

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

2026-09-17

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Introduction

Dictionary v3.0.1 Documentation v2.1.1

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

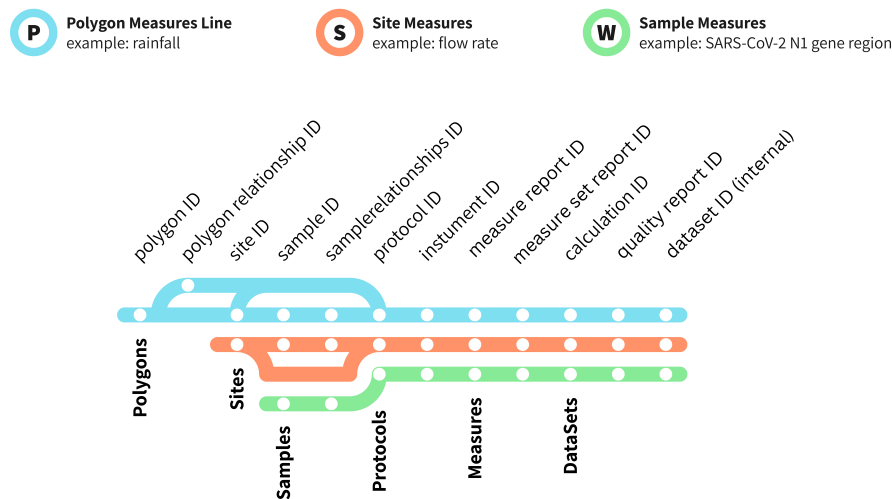


Figure 1.: **Figure 1 - Key ODM tables for recording data**

Introduction

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 interoperability.

 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 watershed or municipality. **Figure**

Introduction

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.

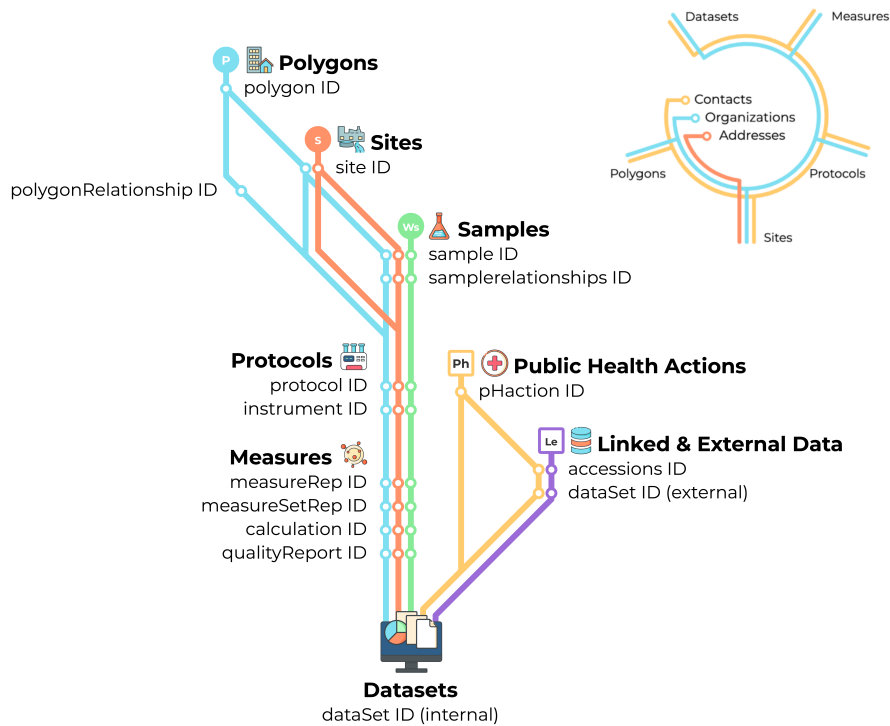


Figure 2.: **Figure 2 - ODM tables and ‘subway’ lines for storing measures**

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 v2.1.1

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 Principles](#).

Background

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

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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](#)

Getting to know the ODM

- [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

“Sets” and the rationale behind sets

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

Getting to know the ODM

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.

Getting to know the ODM

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,

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`qualityFlag` was included as an attribute 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 field has been populated. Similarly, analysis

Translation and language capabilities

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.

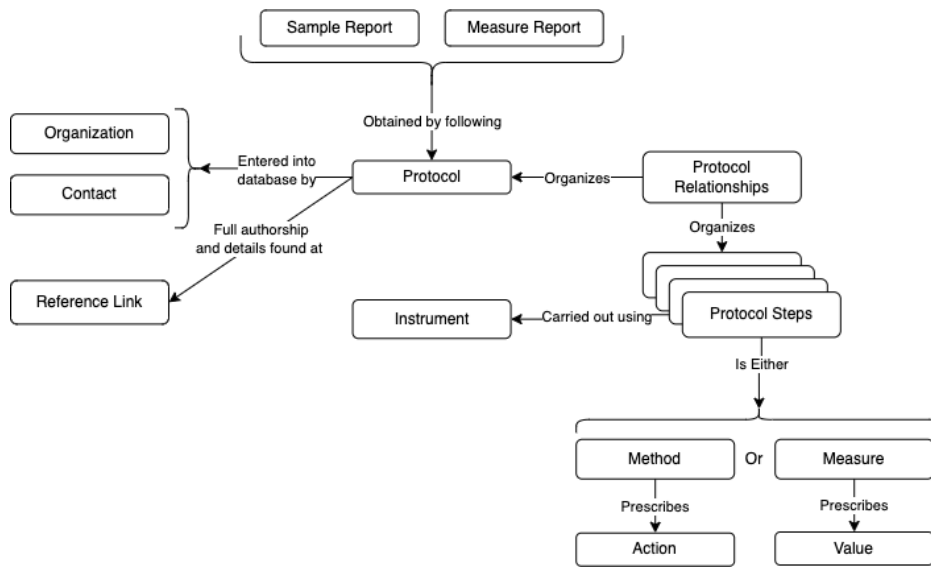


Figure 3.: Figure A: Main entities and relationships used to represent protocols

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	standardizationpmmov15standardizationpmmov1
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	standardizationpmmov15
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	orgID + last 3 letters of part ID of	caOnOtt002Uni-
Step ID	method/measure	Ion
Public	actionType + action + threatTarget	survAlert-
Health	+ actionDT	targSurvsarsCov228022027
Action ID		
Quality	quality flag part ID + either the	flagJcaOnOttOt-
Report ID	measure report ID, the sample ID, or	tawa-
	measure set report ID that the	site1202008021000covN1002
	quality report is for	
Measure	sampleID + part ID of measure +	caOnOt-
report ID	row number	tOtt20200802Covn1002
Measure set	Report ID of first measure in the set	caOnOt-
report ID	+ # measures in the set	tOtt20200801Covn1002003
Sample ID	siteID + collDT/collDTEnd (not	caOnOt-
	including time) + index (if	tOtt20200801
	applicable)	
Site ID	country code (ISO) + province code	caOnOttOtt
	(ISO) + first 2-3 letters of	
	municipality + 3 first letters of site	
	name	
Treatment	calcType + standard + order	standardiza-
ID		tionpmmov1

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

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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 Fisher-brand, 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

Recommended formula for user-generated IDs

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 is 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 quality 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

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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 an issue there so that a team member can respond.

