Storage temp (sTemp). Temperature that the sample is stored at in Celsius. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Strain ID (strainID). The strain identifier for a given organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Stercobilin (stercobilin). Stercobilin is a tetrapyrrolic bile pigment and is one end-product of heme catabolism. It is the chemical responsible for the brown color of human feces and was originally isolated from feces in 1932. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Storage time (stoTim). Length of time that a sample was in storage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Streptococcus pneumoniae (strepPneu). Streptococcus pneumoniae Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sub-variant or lineage (subVar). A unit used to report a specific genetic lineage, or to specify that a reported variant is a sub-variant of another. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sucralose (suc). Sucralose (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Surveillance Level (survLevel). The scale or level of surveillance being done at a site. Ie. Is it institutional, is it only for a single building, or is it for a whol municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

t19r delta-variant gene target (t19r). t19r delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

t3646a delta-variant gene target (t3646a). t3646a delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

t547k omicron-variant gene target (t547k). t547k omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

t9i omicron-variant gene target (t9i). t9i omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

TaqPath N sars-cov-2 gene target (taqpatN). TaqPath N sars-cov-2 mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

TaqPath S sars-cov-2 gene target (taqpatS). TaqPath N sars-cov-2 mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Total Dissolved Solids (TDS) (tds). Total dissolved solids Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sample temperature (temp). Temperature of the sample measured in degrees Celcius Status: active. First released: 1.0.0. Last updated: 2.0.0.

Nucleic acid template volume (tempVol). The volume of DNA or RNA template used for PCR. Status: active. First released: 2.0.0. Last updated: 2.0.0.

TetW Tetracycline-resistance gene target (tetW). The tetW tetracycline anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Total Kjeldahl Nitrogen (tkn). A measure of Total Kjeldahl Nitrogen; ie. the sum of nitrogen bound in organic substances, nitrogen in ammonia (NH3-N) and in ammonium (NH4+-N) in the chemical analysis of soil, water, or waste water. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Total Nitrogen (tn). Total nitrogen concentration, as N. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Treponema pallidum (tPallidum). Treponema pallidum Status: active. First released: 2.2.0. Last updated: 2.2.0.

Total solids concentration (ts). Total solids concentration Status: active. First released: 1.0.0. Last updated: 2.0.0.

Total suspended solids (tss). Total suspended solids Status: active. First released: 1.0.0. Last updated: 2.0.0.

Concentration of total suspended solids (tssConc). Total suspended solids concentration of the wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Turbidity (turb). A measure for the turbidity of water, or a liquid sample, quanitfying the relative clarity or opcaity of a liquid. Highly indicative of water quality. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Trichomonas vaginalis (tVaginalis). Trichomonas vaginalis Status: active. First released: 2.2.0. Last updated: 2.2.0.

Tube weight empty (tWeighE). The weight of the tube used for analysis while empty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Tube weight full (tWeighF). The weight of the tube used for analysis while full of analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ureaplasma (ureaplasma). Ureaplasma Status: active. First released: 2.2.0. Last updated: 2.2.0.

Urobilin or urochrome (urobilin). Urobilin or urochrome is the chemical primarily responsible for the yellow color of urine. It is a linear tetrapyrrole compound that, along with the related colorless compound urobilinogen, are degradation products of the cyclic tetrapyrrole heme. Status: active. First released: 2.2.0. Last updated: 2.2.0.

V1104L Mutation (v1104l). The FLiRT/SLip variant mutation V1104L Status: active. First released: 2.2.0. Last updated: 2.2.0.

v2930l delta-variant gene target (v2930l). v2930l delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

VanA-A Vancomycin-resistance gene target (vanAA). The VanA-A vancomycin anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Vancomycin resistance (vanc). Vancomycin resistant bacteria. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Varicella (varicella). Varicella Status: active. First released: 2.2.0. Last updated: 2.2.0.

Vibrio (vibrio). Vibrio Status: active. First released: 2.2.0. Last updated: 2.2.0.

Size in volume (vol). Total volume of water or sludge sampled. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Volatile suspended solids (vss). Volatile suspended solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Volatile suspended solids - ignition (vssIg). A water quality measure, captured by via the loss on ignition of the mass of measured total suspended solids. This ignition generally takes place in an oven at a temperature of 550 °C to 600 °C. It represents the amount of volatile matter present in the solid fraction of the measured solution. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Verotoxin-producing Escherichia coli (VTEC) (vtec). Verotoxin-producing Escherichia coli (VTEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Wastewater temperature (watTemp). Temperature of the wastewater. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Weather (time of sampling) (weath). A measure for weather captured through qualitative categories; part of a larger suite of weather measures that may be useful when collecting samples from outdoor sources. Status: active. First released: 2.0.0. Last updated: 2.0.0.

West Nile (westNile). West Nile Status: active. First released: 2.2.0. Last updated: 2.2.0.

Wind Speed (wind). A measure for wind speed; part of a larger suite of weather measures that may be useful when collecting samples from outdoor sources. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Delta Variant wt214 gene target (wt214). Delta Variant wt214 gene target Status: active. First released: 2.2.0. Last updated: 2.2.0.

Wastewater treatment plant designed capacity (wwtpCap). A measure for the designed capacity of a wastewater treatment plant, in terms of how much water it was designed to be able to hold and process. Status: active. First released: 1.0.0. Last updated: 2.0.0.

XEC Variant (xecV). The XEC variant of SARS-CoV-2, a subvariant of the Omicron strain. Status: active. First released: 3.0.0. Last updated: 3.0.0.

y505h omicron-variant gene target (y505h). y505h omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Yersinia enterocolitica (yEnterocolitica). Yersinia enterocolitica Status: active. First released: 2.2.0. Last updated: 2.2.0.

Zika (zika). Zika Status: active. First released: 2.2.0. Last updated: 2.2.0.

Andes virus (ANDV) hantavirus (andv). Andes virus (ANDV) is the most common cause of hantavirus pulmonary syndrome (HPS) in South America. Andes virus is transmitted mainly by the long-tailed pygmy rice rat. Orthohantavirus andesense. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Ebola virus, Orthoebolavirus zairense (ebolaV). Orthoebolavirus zairense or Zaire ebolavirus, more commonly known as Ebola virus, is one of six known species within the genus Ebolavirus. Four of the six known ebolaviruses, including EBOV, cause a severe and often fatal hemorrhagic fever in humans and other mammals, known as Ebola virus disease (EVD). Status: active. First released: 3.0.1. Last updated: 3.0.1.

Sudan virus, Orthoebolavirus sudanense (sudanV). Sudan virus (species Orthoebolavirus sudanense) causes Sudan virus disease. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Taï Forest virus, Orthoebolavirus taiense (taiforestV). Orthoebolavirus taiense (formerly Taï Forest ebolavirus) is a rare viral species that causes Taï Forest virus disease in humans. It is one of four orthoebolaviruses known to cause illness in people, with only one confirmed human infection ever recorded. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Bundibugyo virus, Orthoebolavirus bundibugyoense (bundibugyoV). The species Bundibugyo ebolavirus is the taxonomic home of one virus, Bundibugyo virus (BDBV), that forms filamentous virions and is closely related to the Zaire ebolaviruses (EBOV). The virus is one of several that can cause Ebola disease in humans, taking the form of viral hemorrhagic fever. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Ebola Virus Disease (EVD) (EVD). Ebola, also known as Ebola virus disease (EVD) and Ebola hemorrhagic fever (EHF), is a zoonotic viral hemorrhagic fever in humans and other primates, caused by four of the six known ebolaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Hantavirus hemorrhagic fever with renal syndrome (HFRS) (hfrs). Hantavirus hemorrhagic fever with renal syndrome (HFRS) is a hemorrhagic fever caused by hantavirus infection. Symptoms usually occur 2 weeks after exposure to the hantavirus and come in five distinct clinical stages: febrile (toxic), hypotensive, low urine production (oliguric), high urine production (diuretic), and recovery. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Hantavirus pulmonary syndrome (HPS) (hps). Hantavirus pulmonary syndrome (HPS), also called hantavirus cardiopulmonary syndrome (HCPS), is a severe respiratory disease caused by hantavirus infection. The

main features of illness are microvascular leakage and acute respiratory distress syndrome. Symptoms occur anywhere from one to eight weeks after exposure to the virus and come in three distinct phases. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Sin Nombre virus (SNV) hantavirus (snv). Sin Nombre virus (SNV) is the most common cause of hantavirus pulmonary syndrome (HPS) in North America. Sin Nombre virus is transmitted mainly by the western deer mouse (Peromyscus sonoriensis). Status: active. First released: 3.0.1. Last updated: 3.0.1.

Hantaan virus (HTNV) hantavirus (htnv). Hantaan virus (HTNV) is the main cause of hemorrhagic fever with renal syndrome (HFRS) in East Asia. Hantaan virus is transmitted by the striped field mouse (Apodemus agrarius). Status: active. First released: 3.0.1. Last updated: 3.0.1.

Seoul virus (SEOV) hantavirus (seov). Seoul virus (SEOV) is one of the main causes of hemorrhagic fever with renal syndrome (HFRS). Seoul virus is transmitted by the brown rat (Rattus norvegicus) and the black rat (Rattus rattus). Status: active. First released: 3.0.1. Last updated: 3.0.1.

Puumala virus (PUUV) hantavirus (puuv). Puumala virus (PUUV) is the main cause of hemorrhagic fever with renal syndrome (HFRS) in Europe and Russia. Puumala virus is transmitted by the bank vole (Clethrionomys glareolus). Status: active. First released: 3.0.1. Last updated: 3.0.1.

Dobrava-Belgrade virus (DOBV) hantavirus (dobv). Dobrava-Belgrade virus (DOBV) is the main cause of hemorrhagic fever with renal syndrome (HFRS) in southern Europe. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus A (formerly Aichi virus) (aivA). Measures of Aichivirus A, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus B (Bovine kobuvirus) (aivB). Measures of Aichivirus B, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called Bovine kobuvirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus C (Porcine kobuviru) (aivC). Measures of Aichivirus C, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called Porcine kobuvirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus D (kagovirus from black cattles) (aivD). Measures of Aichivirus D, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called kagovirus from black cattle. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus E (Rabbit picornavirus) (aivE). Measures of Aichivirus E, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called Rabbit picornavirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Aichivirus F (Bat kobuvirus) (aivF). Measures of Aichivirus F, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastrorenteritis in human or animal hosts. Also called bat kobuvirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) (hAiV). Viral strain of Aichivirus A known to infect humans, typically of three known genotypes: A, B, or C. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus P1 protein gene (aivP1). A gene target for aichivirus, it is the genomic segment that encodes the structural viral capsid proteins forming the outer shell of the Aichivirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) Genotype A (hAiVGA). Viral strain of Aichivirus A known to infect humans of genotypes A. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) Genotype B (hAiVGB). Viral strain of Aichivirus A known to infect humans of genotypes B. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Aichi virus (AiV) Genotype C (hAiVGC). Viral strain of Aichivirus A known to infect humans of genotypes C. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Bocaparvovirus (bocaparvo). Bocaparvovirus is a genus of viruses in the subfamily Parvovirinae of the virus family Parvoviridae. Humans, cattle, and dogs serve as natural hosts. There are 36 species in this genus. Diseases associated with this genus include, in humans, acute respiratory illness, and in cattle, diarrhea and mild respiratory symptoms. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human bocavirus (HBoV) (hbov). Human bocavirus (HBoV) is the name given to all viruses in the genus Bocaparvovirus of virus family Parvoviridae that are known to infect humans. Some of these viruses cause human disease. HBoV1 is strongly implicated in causing some cases of lower respiratory tract infection, especially in young children, and several of the viruses have been linked to gastroenteritis, although the full clinical role of this emerging infectious disease remains to be elucidated. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Cacipacore virus (Orthoflavivirus cacipacoreense) (cacipacore). Orthoflavivirus cacipacoreense, causitive agent of the rare Cacipacore virus Status: active. First released: 3.0.1. Last updated: 3.0.1.

Porcine Circovirus 1 (PCV-1) (pcv1). Porcine Circoviruses (PCV) are the smallest viruses replicating autonomously in eukaryotic cells. The virions are non-enveloped and spherical with a diameter of 16-18 nm and the covalently closed and single-stranded DNA genomes comprise less than

1800 nucleotides. Porcine circovirus type 1 (PCV1) is not linked with a disease. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Porcine Circovirus 2 (PCV-2) (pcv2). Porcine Circoviruses (PCV) are the smallest viruses replicating autonomously in eukaryotic cells. The virions are non-enveloped and spherical with a diameter of 16-18 nm and the covalently closed and single-stranded DNA genomes comprise less than 1800 nucleotides. Porcine circovirus type 2 (PCV2) is the etiological agent of Postweaning Multisystemic Wasting Syndrome (PMWS), a new emerging and multifactorial disease in swine. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Cosavirus (CosaV) (cosaV). Cosavirus is a genus of viruses in the order Picornavirales, in the family Picornaviridae. Human serve as natural hosts. There are 5 species od enteric viruses in this genus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Deltaretrovirus (deltaretro). Deltaretrovirus is a genus of the Retroviridae family. It consists of exogenous horizontally transmitted viruses found in several groups of mammals. This genus of viruses is known for its propensity to target immune cells and oncogenicity. Infection is usually asymptomatic, but inflammation and cancer can develop over time. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Primate T-lymphotropic virus 1 (priTlym1). Human T-cell lymphotropic virus type 1, Primate T-lymphotropic virus 1, or human T-lymphotropic virus (HTLV-I or HTLV-1), also called the adult T-cell lymphoma virus type 1, is a deltaretrovirus of the human T-lymphotropic virus (HTLV) family. Latin species name: Deltaretrovirus priTlym1. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Primate T-lymphotropic virus 2 (priTlym2). Human T-cell lymphotropic virus 2, or Primate T-lymphotropic virus 2 (HTLV-II or HTLV-2), is a deltaretrovirus of the human T-lymphotropic virus (HTLV) family. Latin species name: Deltaretrovirus priTlym2. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Eastern equine encephalitis virus (EEEV) (eeev). Eastern equine encephalitis virus (EEEV) is defined as a neurotropic alphavirus that causes severe disease in horses, characterized by high mortality rates and pathological lesions in the central nervous system, including inflammation and infiltration of immune cells. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Erythroparvovirus (erythroparvo). Erythroparvovirus is defined as a small DNA virus that belongs to the Parvoviridae family, known for causing various illnesses, including fifth disease, arthritis, and anemia, particularly in immunocompromised individuals. Status: active. First released: 3.0.1. Last updated: 3.0.1.

human parvovirus B19 (B19V) (hParvB19V). Human parvovirus B19 is defined as a nonenveloped, single-stranded DNA virus belonging to the Erythrovirus genus of the Parvoviridae family, which primarily infects humans and can cause a variety of syndromes, including erythema infectiosum, arthropathy, and complications such as aplastic anemia and fetal hydrops. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Giardia duodenalis (gDuodenalis). A protozoan parasite that causes anthroponotic or zoonotic diarrheal disease which can be opportunistic or affect healthy, immunocompetent individuals. Giardia duodenalis is the one commonly described type of Giardia, that is found in mammals including humans. This species complex comprise eight assemblages Status: active. First released: 3.0.1. Last updated: 3.0.1.

Giardia 18S rRNA (g18s). The 18S ribosomal RNA (18S rRNA) gene in Giardia is a primary genetic target used for detecting, identifying, and classifying the microscopic intestinal parasite responsible for giardiasis. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Gammaretrovirus (gammaretro). Gammaretrovirus is a genus in the Retroviridae family. Example species are the murine leukemia virus and the feline leukemia virus. They cause various sarcomas, leukemias and

immune deficiencies in mammals, reptiles and birds. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Lymphocryptovirus (lymphocrypto). Lymphocryptovirus is a genus of viruses in the order Herpesvirales, in the family Orthoherpesviridae, in the subfamily Gammaherpesvirinae. This genus includes the human-infecting Epstein–Barr virus, as well as viruses that infect both Old World monkeys and New World monkeys. Also called gamma-1 herpesviruses, there are nine species in this genus. Diseases associated with this genus include: mononucleosis, Burkitt's lymphoma, and nasopharyngeal carcinoma. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenoviruses (HAdVs) (hadv). Human mastadenoviruses (HAdVs) are non-enveloped, double-stranded icosahedral DNA viruses, approximately 90–100 nm in diameter, with fibre projections on each of the 12 vertices. The genome is approximately 30–35 kilobases in length and encodes more than 30 structural and non-structural proteins. HAdV belongs to the genus Mastadenovirus, one of five genera within the Adenoviridae family. Within Mastadenovirus, seven known groups have been identified (A-G), which can be further classified into 54 serotypes. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group A (hadvA). Group A of the human mastadenovirus genus (HAdV-A). Includes serotypes 12, 18, and 31. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group B (hadvB). Group B of the human mastadenovirus genus (HAdV-B). Includes serotypes 3, and 16. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group C (hadvC). Group C of the human mastadenovirus genus (HAdV-C). Includes serotypes 1, 2, 5, and 6. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group D (hadvD). Group D of the human mastadenovirus genus (HAdV-D). Includes serotypes 8, 17, 19, 23, 36, 51, and 58. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group E (hadvE). Group E of the human mastadenovirus genus (HAdV-E). Includes serotype 4. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human mastadenovirus genotype group F (hadvF). Group F of the human mastadenovirus genus (HAdV-F). Includes serotypes 40 and 41. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Parechovirus (PeV) (hpev). Human parechovirus (HPeV; family Picornaviridae, genus Parechovirus) is a nonenveloped virus with a positive-sense single-stranded RNA genome that infects humans. HPeV strains are currently subdivided into 16 genotypes (i.e., HPeV1 to HPeV16), and HPeV1 and HPeV3 are the genotypes mostly causing gastroenteritis, respiratory syndrome, and febrile illness mainly in young children. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Parechovirus-1 (HPeV1) (hpev1). Human parechovirus (HPeV) of the genotype 1 (HPeV1), capable of causing gastroenteritis, respiratory syndrome, and febrile illness in humans. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Picobirnavirus (picobirna). The single genus of the Picobirnaviridae family, Picobirnavirus, members of which have been identified in the feces of humans, rabbits, and a variety of other species of mammals, reptiles, and birds. Picobirnaviruses have been increasingly recognized with the advent of deep sequencing analysis of fecal specimens from many species of animals, and distinct genetic subgroups are now described. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Polyomavirus (PyV) (pyv). Studies reported human Polyomaviruses (PyV) (mainly strains BK and JC) contaminating water and food. These strains are, respectively, associated with nephropathy and progressive multifocal leukoencephalopathy. Others link them to common respiratory illnesses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

JC Polyomavirus (JCV) (pyvJC). JCPyV, or human polyomavirus JC, is defined a polyomavirus and an etiological agent associated with progressive multifocal leukoencephalopathy, characterized by demyelination in the central nervous system, and has been detected in certain tumors, suggesting a potential but unproven link to cancer development. Status: active. First released: 3.0.1. Last updated: 3.0.1.

BK Polyomavirus (BKV) (pyvBK). BKPyV, or human polyomavirus BK, is defined a polyomavirus and an etiological agent associated with nephropathy. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Roseolovirus (Human Herpesvirus-6) (hhv6). Roseolovirus refers to a group of viruses, including HHV-6A and HHV-6B, that are characterized by their ability to cause various diseases, persist in latency within different cell types, and integrate into the human genome. Their detection does not necessarily indicate causation of disease, highlighting the need for careful interpretation of diagnostic results within clinical contexts. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Herpesvirus-6A (HHV-6A) (hhv6A). HHV-6A is a roseolovirus that has been described as more neurovirulent, and as such is more frequently found in patients with neuroinflammatory diseases such as multiple sclerosis. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Herpesvirus-6B (HHV-6B) (hhv6B). HHV-6B is a roseolovirus and the cause of the common childhood illness exanthema subitum (also known as roseola infantum or sixth disease). It is passed on from child to child. It is uncommon for adults to contract this disease as most people have had it by kindergarten, and once contracted, immunity arises and prevents future reinfection. Additionally, HHV-6B reactivation is common in transplant recipients, which can cause several clinical manifestations such as encephalitis, bone marrow suppression, and pneumonitis. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Salivirus A (Salivirus aklasse) (saliA). Salivirus A (Salivirus aklasse) has been identified in humans and chimpanzees and may cause acute

gastroenteritis in humans, having been detected in 0% to 8.7% of fecal samples collected from gastroenteritis in different human populations. Salivirus is ubiquitous in wastewater of human origin and river water specimens worldwide and represents a potential indicator human RNA virus for monitoring of environmental samples. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus (SAFV) (safv). Saffold virus (SAFV) is an emerging human cardiovirus associated with respiratory and gastrointestinal infection, and, more recently, to symptoms related to the endocrine, cardiovascular, and neurological systems. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 1 (SAFV-1) (safv1). Strain 1 of the saffold virus (SAFV-1). The only strain with global distribution. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 2 (SAFV-2) (safv2). Strain 2 of the saffold virus (SAFV-2) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 3 (SAFV-3) (safv3). Strain 3 of the saffold virus (SAFV-3) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 4 (SAFV-4) (safv4). Strain 4 of the saffold virus (SAFV-4) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 5 (SAFV-5) (safv5). Strain 5 of the saffold virus (SAFV-5) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 6 (SAFV-6) (safv6). Strain 6 of the saffold virus (SAFV-6) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 7 (SAFV-7) (safv7). Strain 7 of the saffold virus (SAFV-7) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Saffold virus 8 (SAFV-8) (safv8). Strain 8 of the saffold virus (SAFV-8) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Tanapox (tanapox). Tanapox (a virus from the genus Yatapoxvirus) was first seen among individuals in the flood plain of the Tana River in Kenya during two epidemics (1957 and 1962) of acute febrile illness accompanied by localized skin lesions. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Torque Teno Virus (ttv). Torque teno virus (TTV) is the type species in the genus Anellovirus. The viruses are small (30–50 nm) and non-enveloped with a circular single-stranded DNA genome that is approximately 3.8 kb in size. More than 90% of adults worldwide are said to be infected with TTV. The viruses have not been conclusively shown to cause disease in humans, although they have been associated with some acute respiratory illnesses in infants. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Human Parechovirus-3 (HPeV3) (hpev3). Human parechovirus (HPeV) of the genotype 3 (HPeV3), capable of causing gastroenteritis, respiratory syndrome, and febrile illness in humans. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Concentration method set

(methodConcSet). A set a concentration methods.

Aloh3 precipitation (aloh3). Aloh3 precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Amicon ultrafiltration (amiconUf). Amicon ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

Beef extract flocculation (beeExtractFloc). Beef extract flocculation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Centricon ultrafiltration (centriconUf). Centricon ultrafiltration. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ceres nanotrap (ceres). Ceres nanotrap. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Hollow fiber dead end ultrafiltration (hollowFiberUF). Hollow fiber dead end ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

Innovaprep ultrafiltration (innovaprepUF). Innovaprep ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polyethyleneglycol (PEG) precipitation (peg). Peg precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Skimmed milk flocculation (skimMilkFloc). Skimmed milk flocculation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ultracentrifugation (untracent). Ultracentrifugation Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with acidification and mgcl2 (mfAcidmgcl2). Membrane filtration with acidification and mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with acidification and mgcl2, membrane recombined with separated solids (mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with addition of mgcl2 (mfMgcl2). Membrane filtration with addition of mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with mgcl2 and separated solids (mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with no amendment (mfNoAmend). Membrane filtration with no amendment Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with no amendment, membrane recombined with separated solids (mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with sample acidification (mfSampleAcid). Membrane filtration with sample acidification Status: active. First released: 2.0.0. Last updated: 2.0.0.

Membrane filtration with sample acidification, membrane recombined with separated solids (mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

No liquid concentration, liquid recombined with separated solids (noliquid). No liquid concentration, liquid recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

No Seperation or Concentration (noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. Status: active. First released: 2.2.0. Last updated: 2.2.0.

promega wastewater large volume tna capture kit (promWW). Nucleic acid extraction performed using the promega wastewater large volume tna capture kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

zymo environ water rna kit (cat. r2042) (zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit (cat. r2042). Status: active. First released: 2.0.0. Last updated: 2.0.0.

membrane filtration with addition of mgcl3 (memMgCl3). membrane filtration with addition of mgcl3 Status: active. First released: 2.2.0. Last updated: 2.2.0.

water concentrating buffer (R2042-1) (watConcBuff). water concentrating buffer (R2042-1) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Flocculation (floc). The process of aggregating suspended particles into larger clusters (flocs) using coagulants to aid in sedimentation or filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Magnetic nanobead binding (magBead). The use of tiny, magnetized beads to selectively capture and isolate biological molecules (e.g., DNA, proteins) in a magnetic field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Precipitation (from solution) (prec). The formation of a solid from a dissolved substance in a solution, typically induced by chemical reactions or changes in temperature/pH. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Methods

(methods). Procedures or steps for collecting samples or performing measures. For example, `methodExtract` is a method that describes the how a sample was extracted. met

AMR Analysis Software (amrSoft). Software use to analyse bacterial genomes and genes for anti-mocrobial resistance (AMR). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bacterial testing method (bactMeth). Description of the bacterial testing/detection method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lineage- or Clade-analysis Software (cladeAn). Software tool or pipeline for determining the clade or lineage of an organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Consensus Sequence Software (conSeqSoft). Software use to run consensus sequence on sequencing analyses. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Deduplication Method (dedup). Sequencing and PCR deduplication method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dehosting Method (dehost). Sequencing and PCR dehosting method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Extraction Blank - Control (extBlank). Binary Y/N indicator for if extraction blank was used as a control for the nucleic acid extraction process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Nucleic acid extraction method (extraction). Description of the nucleic acid extraction method. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Genomic Target Enrichment (gte). The molecular technique used to selectively capture and amplify specific regions of interest from a genome. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Inhibition method (inhibMeth). Description of the method used to evaluate molecular inhibition. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Library Preparation Kit (libraryKit). The name of the DNA/RNA library preparation kit used to generate the library being sequenced. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Concentration method (methodConc). Description of the method to concentrate a wastewater sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Pasteurized sample (pasteur). Binary indicator for whether a sample was pasteurized as part of its processing. Status: active. First released: 2.2.0. Last updated: 2.2.0.

PCR Action/Activity (pcrAct). Describes a given PCR cycle for delineating more method information. Status: active. First released: 2.2.0. Last updated: 2.2.0.

PCR method (pcrmeth). Description of the PCR method. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Population assessment method (popAs). Method for assessing the population count for a site/polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Genetic primer (primer). Method ID used for indicating the primer used for a PCR or sequencing assay. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quaility assurance method (qaqc). Quality assurance and quality control method. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Sequencing Quality Control Method (qcMethod). Method for sequencing quality control or assessment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Raw Sequence Data Processing Method (rawSeqProc). The software/library/pipeline used to process the raw sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing read mapping software name (readMapper). The name of the bioinformatics software tool used to align short DNA or RNA sequence reads (obtained from high-throughput sequencing technologies like Illumina, PacBio, or Oxford Nanopore) to a reference genome or transcriptome. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Resuspension method (resuspension). Describes the method used for resuspending material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Retained Element (retainedElement). The element retained after centrifugation, filtration, solid separation, etc. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Collection other depreciated (sampleTypeOther). Description for other type of method not listed in collection. depreciated. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Genetic sequencing script version (scriptVersion). Used to specify the script or script version used to extract summary information (i.e. coverage and mutation frequency statistics, etc.) from the sequencing output. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Assembly Software (seqAss). The name of the software/toolkit/pipeline used for assembling sequences from reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing Layout (seqLay). The layout of genetic material used in sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing QC Pipeline (seqQC). The quality control pipeline for sequencing or PCR data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing selection method (seqSel). The primer sequence selection method used in sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing Strategy (seqStrat). The sequencing strategy used for an analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Serotyping Method (seroMeth). The method used to determine the serovar. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Shipped on ice (shipOnIce). Was the sample kept cool while being shipped to the lab Status: active. First released: 1.0.0. Last updated: 2.0.0.

Solid seperation (solidSep). Process used to separate solid and liquid phases of the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Spike material (spikeMat). Material into which the recovery efficiency control target is spiked. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Recovery efficiency spike target (spikeTarget). Method specifying the recovery efficiency control target. This matches on to the the spike material method ID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard Curve Calculation Method (stdCurveMet). Describes the specific approach used for calculating a standard curve. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample Storage Medium (stoMed). The medium used to store a sample before final analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nucelic Acid Template Type (tempType). Specifies whether a PCR or sequencing used RNA or DNA as the template for the reaction. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Type other depreciate (tyOtDep). Description for other type of sample not listed in Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Missingness

(missingness). The part type for missingness values. Only used for the dictionary entries of parts.

Data Not Collected (dnc). A missingness value for when when data was not measured or collected; an analysis not run, etc. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Missing data (miss). A general missingness value for missing data, used when data is not included for an unknown reason. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Not applicable (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not a number (nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, …) Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not reported (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Null (NULL). A logical representation of a statement that is neither TRUE nor FALSE. Status: active. First released: 1.0.0. Last updated: 3.0.0.

Restricted data (restrict). Missing data is witheld because it is restricted access. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Undisclosed or Not Provided (undisc). A value has been recorded, however it was not included in the dataset. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Missingness sets

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets.

General missingness set

(genMissingnessSet)The general set for missingness values. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Data Not Collected (dnc). A missingness value for when when data was not measured or collected; an analysis not run, etc. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Missing data (miss). A general missingness value for missing data, used when data is not included for an unknown reason. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Not applicable (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not a number (nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, …) Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not reported (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Null (NULL). A logical representation of a statement that is neither TRUE nor FALSE. Status: active. First released: 1.0.0. Last updated: 3.0.0.

Restricted data (restrict). Missing data is witheld because it is restricted access. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Undisclosed or Not Provided (undisc). A value has been recorded, however it was not included in the dataset. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Geographical Reference Missingness Set

(geoRefMissingnessSet)A missingness set for field populated by the geographical reference tables (countries, zones) Used for fields populated by geographical reference tables to avoid confusion of NA and nr as missingness indicators, vs. legitimate ISO country codes. Status: active. First Released: 3.0.1. Last updated: 3.0.1.

Null (NULL). A logical representation of a statement that is neither TRUE nor FALSE. Status: active. First released: 1.0.0. Last updated: 3.0.0.

Not reported, Not applicable missing set

(nrNAMissingnessSet)Not reported, Not applicable missing set. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Not applicable (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not reported (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Missingness sets

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets.

General missingness set (genMissingnessSet). The general set for missingness values. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Not reported, Not applicable missing set (nrNAMissingnessSet). Not reported, Not applicable missing set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Geographical Reference Missingness Set (geoRefMissingnessSet). A missingness set for field populated by the geographical reference tables (countries, zones) Status: active. First released: 3.0.1. Last updated: 3.0.1.

Measure, method, or attribute sets

(mmaSets). A set of categories. For example, site type has a list of different sites, such as a wastewater treatment plant, a septic tank, or a pumping station. Only used for the dictionary entries of parts.

Public Health Action Type Value Set (actionTypeSet). A set of valid categories for the public health action type field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

All Public Health Actions Set (allActionsSet). A set of all valid categories for public health action, regardless of action type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data Adjustment Standard Value Set (allStandardSet). Set of valid input values for the standard field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Antimicrobial Resistance (AMR) Classification Value Set (amrClassSet). A set of valid categories for the public health action field, where

the action type is 'antimicrobial resistance (AMR) classification'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AMR Software Set (amrSoftSet). The valid set of AMR analysis software categories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bacterial testing method set (bactMethSet). The set capturing containing all of the valid methods for the bacterial testing method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Boolean value set (booleanSet). Set that contains the valid possible values for a boolean measure (TRUE or FALSE). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Calculation type set (calcTypeSet). The set of valid inputs for the calculation type field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lineage- or Clade-analysis Software Set (cladeAnSet). Valid category set for lineage or clade analysis software types. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Collection Approximate Time Period Set (collAppxSet). The category set of valid inputs for the collGenT attribute field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sample collection set (collectSet). Methods for collection samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Consensus Sequence Software Set (conSeqSoftSet). The valid set of consensus sequencing software categories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Control Measure Implementation Value Set (contMeasImpSet). A set of valid categories for the public health action field, where the action type is 'control measure implementation'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data Repository Set (dataRepoSet). The mma set for all valid input categories for the dataRepo field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Deduplication Method Set (dedupSet). The valid set of deduplication method categorical inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Dehosting Method Set (dehostSet). The valid set of dehosting method categorical inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nucleic Acid Extraction set (extractSet). set used for storing all the valid category values for the nucleic acid extraction method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample fraction set (fractionSet). set for the fraction of the sample (solid, liquid, etc.). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Geographic set (geoTypeSet). set for different type of geographic components. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Genomic Target Enrichment Methods Set (gteSet). The set for valid inputs for the Genomic Target Enrichment method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Inhibition set (inhibitionSet). Category set for inhibition methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Instrument set (insTypeSet). List of instruments that are used for measures and methods Status: active. First released: 2.0.0. Last updated: 2.0.0.

Library Preparation Kit Set (libraryKitSet). The valid set of categorical values for sequencing library preparation kits. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Data license set (licSet). The set to describe valid categorical values for the licensing fields for measures or datasets. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample Material Characteristics Set (matCharSet). The set for recording the possible valid values for describing the sample material characteristics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Concentration method set (methodConcSet). A set a concentration methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Original Data Format Set (ogFormSet). The category set for recording the possible original data formats to be recorded in the originalFormat field in the datasets table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Organization level set (orgLevelSet). Categories of organization levels. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organization sector set (orgSectorSet). Cateogries of organization sectors. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organization type set (orgTypeSet). The set for storing organization types. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample Origin set (originSet). The set for storing the valid categorical values of sample origin. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Outbreak declaration Value Set (outbreakSet). set for the valid values of the outbreak measure. Status: active. First released: 2.0.0. Last updated: 3.0.0.

PCR action/activity set (pcrActSet). The set capturing containing all of the valid methods for the PCR activity cycles. Status: active. First released: 2.2.0. Last updated: 2.2.0.

PCR Method set (pcrSet). The set capturing containing all of the valid methods for the PCR method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Public Health Advisory Value Set (phAdviseSet). A set of valid categories for the public health action field, where the action type is 'publi health advisory'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Populated area type set (popAreaSet). Set of valid values used to describe the type of a populated area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population Interval Set (popIntSet). The collection of categorical inputs for population interval measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population assessment method set (popMetSet). The set for valid inputs for the population assessment method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Presampling activity category set (presampSet). The set of valid input values for reporting pre-sampling activity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Genetic primer set (primerSet). The set for genetic primers used in sequencing or PCR assays. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol Relationships set (protocolRelSet). set for valid values of relationshipID in the protocolRelationships table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Purpose set (purposeSet). Purpose set for a sample or measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raw Sequence Data Processing Method Set (rawSeqProcSet). The category set of valid innput values for the software/library/pipeline used

to process the raw sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing read mapping software set (readMapperSet). The set of valid input values for the sequence read mapping software. Status: active. First released: 3.0.0. Last updated: 3.0.0.

General Relationship Set (relSet). set for valid values of relationshipID across all fields and tables. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Replicate Type set (replicateSet). The set for storing valid categorical values of replicate type. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Resuspension method set (resusSet). The set to describe valid categorical values for the resuspension method. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Retained Element Set (retElSet). The set for enumerating the valid possible values of the retained element method. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample material set (sampleMatSet). set for the types of material that can be found in a sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample relationships set (sampleRelSet). set for valid values of relationshipID in the sampleRelationships table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing script version set (scriptSet). The set for script versions Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Assembly Software Set (seqAssSet). The valid set of categorical values for sequence assembly software methods. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing Layout set (seqLaySet). The set for the layout of genetic material used in sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing QC Pipeline Set (seqQCSet). The category set of valid innput values for the software/library/pipeline used to do quality checks on sequencing or PCR data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing selection method set (seqSelSet). The set for the selection method used in sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing Strategy set (seqStratSet). The set for the sequencing strategy used for an analysis Status: active. First released: 2.0.0. Last updated: 2.0.0.

Serotyping Method Set (seroMethSet). The set of categorical inputs for populating the the serotyping method field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Severity set (sevSet). A set for severity indicators. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sampleshed set (shedSet). The set for all valid values of sampleshed. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site Level Category Set (siteLevelSet). The category set containing all valid entries for the siteLevel field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Site set (siteTypeSet). set for the type of sampling site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Solid separation set (solidSeparationSet). set for the separation of solids. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Spike material set (spikeMatSet). set for spikeMat (aterial into which the recovery efficiency control target is spiked). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Recovery efficiency spike target set (spikeTargetSet). The set capturing containing all of the valid categories for the recovery efficiency control (or spike) target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Status set (statusSet). A set for partID = Status to indicate whether a part is in current use or not. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard Curve Calculation Set (stdCurveSet). The set capturing containing all of the valid methods for the PCR standard curve calculations. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample Storage Medium Set (stoMedSet). The set of valid categorical inputs for the stoMed field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Alert Value Set (survAlertSet). A set of valid categories for the public health action field, where the action type is 'surveillance alert'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Level Set (survLevelSet). The list of valid categories for the survLevel measure. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Table column set (tableSet). The set for valid inputs in table columns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Template Set (tempSet). The organizing set for templates. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Threat designation Value Set (threatDesSet). A set of valid categories for the public health action field, where the action type is 'threat designation'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Value treatment value set (valTreatSet). Valid set of values for the value treatment set. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Weather set (weathSet). A set of the valid qualitative categories for the qualitative weather measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Fraction set for wide names (wideFractionSet). Fraction set for wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Polygon Relationship Set (polyRelSet). Value set for polygon relationships. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Set Type Set (setTypeSet). The mmaSet for defining the possible values of setType. Previously undefined but now made explicit in this set. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Nomenclatures

(nomenclatures). A classification system to report the measure class. See partID = nomenclatureID.

International Classification of Diseases (icd). Classification system for diseases in humans. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nomenclature not applicable (naNomenclature). Not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nomenclaturre from the NCBI (ncbiNom). Nomenclaturre from the National Center for Biotechnology Information Status: active. First released: 2.0.0. Last updated: 2.0.0.

NextClade nomenclature (nextclade). Specifies variant or genetic nomenclature as set out by NextClade. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Pangolin nomenclature (pangolin). Specifies variant or genetic nomenclature as set out by the Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin). Status: active. First released: 2.0.0. Last updated: 2.0.0.

WHO nomenclature (who). Specifies variant or genetic nomenclature as set out by the World Health Organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Original Data Format Set

(ogFormSet). The category set for recording the possible original data formats to be recorded in the originalFormat field in the datasets table.

PHES-ODM Version 1 Format (phesODMFormV1). Dataset was originally recorded and/or stored in PHES-ODM version 1 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHA4GE Format (pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

US-CDC NWSS Format (nwssForm). Dataset was originally recorded and/or stored in the US-CDC's NWSS format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NCBI Format (ncbiForm). Dataset was originally recorded and/or stored in NCBI format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ENA Format (enaForm). Dataset was originally recorded and/or stored in ENA format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Norman Format (normanForm). Dataset was originally recorded and/or stored in Norman format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

wSphere Format (wSphereForm). Dataset was originally recorded and/or stored in wSphere format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Other (or proprietary) Format (otherForm). Dataset was originally recorded and/or stored in a format not otherwise described. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHES-ODM Version 2 Format (phesODMFormV2). Dataset was originally recorded and/or stored in PHES-ODM version 2 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PHES-ODM Version 3 Format (phesODMFormV3). Dataset was originally recorded and/or stored in PHES-ODM version 3 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Organization level set

(orgLevelSet). Categories of organization levels.

Local administrative units or neighborhoods (neighborLevel). Local administrative units or neighborhoods Status: active. First released: 2.0.0. Last updated: 3.0.0.

Municipalities or communes (municipalLevel). Municipalities or communes Status: active. First released: 2.0.0. Last updated: 3.0.0.

Departments, states, or provinces (stateProvLevel). Departments, states, or provinces Status: active. First released: 2.0.0. Last updated: 3.0.0.

Administrative regions (admRegLevel). Administrative regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

Countries or sovereign states (countryLevel). Countries or sovereign states Status: active. First released: 2.0.0. Last updated: 3.0.0.

Districts, counties, regions (countyLevel). Districts, counties, regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

Organization sector set

(orgSectorSet). Cateogries of organization sectors.

Health administration or planning agency (healthAdm). Health adminstrative or planning organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

First Nation (fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Utilities sector or organization (utilities). Describes organization that manage or provide utilities services, whether water, gas, heat, etc. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Data collection sector or organization (dataColl). Describes organization who collect compile, analyze, and or manage data as their central focus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Public health agency (pubHealth). Public health agency. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Research sector or organization (research). Describes organizations whose focus is on research generation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Policy and political sector or organization (policy). Describes organizations whose core focus is on policy or political activity. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Wastewater Treatment Agency (wta). An organization type that includes those organizations who manage wastewater treatment programs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater Treatment Plant Operator (wtpo). An organization type that includes those organizations who run and operate wastewater treatment facilities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public Authority (pubAuth). An organization type describing a public agency with authority over a given domain. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Public Administration (pubAdm). An organisation type that describes governmental organizations that manage or administer programs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Laboratory (lab). Laboratory for environmental testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organization type set

(orgTypeSet). The set for storing organization types.

Academic institution (academ). The category of organization type used for academic institutions or research groups. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Government agency (govt). The category of organization type used for government agencies, programs, or crown-owned bodies. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Private sector (priv). The category of organization type used for private sector or non-profit groups that are not otherwise captured by the academic category. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample Origin set

(originSet). The set for storing the valid categorical values of sample origin.

Derived data (derived). Derived data, data that has undergone agregation, standardization, adjustment, or any cleaning prior to reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Field sample (field). Specifies a sample taken from the field; directly collected from an area for testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Synthetic sample (synthetic). A synthetic or artificially generated sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Outbreak declaration Value Set

(outbreakSet). set for the valid values of the outbreak measure.

End of Outbreak (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Outbreak - on-going (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Declared outbreak or Outbreak start (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Public health emergency (outbreak) (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Part types part type

(partTypes). Part types describe the purpose or use of the part. Enivornment data has three main part types: measure (i.e. covN1 viral measures, wasteawater flow rate, temperature), method (e.g. how the measure was taken), and attribute (such as a site name). See description of each of the part types within setID = partTypeCatSets.