How to use the ODM

Dictionary v3.0.1 Documentation v2.1.1

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

How to use the ODM

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.

1) How to use templates

- 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 complete these tables once and then update them as needed.
- ``Protocol steps table`` and ``Protocol relationships table`` are used alongside the ``Protocol``
- 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:

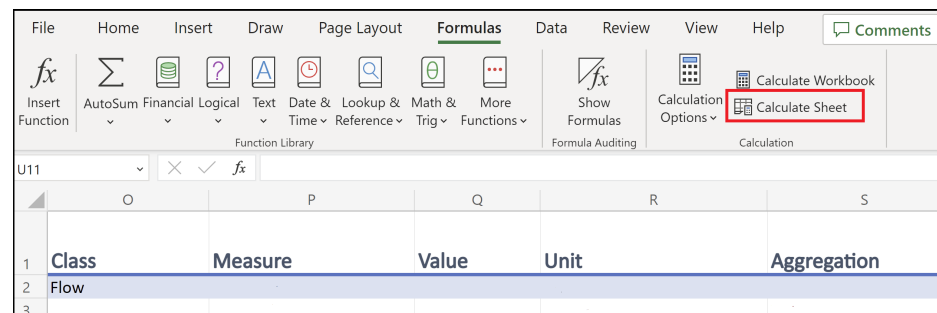
- **Identifier and unique identifier (red):** In these fields you will create a value that will be used to identify something. For instance, **Sample ID** is used to identify each unique sample. An identifier can be repeated between entries, while a unique identifier cannot. There is usually only one 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 contains 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.

How to use the ODM

- **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.



2) *How to report Measures and Measure sets*

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**

How to use the ODM

- **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

How to use the ODM

	A	B	C	D	E	F	G	H	I	J	K
1	Measure Report ID	Sample ID	Site ID	Measure set report ID	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.

Detailed description

- `Measure Report ID` (column A) is the unique identifier for this template, and it can be used to identify the measure in the system.
- You can repeat the other fields between entries (if needed). For instance, if you enter the same measure ID, you can enter different data for the other fields.
- You may have already created these identifiers in another template. For instance, you can use the same measure ID for different measures.

ii) Column D

- `Purpose` has a drop-down menu. If you are unsure what to put, select `Regular` for most measures (see 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 to

iii) Columns O and P

- These measure relevance date fields were added in version 3.0.0 to better contextualize style data. For measures like population counts, for example, which may have time constraints

3. Columns Q to AA

How to use the ODM

	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 dropdown menus. In general these fields are optional, but are recommended (see note below).
- `Compartment` is only truly necessary to report if you are reporting on multiple compartments.
- `Specimen` is mandatory when the ensemble of data you are entering has multiple specimens.
- `Fraction analyzed` applies only for water and wastewater samples. You can also report on other types of samples, but this field is not required.
- Of note is that if you generate wide names, these three fields are also required.

ii) Columns U and V

- `Group` and `Class` help organize the `Measure` field by making specific categories. They 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 ODM is a specific type of measurement.

iv) Column X

- `Value` is where you enter the value of your measure. For instance, you would enter 100 for a value of 100.
- Note: While the value you enter into this field can be of any data type, it must be a number.

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 a dropdown 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 denote if the value is a flag or not.

Detailed description

`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 treatment down menus, and AD is a free text field.
- `Nomenclature` is used when reporting a variant or disease to specify which naming convention is used.
- `Index` (column AD) is used if you have multiple entries with the same values in most other columns.

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 treatment set (`odm.org/sets.html#licSet`).
- `Reportable` (column W) is where you can indicate if the measure should not be used in the report.

iii) Column AG and AH

- These are identifier fields that are used to indicate the organization and contact information.

iv) Column AI, AJ, and AK

- `Last edited` is where you can indicate the date when the entry was last updated. This is a date field.
- `Reference link` is used to point out to an external reference for a single measure, treatment set, or variant.
- `Notes` is free text field for recording any additional details that users may feel are important.

Measure set report template

1. Columns A to G

How to use the ODM

	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 the report.
- For the rest, you can repeat the identifier between entries (if needed).
- You may have already created these identifiers in another template. In this case, you can use the same identifiers.

ii) Columns C and G

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

iii) Column F

- `Last edited` is a date field in which you can enter the date when the report was created.

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.

How to use the ODM

- **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](#).

Detailed Description

- **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 repeated.
- For the rest of the fields, you can repeat values between entries. For instance, if you have multiple samples from the same organization, you can repeat the same organization ID.
- The sample logic applies for sampling protocols (`Protocol ID`), for the individual samples.
- You may have already created these identifiers in another template. For instance you may have a template for sample collection that already has a `Sample ID` column.

How to use the ODM

ii) Columns F to G:

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

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

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

ii) Columns L to M:

- These are free form fields.

Detailed Description

- `Collection period` (column L) refers to the number of hours that you took to collect the sample.
- `Collection number` (column M) refers to the number of subsamples that were used to collect the sample.

iii) Columns O to Q:

- These fields are datetime fields to record details about when exactly a sample was collected. The format is 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 O).
- For composite or aggregated samples, users can use `Collection date time start` (Column P).

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 in 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 collection.
- `EpiWeek Start Date` (Column T) is an optional date field used when recording [epiWeek]

ii) Column S:

How to use the ODM

- `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 data entry.
- `EpiWeek Number` (column U) specifies the number of the EpiWeek (between 1 and 52).
- `Year of the EpiWeek` (column V) specifies the year of the epiWeek.
- In order for epiWeek information to be useful, **all** three pieces of information must be entered.

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 a sample was sent. The format is 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 collection site.
- `Last edited` (Column Z) is where you can enter the date when the entry was last edited.

ii) Columns Y and AA:

Detailed Description

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

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

iii) Columns E and F:

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

How to use the ODM

- `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 anything.

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	gcMI	
6	April_N1-N2_MP.sloq		loq	5	gcMI	
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 step.
- `Protocol step source` (column E) specifies the protocol step that you are reporting on.

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` (column C).

iii) Columns D, F and G:

- These are free form fields.
- `Summary` (column D) is a short description of the protocol step that you are reporting on.
- `Protocol step version` (column F) specifies the version of a given protocol step.
- `Reference link` (column G) is used to report a URL or hyperlink to the protocol step.

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.