Part types part type (partTypes). Part types describe the purpose or use of the part. Enivornment data has three main part types: measure (i.e. covN1 viral measures, wasteawater flow rate, temperature), method (e.g. how the measure was taken), and attribute (such as a site name). See description of each of the part types within setID = partTypeCatSets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Short names (shortName). Shortened names for tables and other important parts for use in wide names. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Aggregations (aggregations). Statistical measures used to report a measure. Each measure reported as a number should be reported with an aggregation. The default aggregation is `sin`, which corresponds to a single measurement. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation scales (aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Attributes (attributes). Attributes describe the who, where, when, and why of environmental surveillance. There are attributes for domain, specimen, compartment, or table. Attributes are one of the three main components or ways to report environment surviellence data. The other two components are measures and methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation sets (aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Categories (categories). A discrete list of values that can be reported for a measure, method or attribute. A use-case example of categories would be how they are used to record the site where a measure is taken (partID = geoType). For the geoType attribute there are different type of sites where samples can be taken: a wastwater treatment plant, airplane holding tank, wastwater pumping station, etc. Each of these site types is recorded as a category that can be identified in categorySetID = sTypeCatSets Status: active. First released: 2.0.0. Last updated: 2.0.0.

Classes (classes). A class is a collection of one or more related measures or methods within a group. A group can have one more more classes to describe different parts or the class. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartments (compartments). The substance from which a sample was taken. For example, wastewater has component of "water". Compartments are attributes of measures, methods, units, and aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment sets (compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured

in people (humans), water, surface, or air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Data types part type (dataTypes). The data type for a part. Data types used in the ODM include: varchar, booleen, float, category, date, time, datetime, url, email. dataType corresponds the the entry or cell within a data table, most commonly within a report table. If the data entry has a unit, then the dataType corresponds to the unit and the dataType refers to 'unit'. If the data entry is a category, then the dataType refers to 'category'. All categories are varchar. Otherwise the dataType is identifed within the part entry. TBA: dataType for dictionary. Status: active. First released: 2.0.0. Last updated: 3.0.1.

Additional dictionary sheets (dictionarySupport). Additional sheets for the Excel version of the ODM dictionary. Sheets or tabs for the ODM Excel dictionary include: all ERD tables (look-up tables and data entry tables) and additional supportig tables. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dictionary set type (dictSets). Sets used to describe and group dictionary tables. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Domains (domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Exceptions Part Type (exceptions). An exception part type for use in creating wide names that do not follow the general structure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Groups (groups). A collection of related measures. Used primary to group measurements and methods, this helps pare down the drop down list for a given measurement or methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measures (measurements). The attribute to describe a part type of measures. All measures have `partType` = "measure". Status: active. First released: 2.0.0. Last updated: 2.0.0.

Methods (methods). Procedures or steps for collecting samples or performing measures. For example, `methodExtract` is a method that describes the how a sample was extracted. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Missingness (missingness). The part type for missingness values. Only used for the dictionary entries of parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Missingness sets (missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measure, method, or attribute sets (mmaSets). A set of categories. For example, site type has a list of different sites, such as a wastewater treatment plant, a septic tank, or a pumping station. Only used for the dictionary entries of parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nomenclatures (nomenclatures). A classification system to report the measure class. See partID = nomenclatureID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Part Support (partSupport). Parts designed to support the metadata definition of other parts in the parts table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicators (qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicator sets (qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Shorthand or Short Name Set Type (shortSets). Sets used to group together short names for tables or part types in ODM. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Specimens (specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See partID = specimentID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specimen sets (specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Tables (tables). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. An example of a table is `site` a collection of attributes such as site name and address to describe where environment samples are taken. PHES-ODM has report tables, but users can create their own tables as well. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Table Support (tableSupport). Parts designed to support the metadata definition oftables in the parts table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Units (units). The unit of the measurement. Every measurement must have a unit. Meaning, `units` are a mandatory field whenever a measurement is recorded. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit sets (unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of 'yes' and 'no'; and set B could contain the values of 'yes', 'no', and 'maybe.' partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PCR action/activity set

(pcrActSet). The set capturing containing all of the valid methods for the PCR activity cycles.

reverse transcription (rt). Describes the reverse transcription cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

polymerase activation (pAct). Describes the polymerase activation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

denaturation (denat). Describes the denaturation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

annealing/extension (anneal). Describes the annealing and/or extension cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

PCR Method set

(pcrSet). The set capturing containing all of the valid methods for the PCR method.

Digital droplet emulsification PCR (bioRadDdpcr). Describes a PCR analysis done using BioRad's digital droplet emulsification PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Fluidigm digital PCR (fluiDpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Life technologies digital PCR (ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

qiagen digital PCR (qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quantitative Real-Time PCR (qpcr). Real-time PCR, also called 'quantAggScale' PCR Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raindance digital PCR (rainDpcr). Describes a PCR analysis done using Raindance's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Singleplex, probe-based, one-step RT-qPCR (sinProbeOne). Describes a PCR method that is singleplex, probe-based, and one-step RT-qPCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Digital PCR (dPCR) (dpcr). Describes a PCR analysis done using digital PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Digital Droplet PCR (ddPCR) (ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

Public Health Advisory Value Set

(phAdviseSet). A set of valid categories for the public health action field, where the action type is 'publi health advisory'.

Travel warning (travWa). A notice advising against travel to certain areas due to health risks. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel ban (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mask recommendation (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Quarantine recommendation (quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hand hygiene advisory (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Change to Vaccine Schedule (vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polygon Relationship Set

(polyRelSet). Value set for polygon relationships.

Child relationship (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Co-located relationship (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical

results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Overlapping relationship (overlap). Locations/polygon have overlapping portions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Neighbouring relationship (neighbour). Locations/polygon are neighbouring eachother. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Populated area type set

(popAreaSet). Set of valid values used to describe the type of a populated area.

Suburban (suburban). Suburban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

Rural (rural). Rural populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

Urban (urban). Urban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population Interval Set

(popIntSet). The collection of categorical inputs for population interval measures.

<10 people (less10). Fewer than 10 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

10 - 100 people (less100). Between 10 and 100 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

10,000 - 100,000 people (less100k). Between 10,000 and 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

1,000 - 10,000 people (less10k). Between 1,000 and 10,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

100 - 1,000 people (less1k). Between 100 and 1,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

100,000 - 1,000,000 people (less1mil). Between 100,000 and 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

1,000,000+ people (more1mil). More than 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population assessment method set

(popMetSet). The set for valid inputs for the population assessment method.

Population census (census). Government or other agency census for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population count (count). A count of residents for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Review of records (rev). A review of records for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Presampling activity category set

(presampSet). The set of valid input values for reporting pre-sampling activity.

Agricultural activity (agri). Agricultural activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Animal husbandry (husb). Animal husbandry occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Industrial activity (indus). Industrial activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Healthcare activity (hcAct). Healthcare activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater treatment (wwTrt). Wastewater treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater filtration (wwFilt). Wastewater filtration occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater grit removal (wwGrit). Wastewater grit removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater microbial treatment (wwMic). Wastewater microbial treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewtaer primary sedimentation (wwPriSed). Wastewtaer primary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater secondary sedimentation (wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater aerobic digestion (wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater anaerobic digestion (wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater screening process (wwScreen). Wastewater screening process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge dewatering (wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge drying (wwDry). Wastewater sludge drying occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater sludge removal (wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

wastewater comminution process (wwCominuated). wastewater comminution process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Genetic primer set

(primerSet). The set for genetic primers used in sequencing or PCR assays.

Use of the articV3 primer (articV3). Initial implementation of an ARTIC bioinformatics platform for nanopore sequencing of nCoV2019 novel coronavirus; Artic Foundation v3 primer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Use of the articV4 primer (articV4). Artic V4 sequencing primer for VOCs and VOIs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

2019-nCoV_N1 forward primer (IDT) (cdcCovN1IDTFor). 2019-nCoV_N1 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N1 reverse primer (IDT) (cdcCovN1IDTRev). 2019-nCoV_N1 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 forward primer (IDT) (cdcCovN2IDTFor). 2019-nCoV_N2 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 reverse primer (IDT) (cdcCovN2IDTRev). 2019-nCoV_N2 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 forward primer (IDT) (cdcCovN3IDTFor). 2019-nCoV_N3 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 reverse primer (IDT) (cdcCovN3IDTRev). 2019-nCoV_N3 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E forward primer (IDT) (cdcCovEIDTFor). Sarbeco_E forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E reverse primer (IDT) (cdcCovEIDTRev). Sarbeco_E reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S forward primer (HF183) (ABI) (bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S reverse primer (BacR287) (ABI) (bact16sABIRev). Bacteroides 16S reverse primer (BacR287) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

PMMV forward primer (ABI) (pmmvABIFor). PMMV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

PMMV reverse primer (ABI) (pmmvABIRev). PMMV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

VSV forward primer (ABI) (vsvABIFor). VSV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

VSV reverse primer (ABI) (vsvABIRev). VSV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Artic V1 Primer Set (articV1). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 1.0.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V2 Primer Set (articV2). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 2.0.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V4.1 Primer Set (articV41). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 4.1.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5 Primer Set (articV500). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.0.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.1 Primer Set (articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2with the attributes of version 5.1.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.2 Primer Set, 1200bp (articV520bp1200). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.2 Primer Set, 400bp (articV520bp400). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Artic V5.3.2 Primer Set (articV532). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.3.2 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Eden V1 Primer Set (edenV1). An amplicon strategy which was developed by John-Sebastian Eden with primers for SARS-CoV-2 and attributes of version 1.0.0 which produces amplicons approximately 2500bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V1 Primer Set (midnightBCCDCv1). An amplicon strategy which is for SARS-CoV-2 and based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V2 Primer Set (midnightBCCDCv2). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V3 Primer Set (midnightBCCDCv3). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 3.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight and BC-CDC V4 Primer Set (midnightBCCDCv4). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 4.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V3 Primer Set (midnightV3). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V1 Primer Set (midnightV1). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore

Technologies with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Midnight scheme V2 Primer Set (midnightV2). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V1a Long Primer Set (nebVarSkipV1aLong). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a long. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V1a short Primer Set (nebVarSkipV1aShort). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a short. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V2a Primer Set (nebVarSkipV2a). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2a. Status: active. First released: 3.0.0. Last updated: 3.0.0.

New England Biolabs VarSKip V2b Primer Set (nebVarSkipV2b). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2b. Status: active. First released: 3.0.0. Last updated: 3.0.0.

2019-nCoV_N1 probe (IDT) (cdcCovN1IDTProbe). 2019-nCoV_N1 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N2 probe (IDT) (cdcCovN2IDTProbe). 2019-nCoV_N2 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

2019-nCoV_N3 probe (IDT) (cdcCovN3IDTProbe). 2019-nCoV_N3 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Bacteroides 16S probe (BacP234) (ABI) (bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

PMMV probe (ABI) (pmmvABIProbe). PMMV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

VSV probe (ABI) (vsvABIProbe). VSV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sarbeco_E probe (IDT) (cdcCovEIDTProbe). Sarbeco_E probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Protocol Relationships set

(protocolRelSet). set for valid values of relationshipID in the protocolRelationships table. Use only for protocolRelationships table relationshipID.

Is Before (before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specifies (specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Is concurrent to (concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Purpose set

(purposeSet). Purpose set for a sample or measure.

Education (education). A measure or sample taken for education or training. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Multiple Purpose (multiple). A measure or sample taken for multiple purposes, not easily captured by the other purpose categories. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Provisional report (provisional). A provisional or interm report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality control (qualityControl). A measure or sample taken for the purpose of quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Regular Pathogen Surveillance (regular). A measure or sample taken for surveillance or epidemiology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol testing (testing). A measure or sample taken to test a new method. These measures are typically used for internal lab uses and not reported to external partners. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Validation study (validationStudy). A meaure or sample taken for a validation study. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Purpose is normalization (norm). The purpose of a measure or sample is for normalization. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Wastewater treatment efficiency assessment (wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Chemical contaminant surveillance (chemSurv). Purpose of sampling/measure is to test for the presence of certain chemicals or chemical contaminants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Drug surveillance (drugSurv). Purpose of sampling/measure is to surveil drug use in a population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Research purposes (researchPurp). Purpose of sampling/measure is for research. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Environmental survey or profiling (profil). Purpose of sampling/measure is to record characteristics and profile a given environment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Random sampling surveillance program (randomSurv). A surveillance sampling strategy in which baseline is established at the beginning of a study or project by the selection of sample units via random sampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Emergency targetted surveillance program (emergSurv). A targeted surveillance strategy which is considered important and/or urgent. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Targeted surveillance program (targetSurv). A surveillance sampling strategy in which an aspired outcome is explicitly stated. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Longitudinal, repeat sampling surveillance program (longSurv). A surveillance strategy in which an individual or site is selected to undergo repeat sampling over a defined period of time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Travel hub surveillance - general (travelSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Domestic travel hub surveillance (domSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to domestic travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

International travel hub surveillance (internatSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to international travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Viral passage experiment (viralPass). A research sampling strategy in which samples are selected in order to perform a viral passage experiment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Calibration purpose (cali). Purpose of calibrating a machine, method, or other. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Quality indicators

(qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts.

Sequence Amplification Artifacts (ampliArtifact). Sequence amplification artifacts detected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Below LOD (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measured levels below LOQ (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

Delayed Arrival or Prolonged Transit (delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Experiment Failed (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

AI - Inhibition present but addressed (flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

B - Trace levels of contamination (flagB). Analytical result may be subject to "trace" levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

FI - Inhibition present and unaddressed (flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

J - Weak signal extrapolation (flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ND - Non-detect (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

UJ - Trace signal extrapolation (flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., "trace" signal observed);

the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

UQ - Unquantifiable (flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample frozen (frozen). Sample was frozen before analysis or processing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low Average Genome Coverage (lAGC). Average coverage of the genome is low/poor. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low breadth of coverage (lBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low depth of coverage (lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Leaked sample (leaked). Sample leaked, some volume and material was lost. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low Coverage of Characteristic Mutations (lowCovMut). Low coverage of characteristic mutations. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low-quality Sequence (lowQualSeq). Low-quality sequence. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low Signal-to-Noise Ratio (lowSNRatio). Low signal-to-noise ratio. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low-volume sample (lowVol). Sample is low-volume, but was run regardless. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low Percent of Genome Captured (lPGC). Only captured a small/low percentage of the genome. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Multiple issues (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No quality concerns (noConcern). A flag to indicate there is are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample not labelled (noLabel). Sample had no label Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample missing time stamp (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NTC Amplification Detected (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Control-plate Flag - NTCs (ntcFlag). quality indicator for when there is observed amplicifation in the non-template controls (NTCs) of a PCR reaction. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

Value out of range (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Value is an outlier (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality concerns (qf1). A flag to indicate there is a quality concern, not otherwise sepcified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sparse coverage (sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Contaminated (seqContam). Sequence is contaminated. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Read Lengths Shorter Than Expected (shortRead). Read lengths are shorter than expected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Sample spilled (spill). Sample contents spilled from container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wide 95% interval (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample stored incorrectly (wrongStorage). Sample was stored inappropriately. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample stored at wrong temperature (wrongTemp). Sample was stored at an inappropriate temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicator sets

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set.

Generic quality flag set

(genQualitySet)A quality set to specify any generic quality concerns about a measure or sample. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

Multiple issues (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No quality concerns (noConcern). A flag to indicate there is are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Quality concerns (qf1). A flag to indicate there is a quality concern, not otherwise sepcified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Measures quality set

(measQualitySet)A quality set for any measure, includes all the quality flag options for any measure. Used as an "any quality set" for measures, but excludes the sample quality flags to avoid confusion and data entry errors. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Below LOD (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measured levels below LOQ (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

Delayed Arrival or Prolonged Transit (delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Experiment Failed (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

AI - Inhibition present but addressed (flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution.

The reported concentration estimate is the updated result after addressing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

B - Trace levels of contamination (flagB). Analytical result may be subject to "trace" levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

FI - Inhibition present and unaddressed (flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

J - Weak signal extrapolation (flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ND - Non-detect (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

UJ - Trace signal extrapolation (flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., "trace" signal observed); the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

UQ - Unquantifiable (flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low breadth of coverage (lBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low depth of coverage (lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Multiple issues (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No quality concerns (noConcern). A flag to indicate there is are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample missing time stamp (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NTC Amplification Detected (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Value out of range (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Value is an outlier (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality concerns (qf1). A flag to indicate there is a quality concern, not otherwise sepcified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sparse coverage (sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wide 95% interval (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PCR quality set

(pcrQualitySet)Quality set for PCR measures. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Below LOD (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measured levels below LOQ (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

Experiment Failed (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

AI - Inhibition present but addressed (flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

B - Trace levels of contamination (flagB). Analytical result may be subject to "trace" levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

FI - Inhibition present and unaddressed (flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

J - Weak signal extrapolation (flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ND - Non-detect (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

UJ - Trace signal extrapolation (flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., "trace" signal observed); the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

UQ - Unquantifiable (flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No quality concerns (noConcern). A flag to indicate there is are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NTC Amplification Detected (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Value out of range (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Value is an outlier (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample quality set

(sampleQualitySet)Quality set for a sample. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Delayed Arrival or Prolonged Transit (delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Sample frozen (frozen). Sample was frozen before analysis or processing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Leaked sample (leaked). Sample leaked, some volume and material was lost. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low-volume sample (lowVol). Sample is low-volume, but was run regardless. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No quality concerns (noConcern). A flag to indicate there is are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample not labelled (noLabel). Sample had no label Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample missing time stamp (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample spilled (spill). Sample contents spilled from container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample stored incorrectly (wrongStorage). Sample was stored inappropriately. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample stored at wrong temperature (wrongTemp). Sample was stored at an inappropriate temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing quality set

(seqQualitySet)Quality set for sequencing measures Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sequence Amplification Artifacts (ampliArtifact). Sequence amplification artifacts detected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Below LOD (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measured levels below LOQ (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

Experiment Failed (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low Average Genome Coverage (lAGC). Average coverage of the genome is low/poor. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low breadth of coverage (lBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low depth of coverage (lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Low Coverage of Characteristic Mutations (lowCovMut). Low coverage of characteristic mutations. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low-quality Sequence (lowQualSeq). Low-quality sequence. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low Signal-to-Noise Ratio (lowSNRatio). Low signal-to-noise ratio. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Low Percent of Genome Captured (lPGC). Only captured a small/low percentage of the genome. Status: active. First released: 2.3.0. Last updated: 2.3.0.

No quality concerns (noConcern). A flag to indicate there is are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample missing time stamp (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NTC Amplification Detected (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Value out of range (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Value is an outlier (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sparse coverage (sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Contaminated (seqContam). Sequence is contaminated. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Read Lengths Shorter Than Expected (shortRead). Read lengths are shorter than expected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Wide 95% interval (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicator sets

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set.

Generic quality flag set (genQualitySet). A quality set to specify any generic quality concerns about a measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Measures quality set (measQualitySet). A quality set for any measure, includes all the quality flag options for any measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

PCR quality set (pcrQualitySet). Quality set for PCR measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample quality set (sampleQualitySet). Quality set for a sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing quality set (seqQualitySet). Quality set for sequencing measures Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raw Sequence Data Processing Method Set

(rawSeqProcSet). The category set of valid innput values for the software/library/pipeline used to process the raw sequencing data.

FastQC (fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Trimmomatic (trimmomatic). A sequencing data processing application that trims adapters and low-quality bases from Illumina sequencing reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cutadapt (cutadapt). A sequencing data processing application that does adapter removal and trimming tool for high-throughput sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Porechop (porechop). A sequencing data processing application that is specifically designed for adapter trimming in Oxford Nanopore Technologies data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap Suite (bbmapSuite). A sequencing data processing application library that includes tools like BBDuk for quality trimming, adapter removal, and quality filtering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AdapterRemoval (adapterRemoval). A sequencing data processing application that removes adapters and filters reads based on quality and length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTX Toolkit (fastXTools). A sequencing data processing application that provides various functions for FASTQ processing, including quality filtering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sickle (sickle). A sequencing data processing application that is a quality-based trimming tool for Illumina data with single-end and paired-end support. Status: active. First released: 3.0.0. Last updated: 3.0.0.

iVar (iVar). A sequencing data processing application that is designed for viral amplicon data, removes primers and can trim low-quality bases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Skewer (skewer). A sequencing data processing application that is a fast tool for adapter trimming and quality trimming in Illumina data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

seqtk (seqtk). A lightweight sequencing data toolkit for FASTQ and FASTA manipulation, including trimming and subsampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Prinseq-lite (prinseqLite). A sequencing data processing application that filters sequences based on complexity and removes low-quality reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SPAdes (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BayesHammer (from SPAdes) (bayesHammer). A sequencing data processing application that does error correction tool specifically for Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fqtrim (fqtrim). A sequencing data processing fast tool for adapter removal, quality trimming, and quality control. Status: active. First released: 3.0.0. Last updated: 3.0.0.

UMI-tools (umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CD-HIT (cdHIT). A sequencing data processing application that clusters and removes duplicate sequences, useful for dereplication. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SortMeRNA (sortMeRNA). A sequencing data processing application that is used for ribosomal RNA filtering in metatranscriptomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTP (fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DeconSeq (deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DADA2 (dada2). A sequencing data processing application that is primarily used in amplicon sequencing for error correction and generating amplicon sequence variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SAMtools (samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA (Burrows-Wheeler Aligner) (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Minimap2 (minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

KneadData (kneadData). A sequencing data processing pipeline for quality control, including trimming and host decontamination (uses Trimmomatic and Bowtie2). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing read mapping software set

(readMapperSet). The set of valid input values for the sequence read mapping software.