Detailed Description

- You can repeat values between entries. For instance, if you are entering two different protocols, you can enter the same protocol ID in two different entries.
- ii) Column K:
- `Value` is a free form field where, if the protocol step is a measure, you can enter a value.
 - Of note, for some measures and methods, they can take enumerated values, so this field can be used to enter those values.
- 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 is used to enter the unit of the measure.
 - `Aggregation` (column M) depends on what you entered in `Unit` (column L). This field is used to enter the aggregation of the measure.
- iv) Columns N and O:
- These are a date field (column N) and a free form field (column O) where you can enter the date and time when the entry was last updated.
 - `Last edited` (column N) is where you can enter the date when the entry was last updated. 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 changed.
 - `Source Protocol ID` (column A), `Organization ID` (column F), and `Contact ID` (column G) are used to link the protocol to the source protocol, organization, and contact.
 - `Source Protocol ID` (column A) is where you can enter the `Protocol ID` of the protocol you are using as a reference.
 - `Organization ID` (column F) records the linked organization who created or designed the protocol.
 - `Contact ID` (column G) records the contact information for questions about the protocol.
- ii) Columns C to E:

How to use the ODM

- These are free form fields in which you can enter the indicated information.
- `Name` (column D) refers to the name that you have decided to give your protocol.
- `Summary` (column D) and `Reference link` (column E) record a narrative of the protocol.

iii) Columns H, J:

- These are free form fields.
- `Protocol version` (column I) is where you can indicate the version of the protocol.
- `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 was last edited.

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-incrementing field.
- All the remaining identifiers (columns B to D; F and G) are either `Protocol ID` or `Step ID`.
- You should only enter a value for one of the two `object` columns (C or D).
- An example will be given in point (ii) below.

ii) Column E:

- `Relationship` contains a drop-down menu; it is where you can select the relationship between the two entities.

5) *How to report metadata*

- 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 enter
- `Last edited` (column G) is where you can enter the date when the entry was last updated

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 represent 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 identifier 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 available 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

How to use the ODM

	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		Responsible 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 typically generated by concatenating the pipeline and treatment IDs together.
- **Pipeline ID:** A unique identifier for the data pipeline, or sequence of calculations/data treatments applied to the data.
- **Treatment ID:** A unique identifier for each treatment or step in the calculation or data pipeline that generated the reported measure.
- **Calculation Type:** An enumerated 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.

How to use the ODM

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

How to use the ODM

	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

How to use the ODM

	A	B	C
1	Polygon relationship ID Polygon 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	flagUI9945_TPMOOS221023_1_covN1_2_2022-11-04	9945_TPMOOS221023_1_covN1_2_2022-11-04	NA	NA	flagUI
5	flagI17969_TPTIMM230215_1_covN2_3_2023-02-17	17969_TPTIMM230215_1_covN2_3_2023-02-17	NA	NA	flagI

this example data is adapted from open data sources using the ODM at the [Ontario Wastewater Surveillance Consortium](#)

How to use the ODM

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.
- **Longitude:** 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

Quick Start

	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 `accessions` table.
- `Measure report ID` (column B), `Measure set report ID` (column C), and `Public Health Action ID` (column D) are identifiers for the measures.
- `Organization ID` (column F) is an field to link the organization who made the publication.

ii) Column E:

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

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:

How to use the ODM

- These are free form fields in which you can enter various information
- `Accession number in Repository` (column G) should be the unique reference
- `Version of Data Hosting Platform/Repository` (column H) sets the version
- `Notes` (column J) is a free text field to record additional comments

ii) Columns I:

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

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, and

ii) Columns B to D, and F:

- These are free form fields in which you can enter various information
- `Address Line 1` (column B) and `Address Line 2` (column C) record spatial

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iii) Columns E and G:

- These are categorical fields that take predetermined enumerated 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.phesodm.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.phesodm.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.

How to use the ODM

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

ii) Columns C and G:

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

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 extra 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 the
- `Pipeline ID` (column B) is a unique identifier for the data pipeline

Quick Start

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

How to use the ODM

- `Equation` (column I) and `Source code` (column K) specify additional information.
- `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, and it must be unique across all datasets.
- For `Parent dataset ID` (column A), you can repeat the value between datasets.

ii) Column C

- `Dataset creation date` (column C) is a date field where you can enter the date.

Quick Start

iii) Columns D, F, and G:

- These are free form fields in which you can enter various information related to the dataset.
- `Name` (column D) and `Summary` (column G) are optional fields to report more detail about the dataset.
- `Reference Link` (column F) points to an external link for additional information, such as a dataset description or a data access link.

iv) Columns E and H:

- These are categorical input fields for reporting additional metadata on the dataset.
- `License` (column E) reports the usage rights of the dataset. For example, whether the dataset is public domain or has a specific license (<https://odm.org/sets.html#licSet>).
- `Language ID` is the ISO-6393 code for the natural language in which the dataset was created and present in the [`languages` reference table] (<https://docs.phesodm.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 a unique identifier for the funder).
- For information regarding Data Custodians, you can enter their `Custody Contact ID` (which is a unique identifier for the data custodian).

How to use the ODM

ii) Columns M, N and O:

- These are a categorical field (column M), date field (column N) and a text field (column O).
- `Original data format` (column M) is used to report the original study identifier. This is used to link the ODM to explain any structural oddities resulting from the mapping process or to provide a link to the original data (e.g. odm.org/sets.html#ogFormSet).
- `Last edited` (column N) is the date when the entry was updated. This is used to track changes to the data.
- `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) and `Model` (column C).
- A `Description` (column E) and `Reference link` (column F) can also be entered.

iii) Columns G to H:

- `Instrument Type` (column G) is a categorical input to better describe the type of instrument (see odm.org/sets.html#insTypeSet).
- `Describe other instrument type, if applicable` (column H) is a free text field to describe other instrument type, if applicable.

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 regarding the instrument.
- You can use `Index` (column I) to differentiate two entries of data that are the same.
- `Last Edited` (column J) is a date field where you can indicate the date when the entry was last edited.
- `Notes` (column K) is for any extra comments or information.

Organization template

1. Columns A to E

How to use the ODM

	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 template.
- For `Address ID` (column D), you can repeat the value between entries.
- You may have already created some of the identifiers in other templates.

ii) Columns B and C:

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

iii) Columns E to G:

- These are fields with drop-down menus where you can select various categorical values.
- For the possible categorical values for `Organization type` (column E) see odm.org/sets.html#orgTypeSet.
- For the possible categorical values for `Organization level` (column F) see odm.org/sets.html#orgLevelSet.
- For the possible categorical values for `Organization sector` (column G) see odm.org/sets.html#orgSectorSet.

iv) Columns H and I:

Quick Start

- These are a date field (column H) and a free form field (column I) where you can enter notes.
- `Last edited` (column H) is the date when the entry was updated. This field is used for tracking changes.
- `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 repeated.
- For `Dataset ID` (column B), you can repeat the value between entries (if needed). For example, you can use the same Dataset ID for multiple polygons within the same dataset.
- 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 the polygon.
- `Name` (column C) is the name of the polygon, and `Description` (column D) offers a brief description of the polygon.
- `European Petroleum Survey Group Coordinates` (or EPSG coordinates) (column F) is a coordinate system identifier. It is used to define the spatial reference of the polygon.
- `Well-known Text` (column G) provides wkt (the text markup language that can be used to represent geometric objects).

How to use the ODM

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

iii) Columns F:

- For `Type of geography` (column E) of the polygon, you can select on the dropdown 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 linking polygons to organizations and contacts.

ii) Column L:

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

iii) Columns M and N:

- `Last edited` (column M) is a date field where you can enter the date when the polygon was last edited.
- `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	Polygon 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 table.
- `Polygon ID subject` (column B) and `Polygon ID object` (column D) reference rows in the Polygon table.

ii) Column C:

- `relationship between entities` (column C) describes the actual relationship between the two entities (see 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 was created or last modified.
- `Notes` (column F) is for any extra comments or information.

Public Helath Actions template

1. Columns A to E

How to use the ODM

	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 each action.
- `Measure Report ID` (column C) and `Measure set report ID` (column D) are used to link actions to measures.
- `Organization ID` (column E) links to the organization orchestrating the action.

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:

- These are categorical fields used to describe the nature and the target of the action.
- `Public health action type` (column G) describes the high-level nature of the action (action types are listed in [[Public Health Action Type Set](https://odm.org/sets.html#actionTypeSet)]), while `public health action` (column H) provides the specific action details (odm.org/sets.html#allActionsSet).

Quick Start

- ``Public health threat targetted by action`` is exactly as it describes, and it takes measurements from 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, while

iii) Columns M to N:

- ``Last edited`` (column M) is a date field where you can enter the date when the entry was last edited.
- ``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 cannot be repeated.
- For the rest of the columns, you can repeat the value between entries (if needed). For instance, you can have the same measure report ID for multiple samples.
- You may have already created some of the identifiers in other templates. For instance, you can have the same measure set report set ID for multiple quality reports.

How to use the ODM

ii) Columns E and F:

- `Quality flag` (column E) is a drop-down menu field where you can select a quality flag. See odm.org/sets.html#qualityIndicators).
- `Severity indicator` (column F) is also a drop-down menu field where you can indicate the severity of the quality flag. See 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 a date.
- `Last edited` (column G) is a date field where you can enter the date.
- `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

Quick Start

- For the rest of the columns, you can repeat the value between entries (if needed). For example, you can repeat the value for the parent site ID.
- `Parent site ID` (column A) refers to the site that is parent to the site that is being created.
- `Address ID` (column H), `Organization ID` (column I), and `Contact ID` (column J) are used to link the site to an address, organization, and contact.

ii) Columns E to G:

- These are drop-down menu fields in which you can specify the `Site Type` (column E), `Shed` (column F), and `Level of Aggregation of a Sampling Site` (column G).
- A list of site types can be found in the [`Site Set`](https://docs.phesodm.org/sets.html#siteTypeSet), and the sheds can be found in the [`Sampleshed Set`](https://docs.phesodm.org/sets.html#shedSet).
- The `Level of Aggregation of a Sampling Site` (column G) is a field to specify the level of aggregation of a sampling site. Possible values for `Level of Aggregation of a Sampling Site` (column G) can be found in the [`Site Level Set`](https://docs.phesodm.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 the site.
- `Name` (column K) and `Description` (column L) are for more internal details describing the site.
- `Health Region for Site` (column O) reports the health region, and should match how the site is categorized in the health region.

How to use the ODM

ii) Columns M and N:

- These are identifier fields that you can use to record additional information.
- These fields 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 information.
- `European Petroleum Survey Group Coordinates` (column Q) is a coordinate

iv) Columns S to T:

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

You have now entered in your metadata, congratulations!

Notes regarding templates

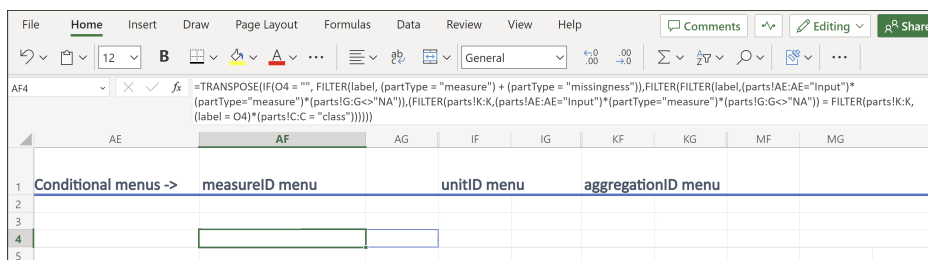
Templates with conditional menus (Measure report and Protocol steps)

Adding more conditional menus

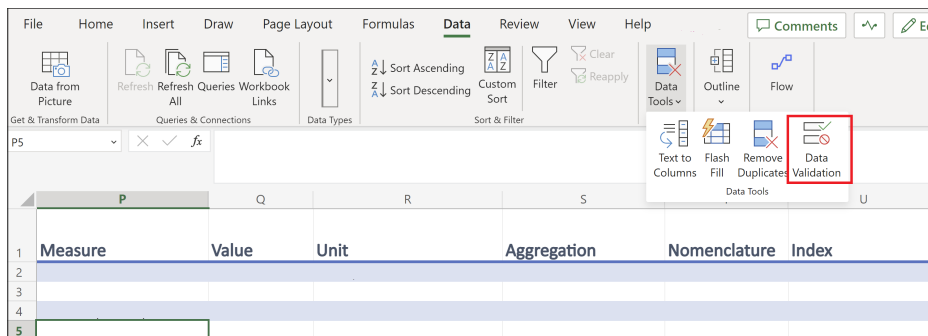
NOTE: The conditional drop-downs in the excel templates are very fragile. They have also been depreciated in version 3+ of the PHES-ODM. Drop-down menus are still available, but not with the conditional menus.

Notes regarding templates

- 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).

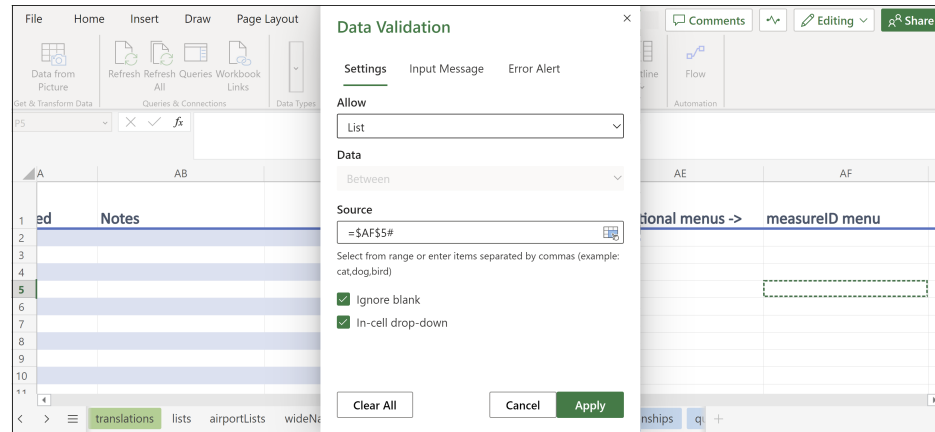


- Then, to create the new menu, you would go to P5 (which is where the new conditional menu will be located). You would select “Data validation”, which is under “Data Tools” in the “Data” tab (it is outlined in red in the image below).



How to use the ODM

- Finally, you would select “List” from the “Allow” menu and then enter the following text “=\$AF\$5#” 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 v2.1.1

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 from. 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.