Bowtie2 (bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that maps reads against a host reference genome to remove aligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BWA (Burrows-Wheeler Aligner) (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

STAR (Spliced Transcripts Alignment to a Reference) (star). STAR (Spliced Transcripts Alignment to a Reference). A general-purpose read mapper. Fast aligner designed for RNA-seq, supports spliced alignment. Best for: Transcriptome data analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

HISAT2 (hisat2). HISAT2. A general-purpose read mapper. Successor to TopHat, optimized for RNA-seq data with splicing awareness. Best for: Large-scale RNA-seq experiments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TopHat (tophat). TopHat. A general-purpose read mapper. An older RNA-seq aligner, splicing-aware. Replaced by HISAT2 in most workflows. Best for: Historical RNA-seq studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Minimap2 (minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBMap (bbmap). BBMap. A general-purpose read mapper. High-sensitivity aligner for DNA and RNA reads. Best for: Error-prone reads from platforms like Nanopore or PacBio. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Subread (subread). Subread. A general-purpose read mapper. Includes the subread-align algorithm for mapping DNA and RNA reads. Best for: High-throughput data with a balance of speed and accuracy. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GEM Mapper (gemMapper). GEM Mapper. A specialized read mapper. High-speed and accurate alignment tool for short reads. Best for: Genomic applications with short reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MapSplice (mapSplice). MapSplice. A specialized read mapper. Designed specifically for spliced alignment of RNA-seq reads. Best for: Transcriptomics with a focus on detecting splice junctions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GMAP (gmap). GMAP. A specialized read mapper. A long-read aligner for genomic mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GSNAP (gsnap). GSNAP. A specialized read mapper. A splice-aware aligner for RNA-seq reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Soap2 (soap2). Soap2. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Soap3 (soap3). Soap3. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Novoalign (novoalign). Novoalign. A specialized read mapper. Commercial aligner known for high accuracy. Best for: Applications requiring precise alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cufflinks (with TopHat integration) (cufflinks). Cufflinks (with TopHat integration). A specialized read mapper. Combines mapping with transcriptome assembly and quantification. Best for: RNA-seq studies with integrated analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NGMLR (Next-Generation Mapping and Long-Read Alignment) (ngmlr). NGMLR (Next-Generation Mapping and Long-Read Alignment). A long-read specific mapper. Specialized for long-read platforms like PacBio and Nanopore. Best for: Structural variant analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GraphMap (graphmap). GraphMap. A long-read specific mapper. Long-read aligner optimized for highly error-prone reads. Best for: De novo assemblies using long-read data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

LAST (Large-Scale Alignment and Search Tool) (last). LAST (Large-Scale Alignment and Search Tool). A long-read specific mapper. Flexible tool for aligning long and error-prone reads. Best for: Comparative genomics with long reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BLASR (Basic Local Alignment with Successive Refinement) (blasr). BLASR (Basic Local Alignment with Successive Refinement). A long-read specific mapper. Optimized for PacBio data. Best for: High-quality long-read alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Snap (snap). Snap. A highly parallelized mapper. Ultrafast, designed for genomic and RNA-seq applications. Best for: Large-scale sequencing projects. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SMALT (smalt). SMALT. A highly parallelized mapper. High-speed aligner for genomic DNA reads. Best for: Applications requiring flexibility with non-standard parameters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

General Relationship Set

(relSet). set for valid values of relationshipID across all fields and tables.

Is Before (before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Is concurrent to (concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specifies (specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Child relationship (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Co-located relationship (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Field sample replicate (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory duplicate (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory control sample duplicate (lcsd). Known amounts of an analyte or representative compounds are added to a second "clean" matrix (lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

Matrix spike duplicate (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Relationship Not Reported (relNR). A relationship ID used in relationship tables across the ODM when two entities are related or connected in some way, but the actual nature of that relationship is not clear or reported. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Replicate Type set

(replicateSet). The set for storing valid categorical values of replicate type.

Co-located relationship (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Field sample replicate (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory duplicate (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory control sample duplicate (lcsd). Known amounts of an analyte or representative compounds are added to a second "clean" matrix (lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

Matrix spike duplicate (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unique sample (unique). A unique sample, not duplicated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Positive experimental control (posCon). A sample or experimental condition where the expected outcome is known to occur, intended to

confirm that the experimental setup is working properly. An example would be a wastewater sample spiked with a known quantity of SARS-CoV-2 virus. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Negative experimental control (negCon). A sample or experimental condition where the expected outcome should not occur, intended to check the original sample matrix for contamination, false positives, or unintended effects. An example would be testing for viral RNA or DNA in a sample known to be free of that virus. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Technical replicate (techRep). A sample that comes from the same biological or environmental source (e.g., the same extracted DNA, the same RNA aliquot, or the same water sample). Helps detect inconsistencies due to pipetting errors, instrument fluctuations, or reagent inconsistencies, rather than biological variation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Biological replicate (bioRep). A biological replicate not otherwise specified - these are parallel measurements of biologically distinct samples that capture random biological variation, which can be a subject of study or a source of noise itself. Biological replicates are important because they address how widely your experimental results can be generalized. They indicate if an experimental effect is sustainable under a different set of biological variables. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sampling Event (sampleEvent). In settings where a person goes out and collects multiple samples, but more accurate location data is not recorded, this is used to group samples from that outing, or 'sampling event'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Subsample (General) (subSamp). A general replicate type for a subsample not otherwise defined. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Derived sample (derivedSamp). A sample that is derived or made from another sample or material. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Unknown sample (unkn). Denotes an unknown sample replicate type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Non-template control (ntc). Denotes a non-template control sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

No amplification control (nac). Denotes a no amplification control replicate sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Standard sample (std). Denotes a standard sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

No target present (ntp). Denotes a sample replicate/control with no target present. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MinusRT (nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Optical calibrator sample (opt). Denotes a sample control or replicate used for optical calibration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Resuspension method set

(resusSet). The set to describe valid categorical values for the resuspension method.

Elution buffer (elutionBuff). Elution buffer is used to resuspend material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Retained Element Set

(retElSet). The set for enumerating the valid possible values of the retained element method.

Solids/Pellet retained (solid). The solids or pellet is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Liquid/Supernatant retained (liquid). The liquid or supernatant is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Eluate/Resuspended filter material retained (eluate). The eluate fraction, or material resuspended from filtration, is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample material set

(sampleMatSet). set for the types of material that can be found in a sample.

Air filter (afu). Air filter as part of filtration or circulating unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Desk or counter (desk). Desk, table, countertop or other flat working surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Fecal matter (faeces). Fecal matter. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Floor (floor). Floor of a building or room. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Holding tank wastewater (htSam). Wastewater sampled from a holding tank, such as from an airplane or ship Status: active. First released: 2.0.0. Last updated: 2.0.0.

Water (nww). Non-wastewater, coming from any kind of water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Primary clarifier effluent (pEfflu). Effluent obtained after primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Primary clarifier sludge (pSludge). Sludge produced by primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Post-grit (pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but priort to a primary clarifier) Status: active. First released: 1.0.0. Last updated: 2.0.0.

Raw sewage at site (rawWW). Wastewater without any form of treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

Raw sewage downstream from a site (rawWWdown). Downstream from a site. See partType = rawWWup. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raw sewage upstream from a site (rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjuctiion with downstream sample. For example, if the site is a long-term care home, but ther is not access to the building or property cleanout. Use two sameple, one sample upstream and one sample downstream. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Secondary clarifier effluent (sEfflu). Effluent obtained after secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Septic tank wastewater (septage). Wastewater from within a septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

Secondary clarifier sludge (sSludge). Sludge produced by secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

Other surface (surface). Surface other than floor or desk. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sewer sediment (swrSed). Sediments obtained in sewer Status: active. First released: 1.0.0. Last updated: 2.0.0.

Wastewater Sludge - non-specified (sludgeNS). Sample material is wastewater sludge - whether primary, secondary or other is unspecified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Wastewater Effluent - non-specified (effluNS). Sample material is wastewater effluent - whether primary, secondary or other is unspecified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sample relationships set

(sampleRelSet). set for valid values of relationshipID in the sampleRelationships table. Use only for sampleRelationships table relationshipID.

Child relationship (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Co-located relationship (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Field sample replicate (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Matrix spike duplicate (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory duplicate (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Laboratory control sample duplicate (lcsd). Known amounts of an analyte or representative compounds are added to a second "clean" matrix (lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

Control sample (control). Denotes a relationship to a primary sample where the object sample serves as a control to the subject sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing script version set

(scriptSet). The set for script versions

Gromstole 1.0 Script (gromstole). Gromstole 1.0 Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Freyja Script (freyja). Freyja Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequence Assembly Software Set

(seqAssSet). The valid set of categorical values for sequence assembly software methods.

SPAdes (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MEGAHIT (megahit). A sequencing software that is a fast and memory-efficient assembler for large metagenomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Velvet (velvet). A sequencing software that is a de novo assembler optimized for short-read data, often used in microbial genomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ABySS (abyss). A sequencing software that is a scalable de novo assembler for large genomes, designed for distributed computing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SOAPdenovo (soapDenovo). A sequencing software that is an assembler for short-read data, suited to large and complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Canu (canu). A sequencing software that is a de novo assembler specifically optimized for long-read data from PacBio and Oxford Nanopore. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Flye (flye). A sequencing software that is an assembler for long-read data, particularly effective on nanopore sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Trinity (trinity). A sequencing software that is an assembler designed specifically for RNA-seq data, creating transcriptome assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

IDBA-UD (idbaUD). A sequencing software that is an iIterative assembler optimized for metagenomics and complex genomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Unicycler (unicycler). A sequencing software that is a hybrid assembler for bacterial genomes, combining short and long reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Miniasm (miniasm). A sequencing software that is a lightweight assembler for long reads, typically followed by polishing steps. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Redundans (redundans). A sequencing software that is a genome assembler that reduces redundancy, useful for fragmented assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NovoPlasty (novoPlasty). A sequencing software that is an assembler tailored for organellar genomes (mitochondrial and chloroplast). Status: active. First released: 3.0.0. Last updated: 3.0.0.

Shasta (shasta). A sequencing software that is a fast assembler optimized for nanopore long-read data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MetAMOS (metAMOS). A sequencing software that is an automated pipeline for metagenomic assembly and annotation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Maryland Super Read Celera Assembler (MaSuRCA) (masurca). A sequencing software that is a hybrid assembler that can integrate both short and long reads for high-quality assemblies, and large, complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DISCOVAR de novo (discovar). A sequencing software that is an assembler optimized for Illumina data in whole-genome sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SSAKE (ssake). A sequencing software that is a simple de novo assembler for highly overlapping short reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

WTDBG (aka wtdbg2) (wtdbg2). A sequencing software that is an assembler for long-read data that generates contigs rapidly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Platanus (platanus). A sequencing software that is an assembler, optimized for large, diploid genome assemblies, particularly plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PEHaplo (pehaplo). A sequencing software that is an assembler that considers heterozygosity in diploid genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ARACHNE (arachne). A sequencing software that is an early assembler optimized for large, complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Celera Assembler (celera). A sequencing software that was initially developed for the Human Genome Project, still used in some workflows for large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AllPaths-LG (allpathsLG). A sequencing software that was designed for high-quality assemblies using large, paired-end Illumina data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing Layout set

(seqLaySet). The set for the layout of genetic material used in sequencing

Single Layout (sinLay). Specifies the single layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

Paired Layout (pairLay). Specifies the paired layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

Mate pair layout (mateLay). Specifies the mate pair layout for a sequencing method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sequencing QC Pipeline Set

(seqQCSet). The category set of valid innput values for the software/library/pipeline used to do quality checks on sequencing or PCR data.

FastQC (fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MultiQC (multiQC). A QC pipeline tool for sequencing data that aggregates QC results from multiple sources (e.g., FastQC, SAMtools) into a single report, useful in large pipelines. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PRINSEQ (prinseq). A QC pipeline tool for sequencing data for assessing and filtering sequences based on complexity, quality scores, and GC content. Status: active. First released: 3.0.0. Last updated: 3.0.0.

QC3 (qc3). A comprehensive QC pipeline for NGS sequencing data that provides summary statistics on sequence quality and contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

AfterQC (afterQC). An automated QC pipeline tool for FASTQ data, combining quality assessment and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FASTP (fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NanoPlot (nanoPlot). A QC pipeline tool for sequencing data that does visualizations for quality assessment of long-read data, particularly from Oxford Nanopore. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TrimGalore! (trimGalore). A QC pipeline tool for sequencing data that integrates Cutadapt and FastQC to assess sequence quality and remove adapters in one step. Status: active. First released: 3.0.0. Last updated: 3.0.0.

EAGER (eager). A QC pipeline tool for sequencing data for ancient DNA, providing quality filtering, contamination estimates, and other QC metrics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Atropos (atropos). A QC pipeline tool for sequencing data that performs adapter trimming and quality filtering with built-in QC reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BBDuk (from BBTools) (bbduk). A QC pipeline tool for sequencing data that is a part of the BBMap suite, performs filtering and trimming, and generates QC statistics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BamQC (from Qualimap) (bamQC). A QC pipeline tool for sequencing data that focuses on quality control for mapped data in BAM format, reporting alignment quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PiSeqQC (piSeqQC). A QC pipeline tool for sequencing data for microbiome and metagenomic sequencing data, including quality filtering and contaminant removal. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DecontaMiner (decontaMiner). A QC pipeline tool for sequencing data for contamination detection and removal in NGS datasets, especially useful in clinical samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

qProfiler2 (qProfiler2). A QC pipeline tool for sequencing data that produces reports with detailed QC metrics for aligned and unaligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqKit stats (seqKitStats). Part of SeqKit, a QC pipeline tool for sequencing data that providing a summary of sequence metrics like length, GC content, and quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FRCbam (frcBam). A QC pipeline tool for sequencing data that assesses read quality and genome assembly quality metrics for high-throughput data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Kraken2 (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

preQC (from Meraculous) (preQC). A QC pipeline tool for sequencing data that evaluates data quality before assembly, particularly for large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PIQMIe (piqmie). A comprehensive QC and contamination assessment pipeline for metagenomic datasets and sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ncov-tools (ncovtools). Tools and plots for perfoming QC on coronavirus sequencing results. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bracken (bracken). A QC pipeline tool for sequencing data and taxonomic profiling that can also be used to identify contamination and assess data quality in metagenomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sequencing selection method set

(seqSelSet). The set for the selection method used in sequencing

Random sequencing selection method (ranSeq). Specifies the random selection method for sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

PCR Sequencing Selection Method (pcrSeq). Specifies the PCR selection method for sequencing, ie. that a pre-determined primer was used. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Sequencing Strategy set

(seqStratSet). The set for the sequencing strategy used for an analysis

Amplicon sequencing (amp). Specifies the amplicon strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

Whole genome sequencing (wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

16S Ribosomal Gene Sequencing (16rgs). An amplicon sequencing assay in which the amplicon is derived from universal primers used to amplify the 16S ribosomal RNA gene from isolate bacterial genomic DNA or metagenomic DNA from a microbioal community. Resulting sequences are compared to reference 16S sequence databases to identify or classify bacteria present within a given sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Whole Metagenome Sequencing (wms). A DNA sequencing assay that intends to provide information on the DNA sequences of multiple genomes

(a metagenome) from different organisms present in the same input sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Whole Virome Sequencing (wvs). A whole metagenome sequencing assay that intends to provide information on multiple genome sequences from different viruses present in the same input sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Serotyping Method Set

(seroMethSet). The set of categorical inputs for populating the the serotyping method field.

Traditional Serotyping methods (tradSero). Traditional Serotyping methods used for serotyping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Salmonella In Silico Typing Resource (SISTR) (sistr). Salmonella In Silico Typing Resource (SISTR). Used for in silico serotyping of Salmonella enterica based on whole-genome sequencing. Combines genomic data with the traditional White-Kauffmann-Le Minor serotyping scheme. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqSero2 (seqSero2). SeqSero2. Specifically designed for Salmonella serotyping using raw sequence reads, assemblies, or even complete genomes. Provides results based on antigenic formulas or serotype names. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SerotypeFinder (serotypeFin). SerotypeFinder. A web-based tool that predicts serotypes for Escherichia coli and other bacteria by detecting genes encoding O-antigens and H-antigens. Developed by the Center for Genomic Epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Kaptive (kaptive). Kaptive. Identifies capsular (K) serotypes in Klebsiella pneumoniae and related species using whole-genome sequence data. Useful for studying capsule diversity and epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CTFinder (ctFinder). CTFinder. Designed for Clostridioides difficile serotyping and subtyping. Identifies capsular polysaccharide synthesis gene clusters to assign serogroups. Status: active. First released: 3.0.0. Last updated: 3.0.0.

BIGSdb (Bacterial Isolate Genome Sequence Database) (bigsdb). BIGSdb (Bacterial Isolate Genome Sequence Database). A flexible platform that supports serotyping alongside sequence typing and other typing schemes. Can be customized for various bacterial species, including Neisseria meningitidis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PBPfinder (pbfinder). PBPfinder. Used for typing and serotyping of Streptococcus pneumoniae through analysis of penicillin-binding proteins and capsular genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Phandango (phandango). Phandango. A visualization tool that integrates serotype predictions with phylogenetic analyses for population studies. Often used alongside other serotyping tools. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SalmonellaTypeFinder (salTypeFin). SalmonellaTypeFinder A specialized tool for predicting Salmonella serotypes based on genomic data, similar to SeqSero. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Streptococcus Serotyping Tool (SSI) (SSI). Streptococcus Serotyping Tool (SSI) A web-based platform for serotyping Streptococcus pneumoniae based on capsular polysaccharide synthesis loci. Status: active. First released: 3.0.0. Last updated: 3.0.0.

CapsuleFinder (capFin). CapsuleFinder Used for typing capsular polysaccharides in a variety of bacteria, especially Escherichia coli and Klebsiella species. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Prokka (with serotyping integration) (prokka). Prokka (with serotyping integration) While primarily an annotation tool, Prokka outputs can be paired with databases for identifying serotypes of certain bacterial pathogens. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Enterobase archives (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Kraken2 (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ARIBA (ariba). ARIBA. Focus: Genotyping, MLST, and serotyping from raw sequencing reads. Applications: Salmonella, Escherichia coli, Klebsiella pneumoniae, and more. Features: Works with custom databases for serotyping and resistance gene identification. Status: active. First released: 3.0.0. Last updated: 3.0.0.

MLST (Center for Genomic Epidemiology) (mlst). MLST (Center for Genomic Epidemiology). Focus: Classical MLST and optional serotype determination. Applications: Compatible with curated schemes for various pathogens. Features: Web-based and command-line versions available. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SRST2 Software (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Pathogenwatch (pathogenwatch). Pathogenwatch. Focus: Integrates MLST, serotyping, and resistance typing with a user-friendly interface. Applications: Primarily used for Salmonella and Escherichia coli. Features: Combines typing results with interactive visualization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Prokka + Roary Pipeline (Nextflow) (prokkaRoary). Prokka + Roary Pipeline. Focus: Genome annotation (Prokka) with MLST and serotyping integration via Roary. Applications: Broad compatibility with bacterial pathogens. Features: Facilitates core-genome MLST and accessory gene analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

SeqTyping (seqTyping). SeqTyping. Focus: Simultaneous MLST and serotyping for Escherichia coli and Salmonella. Applications: Integrated with bacterial genome typing databases. Features: Compatible with short-read sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ChewBBACA (chewBBACA). ChewBBACA. Focus: Core genome MLST (cgMLST) with optional serotyping analysis. Applications: Broad-spectrum bacterial pathogens. Features: Efficient with large datasets and highly customizable. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PubMLST (pubMLST). PubMLST. Focus: Web-based platform for MLST and serotyping analyses. Applications: Neisseria, Campylobacter, Salmonella, and more. Features: Combines curated databases with user-uploaded sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Mykrobe (mykrobe). Mykrobe. Focus: Rapid detection of resistance, MLST, and serotyping. Applications: Mycobacterium tuberculosis and other pathogens. Features: Fast processing and species-specific database compatibility. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Statistical Analysis of Metagenomic Profiles (STAMP) Software (stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. Status: active. First released: 3.0.0. Last updated: 3.0.0.

PGAP (Prokaryotic Genome Annotation Pipeline) (pgap). PGAP (Prokaryotic Genome Annotation Pipeline). Focus: Annotation pipeline that integrates MLST and antigen typing. Applications: Broad bacterial

pathogens. Features: Provided by NCBI, designed for high-throughput workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

ClermonTyping (clermonTyp). ClermonTyping. Focus: MLST and phylogenetic typing for Escherichia coli. Applications: Ideal for epidemiological studies. Features: Combines MLST and phylogroup-specific information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

FastMLST (fastMLST). FastMLST. Focus: Lightweight MLST and serotyping from assembled genomes or raw reads. Applications: Broad bacterial species. Features: Quick and simple, designed for routine use. Status: active. First released: 3.0.0. Last updated: 3.0.0.

GenoTyphi (genoTyphi). GenoTyphi. Focus: Specific MLST and serotyping for Salmonella Typhi. Applications: Outbreak investigations and epidemiology. Features: Highly specialized for typhoidal Salmonella. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Set Type Set

(setTypeSet). The mmaSet for defining the possible values of setType. Previously undefined but now made explicit in this set.