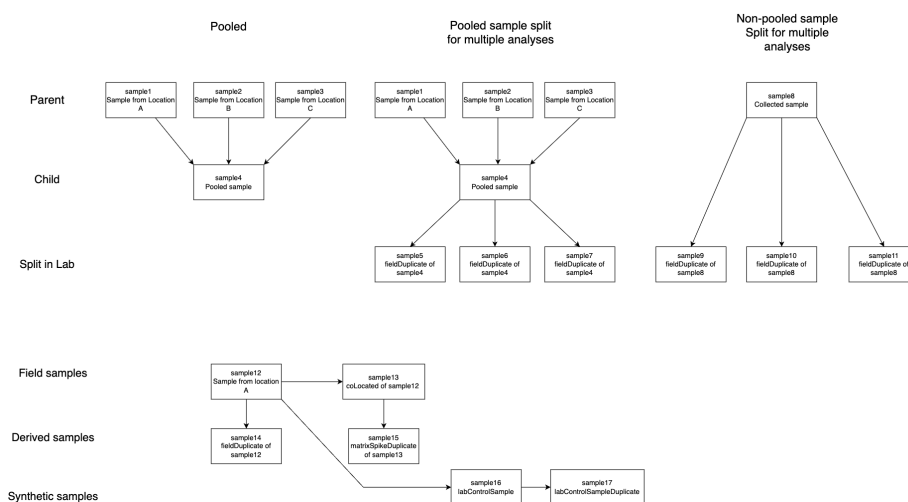


Figure 4.: **Figure A: Various possible sample relationships.**

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`

Sample Relationships

```
- 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.

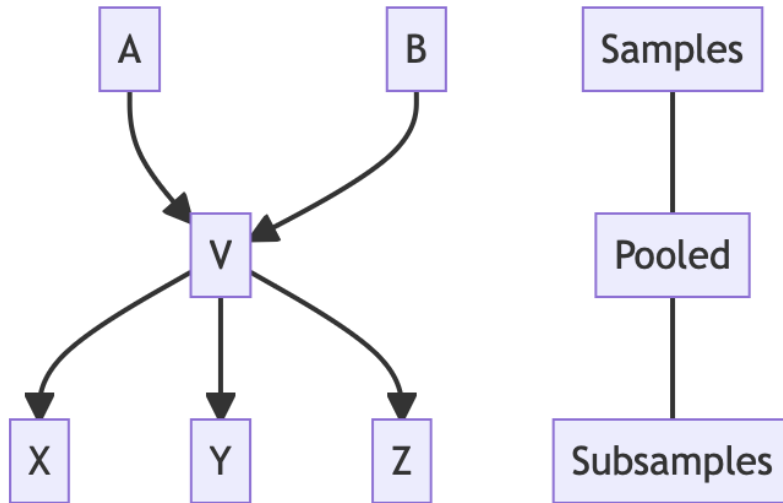


Figure 5.: Example A

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

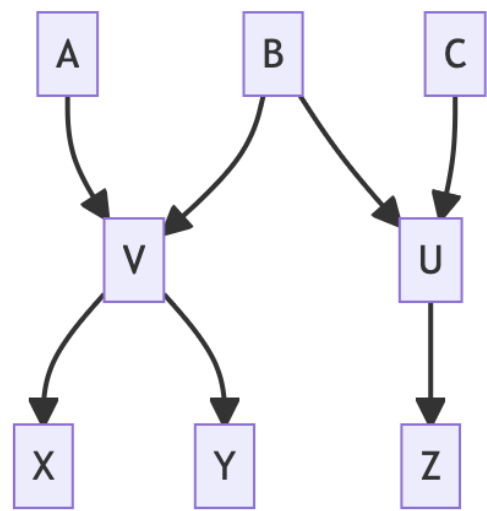


Figure 6.: Example B

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 v2.1.1

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:

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

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).

PHES-ODM approach to wide- and long-formats

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

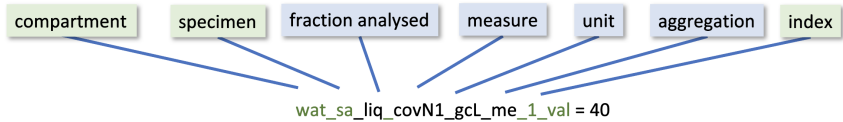


Figure 7.: **Figure 1 - Wide- and Long-names**

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

Long-format:

Samples Table

sampleID	saMaterial	siteID	...
sas100x245	rawWW	ropec	...

Contacts Table

contactID	lastName	email	...
ottawaPer	Doe	Doe@madeUp.ca	...

Wide-format

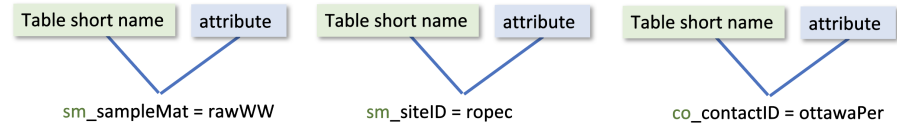


Figure 8.: **Figure 2 - Wide- to Long-format for Attributes**

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

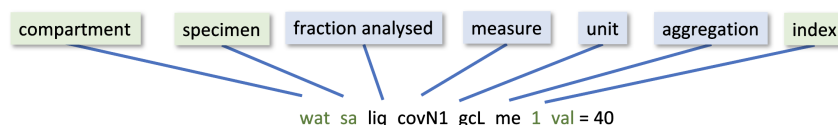


Figure 9.: **Figure 3 - Wide- to Long-format for Measures**

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`.

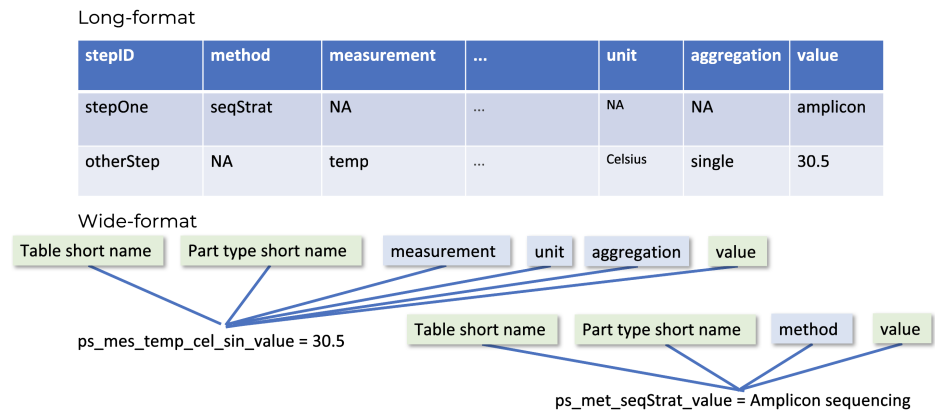


Figure 10.: **Figure 4 - Wide- to Long-format for protocol**

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

For combined long- and wide-formats

`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

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	com-part-ment	speci-men	frac-tion	mea-sure	value	unit	aggre-gation
dec 17	water	sample	liquid	covid N1	32.1	gc/mL	single
dec 17	water	sample	liquid	PM-MoV	16.2	gc/mL	single
dec 17	water	sample	liquid	pH	8.2	unit-less	single
dec 20	water	sample	liquid	covid N1	34.6	gc/mL	single
dec 20	water	sample	liquid	PM-MoV	19.6	gc/mL	single
dec 20	water	sample	liquid	pH	7.9	unit-less	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:

For combined long- and wide-formats

	wat_sa_ liq_covN1_ gcMl_sin_ NR	wat_sa_ liq_pmmov_ gcMl_sin_ NR	wat_sa_ liq_pH_ unitless_ sin_NR
date			
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.

	com- part- ment	spec- imen	frac- tion	mea- sure	value	unit	ag- gre- ga- tion	PM- MoV (gc/ML)	pH (unit- less)
date									
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

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 is 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:

					hCo_hSp_		hCo_hSp_	
					mr_	hCo_hSp_	hFr_pm-unit-	hFr_pm-unit-
					ag-	hFr_pm-unit-	less_	less_
					gre-	mov	gcMl_sis	gcMl_sis
					ga-	NR_valu	NR_valu	NR_valu
					tion	unit	tion	value
mr_	mr_	mr_	mr_	mr_	hCo_hSp_	ag-	hCo_hSp_	hFr_pm-unit-
re-	com-	speci-	frac-	mea-	hFr_hMr_	gre-	hFr_pm-unit-	less_
port	part-	men	tion	sure	hUn_hAggr_	ga-	gcMl_sis	gcMl_sis
Date	ment				NR_valu	unit	NR_valu	NR_valu
dec	wa-	sam-	liq-	covid	32.1	gc/mLsin-	16.2	8.2
17	ter	ple	uid	N1		gle		
dec	wa-	sam-	liq-	covid	34.6	gc/mLsin-	19.6	7.9
20	ter	ple	uid	N1		gle		

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
```