Specimen sets (specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Quality indicator sets (qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Compartment sets (compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured

in people (humans), water, surface, or air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Aggregation sets (aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measure, method, or attribute sets (mmaSets). A set of categories. For example, site type has a list of different sites, such as a wastewater treatment plant, a septic tank, or a pumping station. Only used for the dictionary entries of parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit sets (unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of 'yes' and 'no'; and set B could contain the values of 'yes', 'no', and 'maybe.' partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Shorthand or Short Name Set Type (shortSets). Sets used to group together short names for tables or part types in ODM. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Missingness sets (missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dictionary set type (dictSets). Sets used to describe and group dictionary tables. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Severity set

(sevSet). A set for severity indicators.

Low severity (low). A marker for low severity Status: active. First released: 2.0.0. Last updated: 2.0.0.

Mid-level severity (mid). A marker for med-level severity, where there are some concerns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

High severity (high). Indicates a very sever quality issue, likely meaning the data should not be reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sampleshed set

(shedSet). The set for all valid values of sampleshed.

Airplane (airpln). Airplane sample shed category type Status: active. First released: 1.0.0. Last updated: 2.0.0.

Long-term acute care hospital (ccc). Acute care hospitals, or complex contuing care, that provide care for patients with average length of stay longer than 25 days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Child day care (cdc). Child day care facility. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Correctional facility (corFcil). Correctional facility Status: active. First released: 1.0.0. Last updated: 2.0.0.

Higher education domitory or residential building (dorm). Higher education domitory or residential building Status: active. First released: 2.0.0. Last updated: 2.0.0.

First Nation (fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Hospital (hosptl). Hospital Status: active. First released: 1.0.0. Last updated: 2.0.0.

Long-term care facility (ltcf). A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Long-term care - assisted living or retirement home (ltcfAl). A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other long-term care (ltcfO). Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or assisted living facilities. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Municipality (municp). A complete municipality, this specifies an entire metropolitan area, either a city, town, etc. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Neighbourhood (neigh). A municipal neighbourhood, this specifies a sub-section of a larger municipality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other residential building (orb). Individual residential buildings or institutions not captured in other categories Status: active. First released: 2.0.0. Last updated: 2.0.0.

School (school). A school serving students in the kindergarten to 12th grade range Status: active. First released: 1.0.0. Last updated: 2.0.0.

Ship (ship). A cruise ship or other ship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Social services shelter (sss). Other type of social services shelter Status: active. First released: 2.0.0. Last updated: 2.0.0.

University campus (uCampus). Universityor college campus - comprising an entire campus or part of a campus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Airport (airport). Airport sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

Airport terminal (terminal). Airport terminal sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

Commercial facility - not specified (commFacOth). Specifies a site type which is a commercial facility/worksite that is not otherwise captured or described in the geotype set. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Healthcare facility (hcf). A building for the provision of healthcare, not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Clinic (clinic). A medical clinic, may be used to provide treatment, remedial work, and/or instruction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Educational facility (edFac). A school or other educational facility not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Transport hub - General (tHub). A tansport hub not otherwise specified. i.e. a place where passengers and cargo are exchanged between vehicles

or/and between transport modes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Farm (farm). An aggricultural area, builing, or tract of land. Used for the cultivation of crops or grazing of livestock, including any buildings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Refugee camp (refCamp). A temporary, often makeshift shelter for persons displaced by war, political oppression, or for religious beliefs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Industrial plant (indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occaisonally services, and making them into products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Meat processing plant (meatPl). A processing plant for slaughtering, processing, packaging, labelling, handling, and storing of food animal carcasses, parts of carcasses, and meat products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Pharmaceutical manufacturing plant (pharmPl). An industrial building in which pharamceutical drugs are synthesised and processed on an industrial scale. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Transportation vehicle - general (transp). A vehicle, i.e. a mobile machine, transporting people or cargo, of a type not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Train (train). A series of railroad cars moved as a unit by a locomotive or by integral motors. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Train Station (trStat). A place on a railroad line where trains regularly stop so that passengers can get on or off. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Bus (bus). A large motor vehicle carrying passengers by road, typically one serving the public on a fixed route and for a fare. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Bus Station (busStat). A terminal where buses arrive and depart. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Port or Harbour (port). A harbor is any sheltered body of water where boats or ships may moor or anchor. A port is an installation that has been built around a harbor with facilities for loading and unloading such vessels. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Land-based Transit Hub (landTH). A transport hub is a place where passengers and cargo are exchanged between land-based vehicles and/or between land-based transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Water-based Transit Hub (waterTH). A transport hub is a place where passengers and cargo are exchanged between water-based vehicles and/or between water-based transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Office (office). A workplace where administrative, managerial, or clerical tasks are performed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Restaurant (restaurant). A commercial establishment that prepares and serves food and beverages to customers. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Road (road). A paved or unpaved pathway designed for vehicular and pedestrian travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Roadside (roadside). The area adjacent to a road, including sidewalks, shoulders, or drainage ditches. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Shopping mall (mall). A large commercial complex with multiple retail stores, services, and restaurants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Region (region). Specifies a region that combines multiple urban areas, and/or large rural areas. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Hotel or motel (hotel). A building which 1) contains multiple dwellings of pre-furnished accomodation and 2) is rented for lodging on a short term and/or longer-term basis. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Shorthand or Short Name Set Type

(shortSets). Sets used to group together short names for tables or part types in ODM.

Short Name Set

(shrtNameSet)The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). Status: active. First Released: 2.2.2. Last updated: 2.2.2.

Accessions report table Shorthand (ac). The abbreviated short name used to reference the report table for accessions and accessionIDs. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Address table Shorthand (ad). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). Status: active. First released: 2.2.2. Last updated: 2.2.2.

Calculations Table Short Name (cl). The abbreviated short name used to reference the table for recording data on data treatments and calculations applied to measurements and reported values. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Contact table Shorthand (co). The abbreviated short name used to reference the The table that contains information about a contact; a person who is the contact of a site or laboratory. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Countries look-up tables Shorthand (cu). The abbreviated short name used to reference the Look up table for the possible country inputs. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Dataset table Shorthand (ds). The abbreviated short name used to reference the report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Instrument table Shorthand (in). The abbreviated short name used to reference the The table that contains information about instruments. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Language Look-up table Shorthand (la). The abbreviated short name used to reference the Look up table for all languages, used to give structure to the translation table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Measures Part-type Shorthand (mes). The abbreviated short name used to reference the The attribute to describe a part type of measures. All measures have `partType` = "measurements". Status: active. First released: 2.2.2. Last updated: 2.2.2.

Methods part-type Shorthand (met). The abbreviated short name used to reference the Procedures or steps for collecting samples or performing measures. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Measure report table Shorthand (mr). The abbreviated short name used to reference the The table that contains information and details about a given measure Status: active. First released: 2.2.2. Last updated: 2.2.2.

Measure set report table Shorthand (ms). The abbreviated short name used to reference the The table that identifies sets of measures. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Organization table Shorthand (or). The abbreviated short name used to reference the The table that contains information about a laboratory. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Parts Look-up table Shorthand (pa). The abbreviated short name used to reference the Look up table containing all parts in of the data model. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Public Health Actions Report Table Shortname (pha). The abbreviated short name used to reference the table for recording information on public health actions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polygon table Shorthand (po). The abbreviated short name used to reference the The table that contains information about the geometry of a geographic area. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Polygon Relationships Table Short Name (por). The abbreviated short name used to reference the table for recording the relationships between polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Protocol relationships table Shorthand (pr). The abbreviated short name used to reference the The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Status: active. First released: 2.2.2. Last updated: 2.2.2.

Protocols table Shorthand (pro). The abbreviated short name used to reference the the table that contains the summary information and details about a given protocol. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Protocol steps table Shorthand (ps). The abbreviated short name used to reference the The table for collecting metadata on individual steps in a protocol, methodological process, or assay. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Quality reports table Shorthand (qr). The abbreviated short name used to reference the The table for recording the various quality metrics and indicators for samples and measures. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Sample relationships table Shorthand (sar). The abbreviated short name used to reference the Table for recording the relationships between samples. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Sample report table Shorthand (sas). The abbreviated short name used to reference the The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Sets look-up table Shorthand (se). The abbreviated short name used to reference the Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Sites table Shorthand (si). The abbreviated short name used to reference the The table that contains information about a site; the location where an environmental sample was taken. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Translation look-up table Shorthand (tr). The abbreviated short name used to reference the Look up table for translations of the description,

label, and instruction for all parts. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Wide name table Shorthand (wn). The abbreviated short name used to reference the The table for wide names. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Zones look-up table Shorthand (zo). The abbreviated short name used to reference the Look up table for the possible sub-national region or zone inputs. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Site Level Category Set

(siteLevelSet). The category set containing all valid entries for the siteLevel field.

Country-level Aggregation at Site (countLevel). Specifies that a sewershed/site represents an entire nation or country. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Province-level Aggregation at Site (provLevel). Specifies that a sewershed/site represents a sub-national state, province, or region. Status: active. First released: 3.0.0. Last updated: 3.0.0.

A-Tier Region-level Aggregation at Site (aRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an "A-Tier" region and refers to large, dense urban areas made up of multiple overlapping cities/boroughs. This would be a greater metropolitan area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

B-Tier Region-level Aggregation at Site (bRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an "B-Tier" region, and thus a region within a greater metropolitan area and larger

than a single municipality, but smaller than the entire metropolitan area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Municipality-level Aggregation at Site (muniLevel). Specifies that a sewershed/site represents an entire municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Neighbourhood-level Aggregation at Site (neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a municipaility. Status: active. First released: 3.0.0. Last updated: 3.0.0.

First Nation Territory/Métis Settlement-level Aggregation at Site (fnmiLevel). Specifies that a sewershed/site represents the entirety of a First Nations territory or reservation, or a Métis settlement. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Site set

(siteTypeSet). set for the type of sampling site.

Branch sewer pipleline (bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municpal sewer lines, allowing drainage into the main sewer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Building cleanout (buildCO). Specifies a site type that is a capped pipe that connects to a building's main sewer line. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Estuary, natural water body (estuary). Estuary, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Lake, natural water body (lake). Lake, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Holding tank (htSite). Holding tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

Lagoon system (lagoon). Lagoon system for extensive wastewater treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

Major sewer pipeline (mSwrPpl). Major sewer pipeline Status: active. First released: 1.0.0. Last updated: 2.0.0.

Ocean, natural water body (ocean). Ocean, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Pumping station (pStat). Pumping station - these stations transport sewage or various types of water from one place to another, to facilitate its movement toward treatment plants. Sometimes also referred to as "lift stations". Status: active. First released: 1.0.0. Last updated: 2.0.0.

Retention pond (retPond). Retention pond Status: active. First released: 1.0.0. Last updated: 2.0.0.

River, natural water body (river). River, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sea, natural water body (sea). Sea, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Septic tank (septTnk). Septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

Stabilization pond (stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment to reduce the organic content and remove pathogens from wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sewage truck (swgTrck). Sewage truck Status: active. First released: 1.0.0. Last updated: 2.0.0.

Industrial wastewater treatment plant (wwtpInd). Industrial wastewater treatment plant Status: active. First released: 1.0.0. Last updated: 2.0.0.

Municipal wastewater treatment plant for combined sewage (wwtpMuC). Municipal wastewater treatment plant for combined sewage Status: active. First released: 1.0.0. Last updated: 2.0.0.

Municipal wastewater treatment plant for sanitary sewage only (wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wastewater treatment plant (wwtp). A general site type for wastewater treatment plants. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Upstream sites (upstream). A general site type for upstream wastewater sampling sites. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Back-up wastewater treatment site (wwtpBack). Indicates a wastewater treatment plant where multiple labs are or were sampling, and where secondary samples are being taken taken. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Body of water (bow). An outdoor accumuation of water either on the surface or beneath the ground, no other additional details specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surface water (opWa). An outdoor accumuation of water either on the surface of the earth, no other additional details specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Stream (str). A watercourse which is linear and flows across the solid portion of a planetary surface. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Canal (canal). Artificial watercourse with no flow or a controlled flow used for navigation, drainage or irrigation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Reservoir (res). An artificial body of water, often contained by a dam, constructed for the purpose of water storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Ground water (grWa). Underground water which is located in pore spaces found in rock or unconsolidated deposits such as soil, clay, or gravel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Well (well). A cylindrical hole, pit, or tunnel drilled or dug down to a depth from which water, oil, or gas can be pumped or brought to the surface. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Spring (spr). A surface landform which provides an egress for groundwater or steam to flow out of the ground. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Plumbing drain (pluDra). An artificial channel which transports unwanted water or waste liquids away from their source, either to a more useful area, a receptacle, or into sewers or stormwater mains as waste discharge to be released or processed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sewer (drain) (drain). A pipe that carries water or sewage away from a place, or an opening in a surface that leads to said pipe. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Latrine (latrine). A toilet or outhouse, especially a communal one in a camp or barracks. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Cesspit (cesspit). Cesspit, cesspool and soak pit in some contexts are terms with various meanings: they are used to describe either an underground holding tank (sealed at the bottom) or a soak pit (not sealed at the bottom). A cesspit can be used for the temporary collection and storage of feces,

excreta, or fecal sludge as part of an on-site sanitation system and has some similarities with septic tanks or with soak pits. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Composting toilet (compToi). A self-contained toilet system wherein human waste is designed to be composted. Usually with the addition of secondary materials, like sawdust. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Wastewater Triturator (triturator). The location where wastewater transportation vehicles unload wastewater. Status: active. First released: 2.2.3. Last updated: 2.2.3.

Aeration tank (aerTank). A chamber in wastewater treatment where air is introduced to promote microbial breakdown of organic pollutants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Communitor (communitor). A mechanical device that grinds large solid waste in wastewater into smaller particles to prevent clogging. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Grit chamber (gritCham). A sedimentation basin in wastewater treatment that removes heavy, inorganic particles (e.g., sand, gravel) before biological treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Influent pump station (infPump). A facility that ransports raw wastewater from collection systems to treatment plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Primary clarifer (primClar). A large settling tank that removes solids and floating materials from wastewater before secondary treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Secondary clarifer (secClar). A tank in wastewater treatment that removes biological solids (e.g., microbial flocs) after aeration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sludge dryer (sDryer). A facility or equipment used to reduce moisture content in wastewater sludge for easier handling and disposal. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Bar screen (barScreen). A bar screen is a mechanical device used to remove large solid debris from wastewater or sewage as it enters a treatment plant. It consists of a series of parallel bars or rods, spaced at specific intervals, that allow water to pass through while capturing larger objects. This process prevents damage to downstream equipment and ensures efficient treatment. Bar screens are typically installed at the inlet of wastewater treatment facilities and can be cleaned manually or mechanically, depending on the design and operational requirements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Odour Control Unit (ocu). Odour Control Unit ventilation extends the life of a sewer by reducing the amount of maintenance the pipeline needs, making management of the network much more efficient. The filters used in the Odour Control Unit and ventilation stacks absorb gases such as hydrogen sulphide, which is a common source of odours from sewerage systems. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Solid separation set

(solidSeparationSet). set for the separation of solids.

Centrifugation (cent). Describes solid separation from a wastewater sample via centrifugation. Likely connected to other method steps prior to analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Filtration (filt). Describes solid separation from a wastewater sample via filtration. Proceeds further concentration or analysis of the liquid filtrate. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gravity settling (graSet). Describes solid separation from a wastewater sample where the sample material is allowed to settle by gravity, and then separated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No Seperation or Concentration (noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Specimens

(specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See partID = specimentID.

See Header for Specimen (hSp). An indicator to show in a wide-name that specimen information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Specimen not applicable (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polygon (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specimen sets

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen.

Any specimen set

(anySpecimenSet)A specimen set that inculdes any specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Polygon (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specimen set not applicable

(naSpecimenSet)A specimen set for when specimen/specimen set is not applicable. Use 'not applicable' when there is no specimen/set for the part Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Specimen not applicable (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polygon or site specimen set

(polySiSpecimenSet)A specimen set that inculdes polygon or site specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

Polygon (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polygon specimen set

(polySpecimenSet)A specimen set that inculdes only a polygon specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

Polygon (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population or polygon specimen set

(poPolySpecimenSet)A specimen set that inculdes population or polygon specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

Polygon (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Population or sample set

(poSaSpecimenSet)A specimen set that inculdes population or sample specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population or site set

(poSiSpecimenSet)A specimen set that inculdes population or site specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population specimen set

(poSpecimenSet)A specimen set that inculdes only a population specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample specimen set

(saSpecimenSet)A specimen set that inculdes only a sample specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sample (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site or sample specimen set

(siSaSpecimenSet)A specimen set that inculdes site or sample specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sample (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site specimen set

(siSpecimenSet)A specimen set that inculdes only a site specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Speciment set for wide names

(wideSpecimenSet)Speciment set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

See Header for Specimen (hSp). An indicator to show in a wide-name that specimen information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Specimen not applicable (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polygon (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specimen sets

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen.

Any specimen set (anySpecimenSet). A specimen set that inculdes any specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Specimen set not applicable (naSpecimenSet). A specimen set for when specimen/specimen set is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Polygon or site specimen set (polySiSpecimenSet). A specimen set that inculdes polygon or site specimen. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polygon specimen set (polySpecimenSet). A specimen set that inculdes only a polygon specimen. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population or polygon specimen set (poPolySpecimenSet). A specimen set that inculdes population or polygon specimen. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population or sample set (poSaSpecimenSet). A specimen set that inculdes population or sample specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population or site set (poSiSpecimenSet). A specimen set that inculdes population or site specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population specimen set (poSpecimenSet). A specimen set that inculdes only a population specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample specimen set (saSpecimenSet). A specimen set that inculdes only a sample specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site or sample specimen set (siSaSpecimenSet). A specimen set that inculdes site or sample specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Site specimen set (siSpecimenSet). A specimen set that inculdes only a site specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Speciment set for wide names (wideSpecimenSet). Speciment set for wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Spike material set

(spikeMatSet). set for spikeMat (aterial into which the recovery efficiency control target is spiked).

Clarified sample (clari). Clarified sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sample concentrate (samConc). Sample concentrate. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Dewatered solids (deso). Dewatered solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Lysis buffer (lysi). Lysis buffer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Raw wastewater (raws). Raw wastes water sample Status: active. First released: 1.0.0. Last updated: 2.0.0.

Raw post-pasteurized wastewater (rppw). Raw wastewater sample post-pasteurization Status: active. First released: 1.0.0. Last updated: 2.0.0.

Recovery efficiency spike target set

(spikeTargetSet). The set capturing containing all of the valid categories for the recovery efficiency control (or spike) target.

bcov culture spike target (bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

bcov vaccine spike target (bcovVac). The bovine coronavirus vaccine is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

brsv culture spike target (brsvCul). Cultured bovine respiratory syncytial virus (BRSV) is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

brsv vaccine spike target (brsvVac). The bovine respiratory syncytial virus (BRSV) vaccine is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Heat inactivated sars-cov-2 virus spike target (heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

hep g armored rna spike target (hepGRnaMat). Hepatitis G armored RNA is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

ms2 coliphage spike target (ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

murine coronavirus spike target (muCoMat). Murine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

oc43 spike target (oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

phi6 spike target (phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Puro virus spike target (puroMat). Puro Virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Vesicular stomatitis virus (VSV) target (vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

bcov spike target (unspecified) (bcovGen). The bovine coronavirus (unspecified) is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

murine hepatitis virus (MHV) spike target (mhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Parapoxvirus Orf Virus Spike Target (parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Status set

(statusSet). A set for partID = Status to indicate whether a part is in current use or not.

Active (active). Indicator that a part is in current use. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Development (development). Indicator that a part is under development use. See partID = status Status: active. First released: 2.0.0. Last updated: 2.0.0.

Depreciated (depreciated). Indicator to say that a part is no longer in current use in the model. See partID = status Status: active. First released: 2.0.0. Last updated: 2.0.0.

Standard Curve Calculation Set

(stdCurveSet). The set capturing containing all of the valid methods for the PCR standard curve calculations.

serial dillution (serDil). Describes a serial dilution process for standard curve generation for PCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sample Storage Medium Set

(stoMedSet). The set of valid categorical inputs for the stoMed field.

No sample storage medium used (none). No sample storage medium used Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cary-Blair Transport Medium (cbtm). A buffer solution/medium commonly used for bacterial preservation in stool and wastewater samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

RNAlater (rnaLater). A buffer solution/medium the stabilizes RNA and DNA in samples, effective for preserving nucleic acids in wastewater. Status: active. First released: 3.0.0. Last updated: 3.0.0.