Wide-name exceptions

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)_measure` 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**

Building a wide-format ODM headers

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_measureSetRepID`
- `mr_aDateStart`
- `mr_aDateEnd`
- `mr_reportDate`
- `pa_specimen`
- `pa_fraction`
- `pa_group`
- `pa_class`
- `pa_measure`
- `pa_unit`
- `pa_aggregation`

Tutorials

- 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	com- part- ment	speci- men	frac- tion	measure	value	unit	aggre- ga- tion	index
dec 17	water	sam- ple	liquid	Mpox	32.1	gc/mL	single	1
dec 17	water	sam- ple	mixed	PM- MoV	16.2	gc/mL	single	2
dec 17	air	sam- ple	NA	s2083i omicron- variant gene target	8.2	gc	single	NA
dec 20	water	site	liquid	Flow rate	34.6	ML/dayarith.	mean	NA
dec 20	sur- face	sam- ple	NA	In- fluenza virus A1	19.6	gc/mL	single	NA

Building a wide-format ODM table

date	com- part- ment	speci- men	frac- tion	measure	value	unit	aggre- ga- tion	index
dec 20	water	sam- ple	liquid	pH	7.9	unit- less	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_ report- Date	wat_sa_		wat_si_		wat_sa_ liq_pH	
	wat_sa_ liq_mpo	mix_pm- mov	air_sa_ NA_s2083i	liq_flo- Rate	surf_sa_ NA_fluA1	unit- less_
	_gcml_sin_1_value	_gcml_sin_2_value	_gc_sin_3_value	NA_mld_me_4_value	_gcml_sin_5_value	_sin_2_6_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 template 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

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 v2.1.1

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.

Parts

NA

(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 microbial 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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(a67vDel69Del70). Omicron Variant a67v mutation mutation, and del 69 and del70 mutations co-occurring *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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(absHumidUnitSet). Unit set for absolute humidity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomen-*

Parts

clature: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(ad). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). 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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.1.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(addresses). The table that contains information about addresses. Addresses can be recorded for sites, organizations or contacts (individuals). 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

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

NA

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

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

Parts

naDomain Speciment ID: naSpecimenSet *Compartment Set:* naCompartmentSet *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/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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(airportSheetSet). Worksheets in the full airport surveillance template (list + template). 'ODM_template-planes_{version}.xlsx' *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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(aivA). Measures of Aichivirus A, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis 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*: NA *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: active. Last updated: 3.0.1.

NA

(aivB). Measures of Aichivirus B, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis 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*: NA *Reference Link*: <https://pmc.ncbi.nlm.nih.gov/articles/PMC7223127/> *Data*

Parts

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

NA

(aivC). Measures of Aichivirus C, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis 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:* NA *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: active. Last updated: 3.0.1.

NA

(aivD). Measures of Aichivirus D, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis 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:* NA *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: active. Last updated: 3.0.1.

NA

(aivE). Measures of Aichivirus E, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis 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:* NA *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: active. Last updated: 3.0.1.

NA

(aivF). Measures of Aichivirus F, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis 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:* NA *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: active. Last updated: 3.0.1.

Parts

NA

(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*: NA *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: active. Last updated: 3.0.1.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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://orm-bunkar.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: active. Last updated: 3.0.0.

NA

(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:* NA *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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

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

NA

(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*: NA

Parts

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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

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

NA

(amiMP96). Nucleic 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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(amrGrp). The group for measures and methods pertaining to antimicrobial 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*

Parts

Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.1.0.

NA

(amrSoft). Software use to analyse bacterial genomes and genes for antimicrobial 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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(andBoo). “AND” aggregation. 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: active. Last updated: 2.0.0.

NA

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

Parts

NA

(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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(aradb). 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*: aradb.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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with 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: active. Last updated: 3.0.0.

NA

(articV520bp1200). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: depreciated. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(attributeName). The attribute referenced for the wide name. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment*

Parts

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: active. Last updated: 2.2.0.

NA

(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 surveillance 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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(babesia). Babesia *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* babesiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category*

Parts

Set ID: NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA

Parts

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

NA

(bact16sABIRRev). 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:* 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

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

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(bactMethSet). The set capturing containing all of the valid methods for the bacterial testing method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(bbmap). BBMap. A general-purpose read mapper. High-sensitivity aligner for DNA and RNA reads. Best for: Error-prone reads from platforms like

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(bbMP96). Nucleic 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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(bcfTools). Sequencing software that works with SAMtools to call variants and produce consensus sequences from alignments. *Part Type:* cate-

Parts

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/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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*:

Parts

<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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*:

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

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

NA

(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: active. Last updated:
3.0.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.1.0.

Parts

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(blaCTXM1). CTX-M 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*: NA *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: active. Last updated: 2.2.0.

NA

(blaIMP). Imipenemase (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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: <https://www.mediterranee-infection.com/acces-ressources/base-de-donnees/arg-annot-2/> *Data Type*:

Parts

seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: <https://www.mediterranee-infection.com/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: active. Last updated: 2.2.0.

NA

(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

Parts

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(bocparvGrp). 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: active. Last updated: 3.0.1.

NA

(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

Parts

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

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(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:*

NA *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(booleanSet). Set that contains the valid possible values for a boolean measure (TRUE or FALSE). *Part Type*: mmaSets *Domain*: allDo *Speciment ID*:

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(bow). An outdoor accumulation 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.*

NA

(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: active. Last updated: 3.0.0.*

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:*

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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://choosealicense.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: active. Last updated: 2.2.0.