TE Buffer (Tris-EDTA) (trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Viral Transport Medium (VTM) (vtm). A buffer solution/medium the preserves viral samples during transport, commonly used for wastewater viral studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Phosphate Buffered Saline (PBS) (pbs). An isotonic solution for general sample preservation, used when immediate freezing is available. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Skim Milk–Glycerol Medium (smgm). A buffer solution/medium that protects bacteria in environmental samples, preventing freeze-thaw damage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Amies Transport Medium (atm). A buffer solution/medium that maintains viability of bacteria in wastewater and environmental samples during transport. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sucrose Phosphate Glutamate (SPG) Buffer (spg). A buffer solution/medium that stabilizes viruses, including in wastewater samples, by preventing RNA degradation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

DNA/RNA Shield (dnaRNAshield). A stabilizing solution for nucleic acids in samples, including wastewater, protecting against degradation at room temperature. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Buffered Peptone Water (bpw). A buffer solution/medium used for bacterial enrichment, can also serve as a temporary preservative. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Lactated Ringer's Solution (lrs). A buffer solution/medium sometimes used in combination with other preservatives to stabilize microbial samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sodium Thiosulfate Solution (sts). A buffer solution/medium that neutralizes residual chlorine in wastewater samples, ensuring microbial viability. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Guanidine Thiocyanate (gt). A buffer solution/medium that serves as a strong preservative for viral RNA, commonly used in molecular biology for RNA preservation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Peptone Water with Glycerol (pwWg). A buffer solution/medium used in environmental sampling, especially for preserving microorganisms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Hank's Balanced Salt Solution (HBSS) (hbss). Hank's Balanced Salt Solution (HBSS) - Nutrient-rich buffer that maintains cell and microbial integrity in samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

10% Glycerol Solution (glycerol10). 10% Glycerol Solution - Common cryoprotectant for bacterial and viral storage in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sterile Distilled Water with Sodium Thiosulfate (sDWwST). Sterile Distilled Water with Sodium Thiosulfate - Used to neutralize chlorine for microbiological analysis in wastewater samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Tryptic Soy Broth (TSB) (tsb). Tryptic Soy Broth (TSB) - A nutrient-rich medium for bacterial survival, sometimes used for short-term storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Universal Transport Medium (UTM) (utm). Universal Transport Medium (UTM) - Used for microbial preservation in various environmental samples, including wastewater. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Alert Value Set

(survAlertSet). A set of valid categories for the public health action field, where the action type is 'surveillance alert'.

Targetted surveillance initiated (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Increased surveillance (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Routine surveillance (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Decreased surveillance (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Surveillance Level Set

(survLevelSet). The list of valid categories for the survLevel measure.

Building-level Surveillance (builLev). Surveillance is done only at the level of a single building. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Institution-level Surveillance (instituLev). Surveillance is done at the level of an entire insitution. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Community-level Surveillance (communitLev). Surveillance is done at the level of an entire community. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Multi-Community-level Surveillance (multiComLev). The scope of the surveillance covers multiple communities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Tables

(tables). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. An example of a table is `site` a collection of attributes such as site name and address to describe where environment samples are taken. PHES-ODM has report tables, but users can create their own tables as well.

accessions Table (accessions). Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Address table (addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). The Sites, Organizations, and Contacts tables include a link to the addresses table through Address ID. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Calculations Table (calculations). Table for recording data on data treatments and calculations applied to measurements and reported values. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Contact table (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short

name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Countries look-up tables (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Dataset table (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Instrument table (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Language Look-up table (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Measure report table (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Measure set report table (measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or varients that are identified in a single sample. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Organization table (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Parts Look-up table (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Public Health Actions Report Table (phActions). Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Polygon Relationships Table (polygonRelationships). Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Polygon table (polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Protocol relationships table (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a proceedure) and measureIDs (a measure). An example of a method is centrifugation; where the centriguation rotation speed is described as a measure. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocols table (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Protocol steps table (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Quality reports table (qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Reporter table depreciated (reportersDep). The table that contains information about a reporter of a sample, method, measure, or attribute. The short name for the table (partID) can be found in the instructions field. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Sample relationships table (sampleRelationships). Table for recording the relationships between samples.Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sample report table (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site.Samples can be combined, split, stored and reused. The `Sample relationships` (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets look-up table (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sites table (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an eviromental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the infomation changes often. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Translation look-up table (translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wide name table (wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Zones look-up table (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

Table column set

(tableSet). The set for valid inputs in table columns. These categories are used in the parts list for columns named after tables to indicate the

position and function of a given part in the entity relationship diagram of the data model.

Foreign key (fK). Foreign key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Header (header). Header for a table. Also known as a table variable or entiy relationship 'attribute'. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Input (input). Input for a table. Indicates if a part can be used in a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Primary key (pK). Primary key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Composite Key (cK). Composite key for a table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

Template Set

(tempSet). The organizing set for templates.

DNA Template (dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

RNA Template (rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Threat designation Value Set

(threatDesSet). A set of valid categories for the public health action field, where the action type is 'threat designation'.

Variant of concern (voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Variant of interest (voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

variant under monitoring (vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

De-escalated variant (dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Units

(units). The unit of the measurement. Every measurement must have a unit. Meaning, `units` are a mandatory field whenever a measurement is recorded.

Number of active cases (acti). Number of active cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Number of active cases by Onset date (actiCaseOn). Number of active cases by onset date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by episode date (actiEp). Number of active cases by episode date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by Report date (actiRep). Number of active cases by report date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by test date (actiTest). Number of active cases by test date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Breadth of coverage (>=5x depth) (boc). The percentage of the reference genome covered by the sequenced data, to a prescribed read depth greater or equal to 5. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Base-pairs (bps). A base pair (bp) is a unit of measurement in molecular biology that represents a pair of complementary nucleotides in DNA or RNA. The length of DNA sequences is often measured in base pairs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Episode date of confirmed cases (caseEpDate). Episode date is the earliest of onset, test or reported date for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Onset date of confirmed cases (caseOnDate). Earliest that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Report date of confirmed cases (caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and

this measure is most commonly reported and used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Test date of confirmed cases (caseTestDate). Date that the covid-19 test was performed for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Degrees Celcius (cel). Degrees Celsius. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Colony Forming Units (cfu). Colony forming units Status: active. First released: 3.0.0. Last updated: 3.0.0.

CFU per 100 ml (cfu100). Colony forming units per 100 ml of filtered sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Colony forming units per grams total solids (cfugTS). colony forming units per grams total solids (CFU/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Colony forming units per milliliter (cfumL). colony forming units per milliliter (CFU/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Centimetres (cm). Unit part for the SI unit of centimetres. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Number of confirmed cases (conf). Number of confirmed cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Number of confirmed cases by episode date (confEp). Number of confirmed cases of a given disease, totaled by episode date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed Cases Onset date (confOn). Number of confirmed cases of a given disease, totaled by onset date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed cases by report date (confRep). Number of confirmed cases of a given disease, totaled by report date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed cases test date (confTest). Number of confirmed cases of a given disease, totaled by test date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Gene copies per well (cpWell). Gene or variant copies per well. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cycle threshold or quantification cycle (Ct or Cq) (ct). Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Cycle threshold per quantification cycle (ctcq). cycle threshold (Ct) / quantification cycle (Cq) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Days (days). A unit for indicating a length of time in days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Deaths (death). Units for describing a population measure of patients who have died from a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Detected (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Depth of coverage (doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Efficiency (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Degree Fahrenheit (fah). Unit for temperature, degrees Fahrenheit. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Formazin nephelometric unit (fnu). formazin nephelometric unit (FNU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Feet (foot). foot (ft) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gene copies (gc). Gene or variant copies Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per copy of crAssphage (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per day (gcDay). Unit of measurement of the number of gene copies per day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

gene copies per day per 100,000 people (gcDay100k). The unit for measures reflecting the gene copies per day per 100,000 people in the population. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies per gram solids (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per L (gcL). Gene or variant copies per litre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per mL (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per millilitre per 100,000 people (gcMl100k). Unit of measurement of the number of gene copies per millilitre per 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gene copies per PMMoV copy (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per Reaction (gcRx). Gene or variant copies per reaction in PCR Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gram per kilogram (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gram per liter (gL). gram per liter (g/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gram per cubic metre (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nitrogen per total solids (gNgTS). nitrogen per total solids (gN/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Grams per total solids (gPergTS). Grams per total solids (g/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Orthophosphate per total solids (gPO43gTS). orthophosphate per total solids (gPO43–/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Orthophosphate as phosphorus per total solids (gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Grams (grams). A unit of mass or weight. Status: active. First released: 2.0.0. Last updated: 2.0.0.

General Hospital Admissions (hosa). Hospital admissions or patients newly admitted to hospital. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Hospital Census (hosc). Hospital census or the number of people admitted with an ailment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Hours (hours). A unit for indicating a length of time in hours. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Intensive care unit patients (icu). Units for describing a population measure of patients who are in intensive care due to a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Inch (inch). inch (in) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Intercept (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Kilogram per cubic meter (kgm3). Kilogram per cubic meter (kg/m^3) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Kilogram per second (kgS). Kilograms per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Kilolitres (kl). Kilolitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

Litres (l). Litres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

Litres per day (lday). Unit of litres per day, usually for measuring flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liter per hour (lhour). liter per hour (L/h) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liter per minute (lmin). liter per minute (L/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

log10 gene copies per g (log10cpG). Unit for log10 copies per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

log10 gene copies per L (log10cpL). Unit for log10 copies per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

log10 gene copies per mL (log10cpml). Unit for log10 copies per mililitre Status: active. First released: 2.2.0. Last updated: 2.2.0.

Log10 gene copies per 100 milliliter (log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Log10 gene copies per nanogram total DNA (log10gcngDNA). log10 gene copies per nanogram total DNA Status: active. First released: 3.0.0. Last updated: 3.0.0.

log10 micrograms per g (log10ugG). Unit for log10 micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

log10 micrograms per L (log10ugL). Unit for log10 micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

Liter per second (lsec). liter per second (L/s) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cubic metres per day (m3D). Cubic metres per day. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Cubic metres per hour (m3H). Cubic metres per hour. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Cubic meter per minute (m3min). cubic meter per minute (m^3/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cubic metres per second (m3S). Cubic metre per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Mega-bases or Mega-base-pairs (megaB). A mega-base (Mb) or mega-base-pair (Mbp) is equal to one million base pairs (1,000,000 bp). It is commonly used to describe the size of genomes or large DNA sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milliequivalent per liter (meqL). Unit for alkalinity, miliequivalents per litre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Meter (meter). meter (m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Millions of gallons per day (MG/D) (mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of gallons per day. Also can be used to measure flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Milligrams per litre (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Milligram per liter of calcium carbonate (mgLCaCO3). Unit for alkalinity, miligram per litre of calcium carbonate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams orthophosphate per liter (mgPO43L). milligrams orthophosphate per liter (mg PO43–/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams orthophosphate as phosphorus per liter (mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Minutes (minutes). A unit for indicating a length of time in minutes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Millilitres (ml). Millilitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

Megalitres per day (ML/d) (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Millimetres (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Millimho per centimeter (mmhocm). Millimho per centimeter (mmho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Months (months). A unit for indicating a length of time in months. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Most probable number per 100 milliliters (mpn100mL). most probable number per 100 milliliter (MPN/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Most probable number per milliliter (mpnmL). most probable number per milliliter (MPN/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Metres per second (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

MilliSiemen per centimeter (mScm). MilliSiemens per centimeter (mS/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

MilliVolt (mvolt). milliVolt (mV) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Unit not applicable (naUnit). Not appliable for units. Status: active. First released: 2.0.0. Last updated: 3.0.1.

Population of newly vaccinated persons (newVax). Population of newly vaccinated persons Status: active. First released: 2.0.0. Last updated: 2.0.0.

Nanograms per liter (ngL). nanograms per liter (ng/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nano-molar (nM). the unit of nanomolar. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number per 100 kilo-base-pairs (nPerKbp). This unit expresses the frequency of an event (such as a mutation, binding site, or feature) per 100,000 base pairs (kbp) of DNA or RNA. It normalizes counts across genomic regions of different lengths, making comparisons more meaningful. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nephelometric turbidity unit (ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see "turbidity" under measureIDs). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Other Unit depricated (otunDep). Other measurement of viral copies or wastewater treatment plant parameter. Add description to UnitOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

PCR Quanitification Cycles (pcrCycles). A count unit of how many Polymerase Chain Reaction (PCR) cycles it took to detect a real signal from a sample. Equivalent to the PCR cycle number at which a sample's reaction curve intersects the threshold line. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Number of people (peeps). Unit specifying a number of people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Percent (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Percent recovery (percRec). Percent of the surrogate recovery for a recovery efficiency control assay (as a unit). Status: active. First released: 1.0.0. Last updated: 2.0.0.

Persons for square kilometre (personPerKm). Persons per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Persons per square mile (personPerMile). Persons per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population equivalents (popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a signle person would use. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Percent positive (pp). Percent positive of sample measures. Status: active. First released: 1.0.0. Last updated: 2.0.0.

parts per million (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Percent positivity rate (pprt). Percent positivity rate of tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Percent primary sludge (pps). Percentage of total solids, for primary sludge. Status: active. First released: 1.0.0. Last updated: 2.0.0.

parts per thousand (ppt). Parts per thousand. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Proportion of total (prop). Proportion as a precent of total. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Proportion of variant in sample (propV). Proportion of a variant as percent of total variants. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Practical salinity unit (psu). practical salinity unit (PSU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Number of positive tests (ptot). Number of positive tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

R squared (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ratio (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

Recovered patients (recov). Units for describing a population measure of patients who have recovered from a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Residents per square kilometre (resPerKm). Residents per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Residents per square mile (resPerMile). Residents per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Rate per 100,000 (rP100). Units for describing a population measure of a rate of case incidence per 100,000 people of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Revolutions per minute (RPM) (rpm). RPM stands for "Revolutions per minute." This is how centrifuge manufacturers generally describe how fast the centrifuge is going. The rotor, regardless of its size, is revolving at that rate. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Seconds (seconds). The unit of time, seconds. Status: active. First released: 2.2.0. Last updated: 2.2.0.

slope (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Siemens per meter (sm). Siemens per meter (S/m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Number of tests performed (test). Number of tests performed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Micrograms per gram (ugG). Micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micrograms per litre (ugL). Micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micrograms per milligram (ugmg). Concentration unit of micrograms per milligram. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micro-litres (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micromho per centimeter (umhocm). Micromho per centimeter (mho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Unitless measure (unitless). A unit for unitless measures, like pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Micro-Siemens per centimetre (uSCm). Micro-siemens per centimetre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Frequency of variants detected (varFreq). A description of the frequency of a variants detected. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 1 dose of vaccine (vax1). The population with exactly 1 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 1+ vaccine dose(s) (vax1p). Specifies the portion of the population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 1+ dose(s) of vaccine (vax1plus). The population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 2 or more doses of vaccine (vax2). The population with exactly 2 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 2+ vaccine doses (vax2p). Specifies the portion of the population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 2+ or more doses of vaccine (vax2plus). The population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 3 or more doses of vaccine (vax3). The population with exactly 3 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.2.0.

Proportion of population with 3+ vaccine doses (vax3p). Specifies the portion of the population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 3+ or more doses of vaccine (vax3plus). The population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 4 or more doses of vaccine (vax4). The population with exactly 4 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 4+ vaccine doses (vax4p). Specifies the portion of the population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 4+ or more doses of vaccine (vax4plus). The population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Weeks (weeks). A unit of measuring time in weeks, or periods of seven days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Weight for weight (ww). weight for weight (% w/w) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Relative Centrifugal Force (RCF) or x g units (xg). RCF (Relative Centrifugal Force) denotes the degree of force exerted on a sample. RCF is quantified in multiples of the gravitational acceleration that is standard at the Earth's surface (x g). Thus, the terms RCF and XG are often used

interchangeably in centrifugation protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Years (years). A unit for indicating a length of time in years. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit sets

(unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of 'yes' and 'no'; and set B could contain the values of 'yes', 'no', and 'maybe.' partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused.

Absolute humidity unit set

(absHumidUnitSet)Unit set for absolute humidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Gram per cubic metre (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Alkalinity unit set

(alkalinitySet)Unit set for alkalinity measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Milliequivalent per liter (meqL). Unit for alkalinity, miliequivalents per litre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams per litre (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

parts per million (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Allele unit set

(alleleUnitSet)Unit set for alleles. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Cycle threshold or quantification cycle (Ct or Cq) (ct). Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Detected (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Depth of coverage (doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Efficiency (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies per copy of crAssphage (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

gene copies per day per 100,000 people (gcDay100k). The unit for measures reflecting the gene copies per day per 100,000 people in the population. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies per gram solids (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per mL (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per PMMoV copy (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Intercept (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

R squared (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

slope (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Bacteria unit set

(bacteriaUnitSet)Unit set for bacteria-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Colony Forming Units (cfu). Colony forming units Status: active. First released: 3.0.0. Last updated: 3.0.0.

CFU per 100 ml (cfu100). Colony forming units per 100 ml of filtered sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Colony forming units per grams total solids (cfugTS). colony forming units per grams total solids (CFU/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Colony forming units per milliliter (cfumL). colony forming units per milliliter (CFU/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Most probable number per 100 milliliters (mpn100mL). most probable number per 100 milliliter (MPN/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Most probable number per milliliter (mpnmL). most probable number per milliliter (MPN/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Base-pair unit set

(basePairSet)Unit set for base-pair measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

Base-pairs (bps). A base pair (bp) is a unit of measurement in molecular biology that represents a pair of complementary nucleotides in DNA or RNA. The length of DNA sequences is often measured in base pairs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Mega-bases or Mega-base-pairs (megaB). A mega-base (Mb) or mega-base-pair (Mbp) is equal to one million base pairs (1,000,000 bp). It is commonly used to describe the size of genomes or large DNA sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Number per 100 kilo-base-pairs (nPerKbp). This unit expresses the frequency of an event (such as a mutation, binding site, or feature) per 100,000 base pairs (kbp) of DNA or RNA. It normalizes counts across genomic regions of different lengths, making comparisons more meaningful. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Capacity unit set

(capacityUnitSet)Unit set for capacity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Millions of gallons per day (MG/D) (mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of gallons per day. Also can be used to measure flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Megalitres per day (ML/d) (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population equivalents (popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a signle person would use. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Conductivity unit set

(conductivityUnitSet)Unit set related to conductivity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Millimho per centimeter (mmhocm). Millimho per centimeter (mmho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

MilliSiemen per centimeter (mScm). MilliSiemens per centimeter (mS/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Micromho per centimeter (umhocm). Micromho per centimeter (mho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Micro-Siemens per centimetre (uSCm). Micro-siemens per centimetre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Dissolved gas concentration unit set

(dissGasUnitSet)Unit set for carbon dioxide concentrations measurements in water or air. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Milligrams per litre (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

parts per million (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Electrical potential unit set

(electricPotentSet)Unit set for measurements of electrical potential. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

MilliVolt (mvolt). milliVolt (mV) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Volume flow rate unit set

(flowUnitSet)Unit set for volume flow measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Kilogram per second (kgS). Kilograms per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Litres per day (lday). Unit of litres per day, usually for measuring flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liter per hour (lhour). liter per hour (L/h) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liter per minute (lmin). liter per minute (L/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Liter per second (lsec). liter per second (L/s) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cubic metres per day (m3D). Cubic metres per day. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Cubic metres per hour (m3H). Cubic metres per hour. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Cubic meter per minute (m3min). cubic meter per minute (m^3/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cubic metres per second (m3S). Cubic metre per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Millions of gallons per day (MG/D) (mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of gallons per day. Also can be used to measure flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Megalitres per day (ML/d) (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Genetics unit set

(geneticUnitSet)Unit set for genetic-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Breadth of coverage (>=5x depth) (boc). The percentage of the reference genome covered by the sequenced data, to a prescribed read depth greater or equal to 5. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies per well (cpWell). Gene or variant copies per well. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Cycle threshold or quantification cycle (Ct or Cq) (ct). Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Cycle threshold per quantification cycle (ctcq). cycle threshold (Ct) / quantification cycle (Cq) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Detected (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Depth of coverage (doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Efficiency (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies (gc). Gene or variant copies Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per copy of crAssphage (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per day (gcDay). Unit of measurement of the number of gene copies per day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

gene copies per day per 100,000 people (gcDay100k). The unit for measures reflecting the gene copies per day per 100,000 people in the population. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Gene copies per gram solids (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per L (gcL). Gene or variant copies per litre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per mL (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per millilitre per 100,000 people (gcMl100k). Unit of measurement of the number of gene copies per millilitre per 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gene copies per PMMoV copy (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Gene copies per Reaction (gcRx). Gene or variant copies per reaction in PCR Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Intercept (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

log10 gene copies per g (log10cpG). Unit for log10 copies per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

log10 gene copies per L (log10cpL). Unit for log10 copies per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

log10 gene copies per mL (log10cpml). Unit for log10 copies per mililitre Status: active. First released: 2.2.0. Last updated: 2.2.0.

Log10 gene copies per 100 milliliter (log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Log10 gene copies per nanogram total DNA (log10gcngDNA). log10 gene copies per nanogram total DNA Status: active. First released: 3.0.0. Last updated: 3.0.0.

log10 micrograms per g (log10ugG). Unit for log10 micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

log10 micrograms per L (log10ugL). Unit for log10 micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

PCR Quanitification Cycles (pcrCycles). A count unit of how many Polymerase Chain Reaction (PCR) cycles it took to detect a real signal from a sample. Equivalent to the PCR cycle number at which a sample's reaction curve intersects the threshold line. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Percent recovery (percRec). Percent of the surrogate recovery for a recovery efficiency control assay (as a unit). Status: active. First released: 1.0.0. Last updated: 2.0.0.

Proportion of total (prop). Proportion as a precent of total. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Proportion of variant in sample (propV). Proportion of a variant as percent of total variants. Status: active. First released: 1.1.0. Last updated: 2.0.0.

R squared (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

slope (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

General Humidity Unit Set

(humidUnitSet)A unit set for all types of humidity measurements. Status: active. First Released: 3.0.1. Last updated: 3.0.1.

Gram per cubic metre (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Percent (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Ratio (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit set not applicable

(naUnitSet)Not applicable for unit sets. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Unit not applicable (naUnit). Not appliable for units. Status: active. First released: 2.0.0. Last updated: 3.0.1.