NA

(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

Parts

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municipal 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*:

Parts

Set ID: NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale
Quality Set: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(bwaMEM). A deduplication method that is used with SAMtools or Picard to mark duplicates during read mapping. *Part Type:* categories *Domain:*

Parts

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: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

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

NA

(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: NA *Reference Link:* NA *Data Type:* seeUnitData
Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal
Minimum Length: NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.1.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

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

NA

(capacityUnitSet). Unit set for capacity measurements. *Part Type*: unit-Sets *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(capitalEndonym). The name locals use for their country's capital. Pre-programmed 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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(cardDtbase). Database that provides high-quality reference sequences for resistance genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 2.0.0.

NA

(caseTestDate). Date that the covid-19 test was performed for a confirmed case. *Part Type:* units *Domain:* bio *Specimen 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: active. Last updated: 2.0.0.

NA

(caSmooth). This data treatment smooths the measurement value using central average smoothing. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(categorical). The data type for categorical data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Specimen*

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: active. Last updated: 2.0.0.

NA

(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 wastewater treatment plant, airplane holding tank, wastewater 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: active. Last updated: 2.0.0.*

NA

(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: NA Reference*

Parts

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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.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: active. Last updated: 2.2.0.

NA

(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://choosealicense.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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.3.

NA

(ccbynca40). 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: active. Last updated: 2.2.3.

NA

(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://choosealicense.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: active. Last updated: 2.2.0.

NA

(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:*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: 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: active. Last updated: 2.2.0.

NA

(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: 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: active. Last updated: 2.2.0.

NA

(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: 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: active. Last updated: 2.2.0.

Parts

NA

(cdcCovN1IDTProbe). 2019-nCoV_N1 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:* 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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(cdcCovN2IDTProbe). 2019-nCoV_N2 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:* 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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

Parts

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:*

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum*

Parts

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

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

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*:

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(chewBBACA). ChewBBACA. Focus: Core genome MLST (cgMLST) with optional serotyping analysis. Applications: Broad-spectrum bacterial pathogens. Features: Efficient with large datasets and highly customizable.

Part Type: categories *Domain:* naDomain *Speciment ID:* naSpecimenSet
Compartment Set: naCompartmentSet *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: active. Last
 updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(chlamydiaGrp). A group of measures/methods related to chlamydia bacteria. Used to describe the organism information for general measures. *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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 *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.3.0.

NA

(cladeAn). Software tool or pipeline for determining the clade or lineage of an organism. *Part Type*: methods *Domain*: bio *Specimen 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*: 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: active. Last updated: 3.0.0.

NA

(cladeAnSet). Valid category set for lineage or clade analysis software types. *Part Type*: mmaSets *Domain*: bio *Specimen 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: active. Last updated: 3.0.0.

Parts

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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. *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: active. Last updated: 2.2.2.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(col2Frddg). 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*: NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(collAppxSet). The category set of valid inputs for the collGenT attribute field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:*

Parts

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: active. Last updated: 3.0.0.

NA

(collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection. used when exact time is 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

Type: datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 3.0.0.

NA

(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

Parts

Group: naGroup *Class:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(columnNameDep). Name for the column Depreciated in ODM version 2. Look-up tables are now incorporated 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: depreciated. Last updated: 2.0.0.

NA

(commFacOth). Specifies a site type which is a commercial facility/worksites 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: active. Last updated: 2.2.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA

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

NA

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

NA

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

NA

(comp3h). A 3-hour composite with 3 grab samples each taken once per hour, generally manually performed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Parts

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: depreciated. Last updated: 2.0.0.

NA

(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:* 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: depreciated. Last updated: 2.0.0.

NA

(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:* 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: depreciated. Last updated: 2.0.0.

NA

(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*: 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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(compartmentSet). An identification 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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(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:*

Parts

naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.3.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: NA 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: active. Last updated: 3.0.0.

NA

(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: 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: active. Last updated: 3.0.0.*

NA

(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: active. Last updated: 3.0.0.*

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

Maximum Value: NA *Minimum Length:* 10 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(countriesRequired). Required headers 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:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.1.0.

NA

(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*

Parts

Set: NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* geo-RefMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*:

Parts

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal
Maximum Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal
Maximum Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal
Maximum Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal

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

NA

(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: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA
Maximum Length: NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(cPerfringens). 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: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA
Maximum Length: NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(cphDate). date of reporting for covid-19 measure. Depreciated in ODM version 2. The measure identification is now measureReportID with report

Parts

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*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(cphid). Unique identifier for the table. Depreciated in ODM version 2. The measure identification 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*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*

Parts

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA
Data Type: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal
Maximum Value: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active.
 First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

Parts

NA

(d339h). The FLiRT/SLip variant mutation D339H. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(d377y). d377y delta-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(d3g). d3g omicron-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*:

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(d950n). d950n delta-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*:

Parts

anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(datasetID). The name of the dataset that stores information for MeasureReport, SampleReport and other reporting tables. Where possible, datasetID name should correspond the original 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(datasetsOrder). Specifies the order of the columns in a Datasets 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(dataTypes). The data type for a part. Data types used in the ODM include: varchar, boolean, 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 identified 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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: depreciated. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(days). A unit for indicating a length of time in 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(ddcovN). ddcov_n sars-cov-2 mutation gene target. *Part Type:* measurements *Domain:* bio *Specimen 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). *Part Type:* categories *Domain:* naDomain *Specimen 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:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:*

Parts

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

NA

(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*: NA *Reference Link*: NA
Data Type: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA
Maximum Length: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA
Data Type: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA
Maximum Length: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*

Parts

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.3.

NA

(delta). B.1.617.2 *Part Type:* measurements *Domain:* bio *Specimen 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(deltaGrp). A group of measures/methods related to the SARS-CoV-2 Delta Variant. *Part Type:* groups *Domain:* bio *Specimen 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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

Parts

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(deprecated). 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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 technical and not technical 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*

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

Length: 0 Maximum Length: 30 Part Status: deprecated. First released: deprecated. Last updated: 2.0.0.

NA

(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: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(dilFact). Specifies the extent to which a sample or aliquot was diluted prior 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:* 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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

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

NA

(diphtheriaGrp). A group of measures/methods related to the diphtheria bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* diphtheriaGrp *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*

Parts

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

NA

(discover). 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/discover/blog/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum*

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA
Maximum Length: NA *Part Status:* active. First released: active. Last
 updated: 3.0.1.

NA

(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 variant. *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(dorm). Higher education dormitory 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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data*

Parts

Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.1.

NA

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:*

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*

Parts

Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(embossCons). Sequencing software that is part of the EMBOSS suite,
 generates consensus sequences from multiple alignments. *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*: naU-
 nitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*:
<https://www.bioinformatics.nl/cgi-bin/emboss/help/cons> *Data Type*: var-
 char *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA
Minimum Length: 0 *Maximum Length*: 50 *Part Status*: active. First
 released: active. Last updated: 3.0.0.