Percent unit set

(percentUnitSet)Unit set for percentages. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Percent (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population density unit set

(popDensUnitSet)Unit set for measures of population density of a site. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Persons for square kilometre (personPerKm). Persons per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Persons per square mile (personPerMile). Persons per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Residents per square kilometre (resPerKm). Residents per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Residents per square mile (resPerMile). Residents per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population unit set

(populationUnitSet)Unit set for hospital-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Number of active cases (acti). Number of active cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Number of active cases by Onset date (actiCaseOn). Number of active cases by onset date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by episode date (actiEp). Number of active cases by episode date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by Report date (actiRep). Number of active cases by report date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Number of active cases by test date (actiTest). Number of active cases by test date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Episode date of confirmed cases (caseEpDate). Episode date is the earliest of onset, test or reported date for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Onset date of confirmed cases (caseOnDate). Earliest that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Report date of confirmed cases (caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and this measure is most commonly reported and used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Test date of confirmed cases (caseTestDate). Date that the covid-19 test was performed for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Number of confirmed cases (conf). Number of confirmed cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Number of confirmed cases by episode date (confEp). Number of confirmed cases of a given disease, totaled by episode date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed Cases Onset date (confOn). Number of confirmed cases of a given disease, totaled by onset date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed cases by report date (confRep). Number of confirmed cases of a given disease, totaled by report date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Number of confirmed cases test date (confTest). Number of confirmed cases of a given disease, totaled by test date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

Deaths (death). Units for describing a population measure of patients who have died from a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

General Hospital Admissions (hosa). Hospital admissions or patients newly admitted to hospital. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Hospital Census (hosc). Hospital census or the number of people admitted with an ailment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Intensive care unit patients (icu). Units for describing a population measure of patients who are in intensive care due to a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population of newly vaccinated persons (newVax). Population of newly vaccinated persons Status: active. First released: 2.0.0. Last updated: 2.0.0.

Number of people (peeps). Unit specifying a number of people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Percent positivity rate (pprt). Percent positivity rate of tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Number of positive tests (ptot). Number of positive tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Recovered patients (recov). Units for describing a population measure of patients who have recovered from a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Rate per 100,000 (rP100). Units for describing a population measure of a rate of case incidence per 100,000 people of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Number of tests performed (test). Number of tests performed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Population with 1 dose of vaccine (vax1). The population with exactly 1 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 1+ vaccine dose(s) (vax1p). Specifies the portion of the population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 1+ dose(s) of vaccine (vax1plus). The population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 2 or more doses of vaccine (vax2). The population with exactly 2 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 2+ vaccine doses (vax2p). Specifies the portion of the population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 2+ or more doses of vaccine (vax2plus). The population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 3 or more doses of vaccine (vax3). The population with exactly 3 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.2.0.

Proportion of population with 3+ vaccine doses (vax3p). Specifies the portion of the population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 3+ or more doses of vaccine (vax3plus). The population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Population with 4 or more doses of vaccine (vax4). The population with exactly 4 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Proportion of population with 4+ vaccine doses (vax4p). Specifies the portion of the population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Population with 4+ or more doses of vaccine (vax4plus). The population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Precipitation unit set

(precipitationUnitSet)Unit set for percipitation measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Centimetres (cm). Unit part for the SI unit of centimetres. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Feet (foot). foot (ft) Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Inch (inch). inch (in) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Meter (meter). meter (m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Millimetres (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Relative humidity unit set

(relHumidUnitSet)Unit set for relative humidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Percent (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Salinity unit set

(salinityUnitSet)Unit set for salinity measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

Gram per kilogram (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Gram per liter (gL). gram per liter (g/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

parts per thousand (ppt). Parts per thousand. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Practical salinity unit (psu). practical salinity unit (PSU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Weight for weight (ww). weight for weight (% w/w) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Specific humidity unit set

(specHumidUnitSet)Unit set for specific humidity. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Ratio (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

Speed Unit Set

(speedUnitSet)Unit set for reporting speeds (centrifugation speed, etc.) Status: active. First Released: 2.2.0. Last updated: 2.2.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Metres per second (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Revolutions per minute (RPM) (rpm). RPM stands for "Revolutions per minute." This is how centrifuge manufacturers generally describe how fast the centrifuge is going. The rotor, regardless of its size, is revolving at that rate. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Relative Centrifugal Force (RCF) or x g units (xg). RCF (Relative Centrifugal Force) denotes the degree of force exerted on a sample. RCF is quantified in multiples of the gravitational acceleration that is standard at the Earth's surface (x g). Thus, the terms RCF and XG are often used interchangeably in centrifugation protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Standard concentration unit set

(stdConcentrationUnitSet)Unit set for concentration measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Gram per kilogram (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nitrogen per total solids (gNgTS). nitrogen per total solids (gN/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Grams per total solids (gPergTS). Grams per total solids (g/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Orthophosphate per total solids (gPO43gTS). orthophosphate per total solids (gPO43–/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Orthophosphate as phosphorus per total solids (gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Kilogram per cubic meter (kgm3). Kilogram per cubic meter (kg/m^3) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams per litre (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Milligram per liter of calcium carbonate (mgLCaCO3). Unit for alkalinity, miligram per litre of calcium carbonate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams orthophosphate per liter (mgPO43L). milligrams orthophosphate per liter (mg PO43–/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Milligrams orthophosphate as phosphorus per liter (mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nanograms per liter (ngL). nanograms per liter (ng/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Nano-molar (nM). the unit of nanomolar. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Percent (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

parts per million (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Percent primary sludge (pps). Percentage of total solids, for primary sludge. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Micrograms per gram (ugG). Micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micrograms per litre (ugL). Micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micrograms per milligram (ugmg). Concentration unit of micrograms per milligram. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Micro-litres (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Temperature unit set

(temperatureUnitSet)Unit set for temperature measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Degrees Celcius (cel). Degrees Celsius. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Degree Fahrenheit (fah). Unit for temperature, degrees Fahrenheit. Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Time unit set

(timeUnitSet)The unit set for measures of time. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Days (days). A unit for indicating a length of time in days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Hours (hours). A unit for indicating a length of time in hours. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Minutes (minutes). A unit for indicating a length of time in minutes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Months (months). A unit for indicating a length of time in months. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Seconds (seconds). The unit of time, seconds. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Weeks (weeks). A unit of measuring time in weeks, or periods of seven days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Years (years). A unit for indicating a length of time in years. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Turbidity unit set

(turbidityUnitSet)Unit set for turbidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Formazin nephelometric unit (fnu). formazin nephelometric unit (FNU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Nephelometric turbidity unit (ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see "turbidity" under measureIDs). Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unitless unit set

(unitlessUnitSet)Unit set for measurements that does not have units. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Unitless measure (unitless). A unit for unitless measures, like pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Volume unit set

(volumeUnitSet)Unit set of volume measurements. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

Grams (grams). A unit of mass or weight. Status: active. First released: 2.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Kilolitres (kl). Kilolitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

Litres (l). Litres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

Millilitres (ml). Millilitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

Millimetres (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Percent positive (pp). Percent positive of sample measures. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sub-variant or lineage (subVar). A unit used to report a specific genetic lineage, or to specify that a reported variant is a sub-variant of another. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Micro-litres (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Frequency of variants detected (varFreq). A description of the frequency of a variants detected. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Wind speed unit set

(windSpeedUnitSet)Unit set for wind speed measurements. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

See Header for Unit (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 3.0.1.

Metres per second (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit sets

(unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of 'yes' and 'no'; and set B could contain the values of 'yes', 'no', and 'maybe.' partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and

units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused.

Absolute humidity unit set (absHumidUnitSet). Unit set for absolute humidity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Alkalinity unit set (alkalinitySet). Unit set for alkalinity measurements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Allele unit set (alleleUnitSet). Unit set for alleles. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Bacteria unit set (bacteriaUnitSet). Unit set for bacteria-related measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Base-pair unit set (basePairSet). Unit set for base-pair measurements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Capacity unit set (capacityUnitSet). Unit set for capacity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Conductivity unit set (conductivityUnitSet). Unit set related to conductivity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Dissolved gas concentration unit set (dissGasUnitSet). Unit set for carbon dioxide concentrations measurements in water or air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Electrical potential unit set (electricPotentSet). Unit set for measurements of electrical potential. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Volume flow rate unit set (flowUnitSet). Unit set for volume flow measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Genetics unit set (geneticUnitSet). Unit set for genetic-related measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unit set not applicable (naUnitSet). Not applicable for unit sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Percent unit set (percentUnitSet). Unit set for percentages. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population density unit set (popDensUnitSet). Unit set for measures of population density of a site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Population unit set (populationUnitSet). Unit set for hospital-related measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Precipitation unit set (precipitationUnitSet). Unit set for percipitation measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Relative humidity unit set (relHumidUnitSet). Unit set for relative humidity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Salinity unit set (salinityUnitSet). Unit set for salinity measurements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Specific humidity unit set (specHumidUnitSet). Unit set for specific humidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Speed Unit Set (speedUnitSet). Unit set for reporting speeds (centrifugation speed, etc.) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Standard concentration unit set (stdConcentrationUnitSet). Unit set for concentration measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Temperature unit set (temperatureUnitSet). Unit set for temperature measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Time unit set (timeUnitSet). The unit set for measures of time. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Turbidity unit set (turbidityUnitSet). Unit set for turbidity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Unitless unit set (unitlessUnitSet). Unit set for measurements that does not have units. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Volume unit set (volumeUnitSet). Unit set of volume measurements. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Wind speed unit set (windSpeedUnitSet). Unit set for wind speed measurements. Status: active. First released: 1.0.0. Last updated: 2.0.0.

General Humidity Unit Set (humidUnitSet). A unit set for all types of humidity measurements. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Value treatment value set

(valTreatSet). Valid set of values for the value treatment set.

Raw data (raw). Raw data, without adjustment or additional treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Derived data (derived). Derived data, data that has undergone agregation, standardization, adjustment, or any cleaning prior to reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Estimated data (estimate). Estimated data, data that should be understood to be an estimation, possiblynot taken directly from sample measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Predicted data (predicted). Predicted data, data generated by predictove models or algorithims, not taken directly from sample measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Weather set

(weathSet). A set of the valid qualitative categories for the qualitative weather measure.

Cloudy (cloudy). Qualitative category for the weather measure, specifying an overcast day with no rain. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Foggy (foggy). Qualitative category for the weather measure, specifying a foggy or hazy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Rainy (rainy). Qualitative category for the weather measure, specifying a rainy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Snowy (snowy). Qualitative category for the weather measure, specifying a snowy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sunny (sunny). Qualitative category for the weather measure, specifying a clear and sunny day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

No rain (noRain). Qualitative category for the weather measure, specifying no rainfall for a given day. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Stormy Weather (stormy). Stormy weather Status: active. First released: 3.0.0. Last updated: 3.0.0.

Fraction set for wide names

(wideFractionSet). Fraction set for wide names. For wide names.

Liquid fraction (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Mixed/homogenized sample (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Solid fraction (general) (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Not applicable (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

See Header for Fraction Analyzed (hFr). An indicator in wide-names to show that information on the fraction analyzed in found under a separate header. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Solid fraction (Wet) (solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Solid Fraction (Dry) (solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Multiple fraction (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Not reported (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Tables

Dictionary v3.0.1 Documentation v3.0.1

The ODM database model has 26 tables in its full relational database, with 19 tables for reporting data, and 7 look-up or reference tables. Of these report tables, only 3 are mandatory for the simplest micro-report template. In addition to many of the tables being optional, each table also has a mix of mandatory and optional headers. The full model is commonly referred to as "long" tables as it stores data with one measurement per row, though wide versions are also possible (see section on wide names).

> **Data storage**
>
> While storing data in the full suite of 26 tables in the PHES-ODM ensures optimal interoperablity and support by the ODM validation toolkit and other ODM libraries, as long as data is recorded in some of the tables, the validation library and other tools will still be functional and will ensure compliance with the data structure. Not all tables are relevant for all programs, just as not all fields are relevant for all programs. The PHES-ODM is modular, setting up a standard structure and vocabulary so that data can be compared and combined accurately - regardless of program, collection, or analysis approach. Users can also create custom tables or 'views' by merging fields from any table. A common format for data entry format is the "wide" table format, with *one day per row* and multiple measures or attributes per row (as opposed to the "long" *one measure per row* approach). This page does not provide guidance on generating wide tables, but

> there is a wide name and wide table section that can support efforts to implement that structure.

Table types

There are three general table types, which can be further thematically categorized:

1) **Results tables**. These are the main tables of interest for environmental surveillance reporting, which store information on samples and on the results of analysis of samples. Tables in this category include the `measures` and `samples` tables, which are used for regular reporting of new measurements and information on sample collection. There are three additional results tables that support regular reporting, but that are optional: - `measureSets` (optional) is used to link measures, - `sampleRelationships` (optional) is used when samples are pooled or split, and - `qualityReports` (optional) is used for detailed quality assurance and control measures.

2) **Program description tables**. Tables in this category store administrative information about the organizations involved in testing, locations where tests were conducted, protocols used, etc. These are tables that are updated much more infrequently than results tables. These can be further divided into:

- **Contact information tables**. The `organizations`, `contacts`, and `addresses` tables store contact information for the testing site and/or the person who performed the testing.
- **Protocol or methods tables**. The `protocols` and `instruments` tables hold information on the methods used for sample collection or measurement. `protocolSteps` and `protocolRelationships` tables are used in conjunction with the `protocols` table.

- **Data source & processing tables**. The `accessions`, `datasets`, and `calculations` tables record details about data provenance and ownership. `accessions` provides links to external datasets were either complimentary data (ie. sequencing ouptputs) or the original data may be found. The `datasets` table includes information on the data custodian and owner, as well as licensing.`calculations` records the kinds of calculations, models, or data treatments used to generate the data from raw inputs.
- **Geospatial tables**. The `polygons` and `sites` tables stores information on the sample area. `sites` records details about the physical sampling site and its context, while `polygons` records geospatial data about the area the aa site may reflect - for example if the site is a wastewater treatment plant, the polygon would reflect the treatment plant's catchment area. The `polygonRelationships` table is used in conjunction with the `polygons` table.

3) **Dictionary reference tables**. The `parts` table describes all elements of the ODM, including tables, table headers, measures, methods, categories, and units. The `sets` table stores collections of parts, such as units grouped together in a unitSet. The `languages` and `translations` tables support translations for the `parts` and `sets` tables. The `countries` and `zones` tables standardize location information to the ISO-2 and ISO-3 to reduce ambiguity and free-text errors when populating these fields, while improving interoperability of location metadata. `wideNames` is used for recording "wide names" (ie. variables or table headers for "wide" format data) in current use across various PHES-ODM templates, and has built in code to assist users in generating their own ODM-compatible "wide names".

Header roles

Each table in the PHES-ODM has column headers, also known as table variables, fields, or entity relationship attributes. The header serves as the

top row and contains the variable name.

Primary key (PK) - All tables have one primary key. The primary key serves as a unique identifier for each row in the table, meaning that a primary key value cannot be repeated.

Foreign key (FK) - Tables may have one or more foreign keys. A foreign key is when a primary key being referenced in another table, connecting an entry in one table to an entry in another table. This allows for relationships to be established between tables, making it possible to link data between different tables.

Header (header) - This label is used in a table description when a header is not a primary or foreign key.

Mandatory, optional, mandatoryIf

Each header may be classified as either `mandatory` or `optional`. In the `measures` table, examples of mandatory headers are the `measureID` and `aDateEnd`. The PHES-ODM validation toolkit can be used to validate data, and will return an error if a table lacks a mandatory header or if there are missing row entries for mandatory fields.

Additionally, there are special headers called `mandatoryIf` headers. These headers are mandatory if certain conditions apply. For example, the `protocol steps` table has row entries that are either `measures` or `methods`. If the row entry is a `measure`, then a `unit` becomes `mandatory` since all measures must have a unit. Therefore, units are `mandatoryIf` in the protocol steps table.

Table list

accessions Table

Address table

Calculations Table

Contact table

Countries look-up tables

Dataset table

Instrument table

Language Look-up table

Measure report table

Measure set report table

Organization table

Parts Look-up table

Public Health Actions Report Table

Polygon Relationships Table

Polygon table

Protocol relationships table

Protocols table

Protocol steps table

Quality reports table

Sample relationships table

Sample report table

Sets look-up table

Sites table

Translation look-up table

Wide name table

Zones look-up table

accessions Table

partID: accessions. Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field. ac

Accession Number in Repository (accessNum). The accession number for the data entry in the given data repository or hosting platform.Role: Header.Requirement: mandatory.Data type: varchar.

Version of Data Hosting Platform/Repository (hostVersion). The version of the data repository or hosting platform being used.Role: Header.Requirement: optional.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Address table

partID: addresses. The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). The Sites, Organizations, and Contacts tables include a link to the addresses table through Address ID. The short name for the table (partID) can be found in the instructions field. ad

Address Line 1 (addL1). Line 1 (the street name, number and direction) for a given address.Role: Header.Requirement: mandatory.Data type: varchar.

Address Line 2 (addL2). Line 2 (the unit number) for a given address.Role: Header.Requirement: optional.Data type: varchar.

City (city). The city where a site or organization is located; part of the address.Role: Header.Requirement: mandatory.Data type: varchar.

Postal or Zip Code (pCode). The zip code or postal code for a given address, specifying a specifc geographic area.Role: Header.Requirement: optional.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Calculations Table

partID: calculations. Table for recording data on data treatments and calculations applied to measurements and reported values. cl

Treatment ID (treatmentID). A unique identifier for a single calculation/data treatment, a single data treatment identifier.Role: Header.Requirement: mandatory.Data type: varchar.

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: optional.Data type: varchar.

Summary worksheet (summary). Summary sheet of the dictionary.xlxs file.Role: Header.Requirement: optional.Data type: varchar.

Sequence Order (order). The order a single calculation/data treatment takes within the full container pipeline/workflow.Role: Header.Requirement: recommended.Data type: integer.

Equation (equation). The equation used in the calculation/data treatment.Role: Header.Requirement: recommended.Data type: varchar.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Source Code (sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps.Role: Header.Requirement: recommended.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Contact table

partID: contacts. The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. co

First name of contact (firstName). Specifies the first name of a given contact.Role: Header.Requirement: optional.Data type: varchar.

Last name of contact (lastName). Specifies the last name of a given contact.Role: Header.Requirement: optional.Data type: varchar.

Contact email (email). Contact e-mail address, for the lab.Role: Header.Requirement: mandatory.Data type: varchar.

Contact phone (coPhone). Contact phone number, for the lab.Role: Header.Requirement: optional.Data type: varchar.

Role of contact (role). Specifies the organizational role of a given contact.Role: Header.Requirement: optional.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Countries look-up tables

partID: countries. Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. cu

ISO 3166-1 alpha-3 country code (isoCodeX). The ISO 3166-1 alpha-3 code, a three-letter country code which may allow a better visual association between the code and the country names than the 3166-1 alpha-2 code.Role: Header.Requirement: mandatory.Data type: varchar.

ISO 3166-1 numeric country code (numCode). The ISO 3166-1 numeric code, a three-digit country code which is identical to that developed and maintained by the United Nations Statistics Division, with the advantage of script (writing system) independence, and hence useful for people or systems using non-Latin scripts.Role: Header.Requirement: mandatory.Data type: varchar.

Country code top-level domain (tld). The internet top-level domain generally used or reserved for a country, sovereign state, or dependent territory identified with a country code.Role: Header.Requirement: mandatory.Data type: varchar.

English name for countries (nameEngl). English-language name of a given country.Role: Header.Requirement: mandatory.Data type: varchar.

Official state name (nameOfficial). Official english-language name of a given state.Role: Header.Requirement: mandatory.Data type: varchar.

Sovereign status of a country (sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory.Role: Header.Requirement: mandatory.Data type: varchar.

Country exonym (countryExonym). The English name foreigners use for the country.Role: Header.Requirement: mandatory.Data type: varchar.

Capital city exonym (capitalExonym). The English name foreigners use for the country's capital.Role: Header.Requirement: mandatory.Data type: varchar.

Country endonym (countryEndonym). The name locals use for their country.Role: Header.Requirement: mandatory.Data type: varchar.

Capital city endonym (capitalEndonym). The name locals use for their country's capital.Role: Header.Requirement: mandatory.Data type: varchar.

National language script (langScript). The language(s) and script(s) used for the country's capital endonyms.Role: Header.Requirement: mandatory.Data type: varchar.

Country national phone prefix (phone). International dialing code for the country.Role: Header.Requirement: mandatory.Data type: varchar.

Coordinated universal time (UTC) zone (utc). UTC – Time zone.Role: Header.Requirement: mandatory.Data type: varchar.

Coordinated universal time (UTC) zone in daylight savings (utcDST). Time zone during Daylight Saving Time.Role: Header.Requirement: mandatory.Data type: varchar.

Dataset table

partID: datasets. A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. ds

Dataset creation date (datasetDate). Specifies the date a given dataset was created.Role: Header.Requirement: recommended.Data type: datetime.

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

Description (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Original Data Format (originalFormat). The original structure or model used to record and store the data. This helps indicate if data have been transformed or mapped into the ODM structure.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: ogFormSet

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Instrument table

partID: instruments. The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. in

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

Model (model). Model number or version of the instrument.Role: Header.Requirement: mandatory.Data type: varchar.

Manufacturer (manufacturer). Manufacturer of an instrument.Role: Header.Requirement: optional.Data type: varchar.

Description (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Describe other instrument type, if applicable (insTypeOth). Description of the instrument in case it is not listed in instrumentType.Role: Header.Requirement: optional.Data type: varchar.

Index (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Language Look-up table

partID: languages. Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. la

Language family (langFam). Specifies the language family of a given language for translation and language tracking purposes.Role: Header.Requirement: mandatory.Data type: varchar.

Language name (langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes.Role: Header.Requirement: mandatory.Data type: varchar.

Native Name (natName). The native name of the language, i.e. what the language is called by its speakers.Role: Header.Requirement: mandatory.Data type: varchar.

ISO639-1 (iso6391). The first part of the ISO 639 series of international standards for language codes. Part 1 covers the registration of two-letter codes. There are 183 two-letter codes registered as of June 2021. The registered codes cover the world's major languages.Role: Header.Requirement: mandatory.Data type: varchar.

ISO639-2T (iso6392T). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'T' specifies the terminological code (T code).Role: Header.Requirement: mandatory.Data type: varchar.

First released version (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

Last updated version (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

Changes column (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Measure report table

partID: measures. The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. mr

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: optional.Data type: varchar.

Analysis date start (aDateStart). Date the measurement or analysis was started.Role: Header.Requirement: optional.Data type: datetime.

Analysis date end (aDateEnd). Date the measurement or analysis was completed.Role: Header.Requirement: mandatory.Data type: datetime.

EpiWeek Start Date (epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start dat resolves the possible ambiguity.Role: Header.Requirement: optional.Data type: date.

EpiWeek Number (epiWeek). The number of the epi week in which a sample what collected, or to which a measure would apply.Role: Header.Requirement: optional.Data type: integer.

Year of the EpiWeek (epiYear). The year in which the epi week is occuring.Role: Header.Requirement: optional.Data type: integer.

Measure relevance start date (relDateStart). The start date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons.Role: Header.Requirement: mandatoryIf.Data type: datetime.

Measure relevance end date (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons.Role: Header.Requirement: mandatoryIf.Data type: datetime.

Report date (reportDate). The date a measure was reported.Role: Header.Requirement: optional.Data type: datetime.

Value (value). Value of a measure, observation or attribute.Role: Header.Requirement: mandatory.Data type: varchar.

Value Treatment (valTreat). A field which specifies what kinds of data treatments or the nature of the measurement value.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: valTreatSet

Index (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

Measure license (measureLic). Specifies the access and use licensing for a given single measurement.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: licSet

Reportable (reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied.Role: Header.Requirement: optional.Data type: boolean.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Measure set report table

partID: measureSets. The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or varients that are identified in a single sample. The short name for the table (partID) can be found in the instructions field. ms

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: optional.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Organization table

partID: organizations. The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. or

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

Description (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

Organization Type (orgType). Specifies the type or purpose of a given organization.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: orgTypeSet

Organization level (orgLevel). The geographic level of an organization.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: orgLevelSet

Organization sector (orgSector). The sector of an organizationRole: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: orgSectorSet

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Parts Look-up table

partID: parts. Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. pa

Label (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

Part type column (Reported) (partType). The recorded part type for every part in the part table. This is the attribute in the parts table, not to be confused with partTypes, the part type.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: partTypes

Part description (partDesc). The description of the part.Role: Header.Requirement: mandatory.Data type: varchar.

Part instruction (partInstr). Additional notes and instructions on how a part is used and/or defined.Role: Header.Requirement: optional.Data type: varchar.

Foreign Key Alias ID (fKAliasID). The primary key that is being referenced by another name in another table as a foreign key.Role: Header.Requirement: mandatoryIf.Data type: varchar.

Domain (domain). Domain is the highest level of describing of a measure.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: domains

Group (group). Unique identifier for a group of measures. Mostly applicable for measures, methods, units, and aggregations.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: groups

Class (class). A unique identifier for a class, which is akin to a subgroup; it's a way of grouping parts within a given group. A group can have one or more classes to describe different parts of the class.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: classes

Nomenclature (nomenclature). A classification system to report the measure class. Only applicable to variants, mutations, and diseases.Role:

Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: nomenclatures

Ontology reference (ontologyRef). Ontology reference for a part.Role: Header.Requirement: optional.Data type: varchar.

LaTeX expression (latExp). LaTeX expression used to generate formulas, symbols, etc. Mainly relevant for units.Role: Header.Requirement: mandatoryIf.Data type: varchar.

Aggregation scale (aggregationScale). A scale used for an aggregation. Only applicable for measures and units.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: aggregationScales

Status (status). Whether the part is still active and can be used in the most current ODM version. Values are 'active' or 'inactive'.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: statusSet

First released version (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

Last updated version (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

Changes column (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

Protocol steps table (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Protocol steps table required headers (protocolStepsRequired). Specifies the columns required in a Protocol Steps table.Role: Header.Requirement: optional.Data type: varchar.

Protocol steps table column order (protocolStepsOrder). Specifies the order of the columns in a Protocol Steps table.Role: Header.Requirement: optional.Data type: integer.

Protocol relationships table (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a proceedure) and measureIDs (a measure). An example of a method is centrifugation; where the centriguation rotation speed is described as a measure. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Protocol Relationship table required headers (protocolRelationshipsRequired). Specifies the columns required in the Protocol Organization table.Role: Header.Requirement: optional.Data type: varchar.

Protocol relationships table column order (protocolRelationshipsOrder). Specifies the order of the columns in the Protocol Organization table.Role: Header.Requirement: optional.Data type: integer.

Measure report table (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Measures table required headers (measuresRequired). Specifies the columns required in a Measures table.Role: Header.Requirement: optional.Data type: varchar.

Measures table column order (measuresOrder). Specifies the order of the columns in a Measures table.Role: Header.Requirement: optional.Data type: integer.

Measure set report table (measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or varients that are identified in a single sample. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Measure sets table column order (measureSetsOrder). Specifies the order of the columns in a Measure Sets table.Role: Header.Requirement: optional.Data type: integer.

Measure Set table required headers (measureSetsRequired). Specifies the columns required in a Measure Sets table.Role: Header.Requirement: optional.Data type: varchar.

Dataset table (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Dataset table required headers (datasetsRequired). Specifies the columns required in a Datasets table.Role: Header.Requirement: optional.Data type: varchar.

Datasets table column order (datasetsOrder). Specifies the order of the columns in a Datasets table.Role: Header.Requirement: optional.Data type: integer.

Sites table (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an eviromental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the infomation changes often. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Sites table required headers (sitesRequired). Specifies the columns required in a Sites table.Role: Header.Requirement: optional.Data type: varchar.

Sites table column order (sitesOrder). Specifies the order of the columns in a Sites table.Role: Header.Requirement: optional.Data type: integer.

Sample report table (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site.Samples can be combined, split, stored and reused. The `Sample relationships` (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Sample table required headers (samplesRequired). Specifies the columns required in a Samples table.Role: Header.Requirement: optional.Data type: varchar.

Samples table column order (samplesOrder). Specifies the order of the columns in a Samples table.Role: Header.Requirement: optional.Data type: integer.

Address table (addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). The Sites, Organizations, and Contacts tables include a link to the addresses table through Address ID. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Address table required headers (addressesRequired). Specifies the columns required in a Addresses table.Role: Header.Requirement: optional.Data type: varchar.

Addresses table column order (addressesOrder). Specifies the order of the columns in the Addresses table.Role: Header.Requirement: optional.Data type: integer.

Contact table (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Contact table required headers (contactsRequired). Specifies the columns required in a Contacts table.Role: Header.Requirement: optional.Data type: varchar.

Contacts table column order (contactsOrder). Specifies the order of the columns in a Contacts table.Role: Header.Requirement: optional.Data type: integer.

Organization table (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Organziation table required headers (organizationsRequired). Specifies the columns required in a Organizations table.Role: Header.Requirement: optional.Data type: varchar.

Organizations table column order (organizationsOrder). Specifies the order of the columns in a Organizations table.Role: Header.Requirement: optional.Data type: integer.

Public Health Actions Report Table (phActions). Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: mandatory.Data type: varchar.

Public health actions table required headers (phActionsRequired). Required headers in the public health actions table.Role: Header.Requirement: mandatory.Data type: varchar.

Public health actions table column order (phActionsOrder). Specifies the order of the columns in the public health actions table.Role: Header.Requirement: mandatory.Data type: integer.

Calculations Table (calculations). Table for recording data on data treatments and calculations applied to measurements and reported values.Role: Header.Requirement: optional.Data type: varchar.

Calculations table required headers (calculationsRequired). Required headers in the calculations table.Role: Header.Requirement: mandatory.Data type: varchar.

Calculations table column order (calculationsOrder). Specifies the order of the columns in the calculations table.Role: Header.Requirement: mandatory.Data type: integer.

Instrument table (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Instrutment table required headers (instrumentsRequired). Specifies the columns required in the Instruments table.Role: Header.Requirement: optional.Data type: varchar.

Instruments table column order (instrumentsOrder). Specifies the order of the columns in the Instruments table.Role: Header.Requirement: optional.Data type: integer.

Polygon Relationships Table (polygonRelationships). Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Polygon relationships table required headers (polygonRelationshipsRequired). Required headers in the polygon relationships table.Role: Header.Requirement: mandatory.Data type: varchar.

Polygon relationships table column order (polygonRelationshipsOrder). Specifies the order of the columns in the polygon relationships table.Role: Header.Requirement: mandatory.Data type: integer.

Polygon table (polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Polygon table required headers (polygonsRequired). Specifies the columns required in a Polygons table.Role: Header.Requirement: optional.Data type: varchar.

Polygons table column order (polygonsOrder). Specifies the order of the columns in a Polygons table.Role: Header.Requirement: optional.Data type: integer.

accessions Table (accessions). Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Accessions table required headers (accessionsRequired). Required headers in the accessions table.Role: Header.Requirement: mandatory.Data type: varchar.

Accessions table column order (accessionsOrder). Specifies the order of the columns in the accessions table.Role: Header.Requirement: mandatory.Data type: integer.

Language Look-up table (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Language table required headers (languagesRequired). Required headers in the Languages table.Role: Header.Requirement: optional.Data type: varchar.

Language table column order (languagesOrder). Specifies the order of the columns in the Languages table.Role: Header.Requirement: optional.Data type: integer.

Translation look-up table (translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Translation table required headers (translationsRequired). Required headers in the Translations table.Role: Header.Requirement: optional.Data type: varchar.

Translation table column order (translationsOrder). Specifies the order of the columns in the Translation table.Role: Header.Requirement: optional.Data type: integer.

Parts Look-up table (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Parts table required headers (partsRequired). Required headers in the Parts table.Role: Header.Requirement: optional.Data type: varchar.

Parts table column order (partsOrder). Order of headers in the Parts table.Role: Header.Requirement: optional.Data type: integer.

Sets look-up table (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Sets table required headers (setsRequired). Required headers in the Sets table.Role: Header.Requirement: optional.Data type: varchar.

Sets table column order (setsOrder). Specifies the order of the columns in the Sets table.Role: Header.Requirement: optional.Data type: integer.

Quality reports table (qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Quality report table required headers (qualityReportsRequired). Specifies the columns required in the Quality Reports table.Role: Header.Requirement: optional.Data type: varchar.

Quality rerpots table column order (qualityReportsOrder). Specifies the order of the columns in the Quality Reports table.Role: Header.Requirement: optional.Data type: integer.

Sample relationships table (sampleRelationships). Table for recording the relationships between samples.Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Sample relationships table required headers (sampleRelationshipsRequired). Specifies the columns required in a Sample Relationships table.Role: Header.Requirement: optional.Data type: varchar.

Sample relationships table column order (sampleRelationshipsOrder). Specifies the order of the columns in a Sample Relationships table.Role: Header.Requirement: optional.Data type: integer.

Protocols table (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Protocols table required headers (protocolsRequired). Specifies the columns required in the Protocols table.Role: Header.Requirement: optional.Data type: varchar.

Protocols table column order (protocolsOrder). Specifies the order of the columns in the Protocols table.Role: Header.Requirement: optional.Data type: integer.

Countries look-up tables (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Counries table required headers (countriesRequired). Required headers in the countries table.Role: Header.Requirement: optional.Data type: varchar.

Countries table column order (countriesOrder). Specifies the order of the columns in the countries table.Role: Header.Requirement: optional.Data type: integer.

Zones look-up table (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Zones table required headers (zonesRequired). Required headers in the zones table.Role: Header.Requirement: optional.Data type: varchar.

Zones table column order (zonesOrder). Specifies the order of the columns in the zones table.Role: Header.Requirement: optional.Data type: integer.

Wide name table (wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

Wide name table required (wideNamesRequired). Column for indicating which fields in the wide names table are mandatory.Role: Header.Requirement: optional.Data type: varchar.

Wide name table order (wideNamesOrder). Column for indicating the order of the fields in the wide names table.Role: Header.Requirement: optional.Data type: integer.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Data Type column (Reported) (dataType). The recorded data type for every part in the part table. This is the attribute in the parts table, not to be confused with dataTypes, the part type.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: dataTypes

Minimum value part support (minValue). The minimum value of part.Role: Header.Requirement: mandatoryIf.Data type: varchar.

Maximum value part support (maxValue). The maximum value of a part.Role: Header.Requirement: mandatoryIf.Data type: varchar.

Minimum length (minLength). The maximum value of measure.Role: Header.Requirement: mandatoryIf.Data type: integer.

Maximum length (maxLength). The maximum length of the value of a part or measure.Role: Header.Requirement: mandatoryIf.Data type: integer.

Public Health Actions Report Table

partID: phActions. Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. pha

Public health action datetime (actionDT). The date and Time of the public health action.Role: Header.Requirement: optional.Data type: datetime.

Measure relevance start date (relDateStart). The start date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons.Role: Header.Requirement: optional.Data type: datetime.

Measure relevance end date (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons.Role: Header.Requirement: optional.Data type: datetime.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Polygon Relationships Table

partID: polygonRelationships. Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. por

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Polygon table

partID: polygons. The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. po

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

Description (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

Type of geography (geoType). Type of geography that is represented by the polygon.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: geoTypeSet

European Petroleum Survey Group Coordinates (geoEPSG). The unique EPSG code specifying a given geospatial area.Role: Header.Requirement: mandatory.Data type: float.

Well-known text (geoWKT). Well-known text of the polygonRole: Header.Requirement: mandatory.Data type: varchar.

File location of polygon (fileLocation). The location of the file containing the geometry of the polygon.Role: Header.Requirement: optional.Data type: varchar.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Polygon License (poLic). The license for the availability of the polygon shapefile.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: licSet

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Protocol relationships table

partID: protocolRelationships. The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a proceedure) and measureIDs (a measure). An example of a method is centrifugation; where the centriguation rotation speed is described as a measure. The short name for the table (partID) can be found in the instructions field. pr

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Protocols table

partID: protocols. The table for protocols. The short name for the table (partID) can be found in the instructions field. pro

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: optional.Data type: varchar.

Summary (summ). Short description of the assay and how it is different from the other assay methods.Role: Header.Requirement: optional.Data type: varchar.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Protocol version (protocolVersion). Specifies the version of a method set.Role: Header.Requirement: optional.Data type: integer.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Protocol steps table

partID: protocolSteps. The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. ps

Summary (summ). Short description of the assay and how it is different from the other assay methods.Role: Header.Requirement: optional.Data type: varchar.

Protocol step version (stepVer). Specifies the version of a given protocol step.Role: Header.Requirement: optional.Data type: varchar.

Reference link (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

Value (value). Value of a measure, observation or attribute.Role: Header.Requirement: mandatoryif.Data type: varchar.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Quality reports table

partID: qualityReports. The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. qr

Quality flag (qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample or measure.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: qualityIndicators

Severity indicator (severity). An indicator of the severity or seriousness of a quality flag.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: sevSet

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Sample relationships table

partID: sampleRelationships. Table for recording the relationships between samples.Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field. sar

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Sample report table

partID: samples. The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site.Samples can be combined, split, stored and reused. The `Sample relationships` (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. sas

Sample origin (origin). An attribute of a sample specifying the origin.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: originSet

Collection period (collPer). Collection period. The time period over which the sample was collected, in hours. Alternatively, use collectionStart and collectionEnd.Role: Header.Requirement: mandatory.Data type: float.

Collection number (collNum). The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling.Role: Header.Requirement: mandatory.Data type: integer.

Pooled (pooled). Is this a pooled sample, and therefore composed of multiple child samples obtained at different sitesRole: Header.Requirement: optional.Data type: boolean.

Collection date time (collDT). For grab samples this is the date, time and timezone the sample was taken.Role: Header.Requirement: mandatory.Data type: datetime.

Collection date time start (collDTStart). For integrated time averaged samples this is the date, time and timezone the sample was started being taken.Role: Header.Requirement: optional.Data type: datetime.

Collection date time end (collDTEnd). For integrated time average samples this is the date, time and timezone the sample was finished being taken.Role: Header.Requirement: optional.Data type: datetime.

Collection Date (time not included) (collDate). Sample collection date, where time is reported in a separate field.Role: Header.Requirement: optional.Data type: date.

Collection Approximate Time Period (collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: collAppxSet

EpiWeek Start Date (epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start dat resolves the possible ambiguity.Role: Header.Requirement: optional.Data type: date.

EpiWeek Number (epiWeek). The number of the epi week in which a sample what collected, or to which a measure would apply.Role: Header.Requirement: optional.Data type: integer.

Year of the EpiWeek (epiYear). The year in which the epi week is occuring.Role: Header.Requirement: optional.Data type: integer.

Date sample was sent (sentDate). Date that the sample was sent from the collection site to the lab.Role: Header.Requirement: optional.Data type: datetime.

Date sample recieved (recDate). The date the sample was received at the laboratory for analysis.Role: Header.Requirement: optional.Data type: datetime.

Reportable (reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied.Role: Header.Requirement: optional.Data type: boolean.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Sets look-up table

partID: sets. Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. se

Set type (setType). The type of set. i.e. quality set, aggregation set, unit setRole: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: setTypeSet

Label (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

Enumeration for set values (enumeration). The numeric value that corresponds to a given value in a set, defined in the sets table.Role: Header.Requirement: mandatory.Data type: integer.

Status (status). Whether the part is still active and can be used in the most current ODM version. Values are 'active' or 'inactive'.Role:

Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: statusSet

First released version (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

Last updated version (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

Changes column (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Sites table

partID: sites. The table that contains information about a site; the location where an environmental sample was taken. The site of an eviromental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the infomation changes often. The short name for the table (partID) can be found in the instructions field. si

Sample shed (sampleShed). A geographic area, physical space, or structure. A sample is taken from a sampleshed for a representative measurement of a substance(s).Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: shedSet

Level of Aggregation of a Sampling Site (siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type of region is represented by the base sewershed. This can be used to pool together or average results across similar sewersheds, and avoid trying to average different scales of sewershed together without a correction for size.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: siteLevelSet

Name (name). Human-readable name of an entity; such as the name of a site, domain, specimen, group, class, attribute, unit, nomenclature or other entity. Specific naming conventions vary by usecase and are user-generated. To differenciate between the `name` field in different tables, please use attribute-specific widenames per widename rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

Description (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

Health Region for a Site (healthRegion). A free-text variable for listing the health region for a given site.Role: Header.Requirement: optional.Data type: varchar.

Latitude (geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721)Role: Header.Requirement: mandatoryIf.Data type: float.

Longitude (geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000)Role: Header.Requirement: mandatoryIf.Data type: float.

European Petroleum Survey Group Coordinates (geoEPSG). The unique EPSG code specifying a given geospatial area.Role: Header.Requirement: mandatoryIf.Data type: float.

Last edited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Translation look-up table

partID: translations. Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. tr

Label (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

Part description (partDesc). The description of the part.Role: Header.Requirement: mandatory.Data type: varchar.

Part instruction (partInstr). Additional notes and instructions on how a part is used and/or defined.Role: Header.Requirement: optional.Data type: varchar.

First released version (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

Last updated version (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

Changes column (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

Notes (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

Wide name table

partID: wideNames. The table for wide names. The short name for the table (partID) can be found in the instructions field. wn

Label (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

character length (charLength). The number of characters used for the wide names.Role: Header.Requirement: optional.Data type: integer.

Description (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: mandatory.Data type: varchar.

Wide name source (source). The database or table sourced for the wide name.Role: Header.Requirement: mandatory.Data type: varchar.

Measure identification (wide table) (wideMeasure). Unique identifier for a measure in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

Specified protocol (wide table) (wideProtocol). Unique identifier for a protocol in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

Specified attribute (wide table) (wideAttribute). Unique identifier for an attribute in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

Report table name (wide table) (reportTableName). The report table that the wide name calls from.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: tables

Part type name (wide table) (partTypeName). The part type being used in a wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: partTypes

Compartment name (wide table) (compartmentName). The compartment referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: compartments

Specimen name (wide table) (specimenName). The specimen referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: specimens

Fraction name (wide table) (fractionName). The fraction analyzed referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: fractionSet

Measure name (wide table) (measureName). The measure referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: measurements

Method name (wide table) (methodName). The method referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: methods

Unit name (wide table) (unitName). The unit referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: units

Aggregation name (wide table) (aggregationName). The aggregation referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: aggregations

Index (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

Attribute name (wide table) (attributeName). The attribute referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: attributes

Wide name measurement and linkage tag (tag). A tag used in wide names to clarify relationship and linkage in the flattened, single table format.Role: Header.Requirement: optional.Data type: varchar.

Zones look-up table

partID: zones. Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. zo

English name of country sub-domains (zoneName). The english-language name for a given country sub-domain.Role: Header.Requirement: mandatory.Data type: varchar.

Page created on Thu Sep 17 00:00:00 2026.