NA

(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: active. Last updated:
 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(enaNotes). ENA notes *Part Type: attributes Domain: naDomain Specimen ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass 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: active. Last updated: 2.0.0.*

NA

(enterobase). Enterobase archives. *Part Type: categories Domain: naDomain Specimen ID: naSpecimenSet Compartment Set: naCompartmentSet 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: active. Last updated: 3.0.0.*

NA

(enterovirus). Enterovirus *Part Type: measurements Domain: bio Specimen ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: enterovirusGrp Class: organism Nomenclature: organism Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale:*

Parts

seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(enviroInst). Local probe instruments 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: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: genMissingnessSet *Minimum Value*:

Parts

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

NA

(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*: NA *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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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 date resolves the possible ambiguity. *Part Type:* attributes *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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: active. Last updated: 3.0.0.

NA

(epiYear). The year in which the epi week is occurring. Used in conjunction with the epiWeek field. *Part Type:* attributes *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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: active. Last updated: 3.0.0.

NA

(epi10). The licensing for the measure or data set is managed under the Eclipse Public License 1.0. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(erdTableSet). All tables listed in the Entity Relationship Diagram. The full ODM model is commonly referred to as “long” tables as it stores

Parts

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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

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

NA

(esp). exclusions based sample preparation (ESP) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology*

Parts

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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(estimate). Estimated data, data that should be understood to be an estimation, possibly 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

Parts

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

NA

(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:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

Parts

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA

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: active. Last updated: 2.0.0.

NA

(f456l). The FLiRT/SLip variant mutation F456L. *Part Type:* measurements *Domain:* bio *Specimen 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(faeces). Fecal matter. *Part Type:* categories *Domain:* naDomain *Specimen 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: active. Last updated: 2.0.0.

NA

(faFlow). A quality of a body of water wherein there is a fast flow. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Com-*

Parts

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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(farm). An agricultural area, building, 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

Aggregation Scale: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(fecContam). A contamination quality in which fecal matter is a key component of the contamination. *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(fiNa). Used to categorize a sample 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 question. *Part Type:* categories *Domain:* naDomain *Specimen 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: active. Last updated: 2.0.0.

NA

(finVol). The final volume of a testing solution or sample. *Part Type:* measurements *Domain:* che *Specimen 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:* 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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(flagB). Analytical result may be subject to “trace” levels of contamination; the target analyte was also detected in negative controls on the same run

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.*

NA

(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*

Parts

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

NA

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

NA

(flavivirusGrp). A group of measures/methods related to flaviviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Specimen 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(flirtV). FLiRT is the name given to an entire family of COVID-19 sub-variants 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*: NA
Reference Link: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA
Maximum Length: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* 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: depreciated. Last updated: 2.0.0.

Parts

NA

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

NA

(flowInst). Flow meter instruemnts; 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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(flowUnitSet). Unit set for volume flow measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-CompartmentSet *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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(fluA). Influenza A virus. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: fluA-Grp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness*

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(fluA2). influenza virus A2 type *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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

Parts

Quality Set: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(fluidpcer). 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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(flye). A sequencing software that is an assembler for long-read data, particularly effective on nanopore 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://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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*: fraction-Set *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(fullDictionarySheetSet). Worksheets in the full Excel dictionary. The full dictionary is 'ODM_full-dictionary.xlsx' *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

Parts

NA

(g215c). g215c 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(g339d). g339d 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum*

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

NA

(g662s). g662s delta-variant mutation gene target *Part Type:* measure-
 ments *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 *Aggrega-*
tion Scale: seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data*
Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:*
 seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*
Length: NA *Part Status:* active. First released: active. Last updated:
 2.0.0.

NA

(gam). P.1 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpeci-
 menSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:*
 variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:*
 NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality*
Set: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:*
 genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeU-
 nitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active.
 First released: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.1.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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/GEM-Mapper.html> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(genoTyphi). GenoTyphi. Focus: Specific MLST and serotyping for Salmonella Typhi. Applications: Outbreak investigations and

Parts

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/genotypphi> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.2.0.

NA

(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

Parts

Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(g/L). 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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

Parts

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

NA

(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:* quantAggrScale *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(grabInst). Grab sampler instruments; manually collect a single sample at a point in time. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(grams). A unit of mass or weight. *Part Type:* units *Domain:* phy *Specimen ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggrScale *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(grb). A single large representative grab sample. If the sample was collected over a series of hours or is a composite sample, 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:* NA *Reference Link:* NA
Data Type: varchar *Missingness Set:* NA *Minimum Value:* NA
Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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 that 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 *Specimen 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: active. Last updated: 2.0.0.

NA

(groups). A collection of related measures. Used primarily to group measurements and methods, this helps pare down the drop down list for a given measurement or methods. *Part Type*: partTypes *Domain*: naDomain *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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.cnbc.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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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 *Specimen 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*: NA *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: active. Last updated: 3.0.1.

NA

(hadvA). Group A of the human mastadenovirus genus (HAdV-A). Includes serotypes 12, 18, and 31. *Part Type*: measurements *Domain*: bio *Specimen ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*:

Parts

mastadenoGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *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: active. Last updated: 3.0.1.

NA

(hadvB). Group B of the human mastadenovirus genus (HAdV-B). Includes serotypes 3, and 16. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *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: active. Last updated: 3.0.1.

NA

(hadvC). Group C of the human mastadenovirus genus (HAdV-C). Includes serotypes 1, 2, 5, and 6. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *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: active. Last updated: 3.0.1.

NA

(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 *Specimen 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*: NA *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: active. Last updated: 3.0.1.

NA

(hadvE). Group E of the human mastadenovirus genus (HAdV-E). Includes serotype 4. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *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: active. Last updated: 3.0.1.

Parts

NA

(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*: NA *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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.2.0.

NA

(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:
 active. Last updated: 2.2.0.

NA

(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:* NA *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: active. Last updated: 3.0.1.

NA

(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:* NA *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: active. Last updated: 3.0.1.

Parts

NA

(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*: NA *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: active. Last updated: 3.0.1.

NA

(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*: NA *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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:*

Parts

seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

Parts

NA

(header). Header for a table. Also known as a table variable or entity 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: active. Last updated: 2.0.0.

NA

(healthAdm). Health administrative 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control target. *Part Type*: categories *Domain*: naDomain *Specimen 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: active. Last updated: 2.0.0.

NA

(hel). SARS-CoV-2 hel gene (nsp13) *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(hepA). Hepatitis A *Part Type*: measurements *Domain*: bio *Specimen ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: hepGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale

Parts

Quality Set: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(hf183). Human-Specific HF183 Bacteriodes 16S rRNA *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bacteriodesGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum*

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

NA

(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: active. Last updated: 2.2.0.

NA

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

Parts

NA

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

NA

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

NA

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

NA

(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: active. Last updated: 3.0.1.

Parts

NA

(h1aa5). A serotonin metabolite used for normalizing wastewater surveillance signal. Analysis of 5-HIAA is done in clinical settings to assess the possibility of carcinoid syndrome in patients, and used in wastewater analysis to estimate human population numbers. Studies have shown that 5-HIAA can be quantified 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 *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(high). Indicates a very severe quality issue, likely meaning the data should not be reported. *Part Type*: categories *Domain*: naDomain *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data*

Parts

Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(hma). Handheld measurement analyzer. A handheld measurement analyzer. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpec-

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

NA

(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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

Parts

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(hotel). A building which 1) contains multiple dwellings of pre-furnished accommodation 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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

Group: erythroparvoGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

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

NA

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

NA

(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 ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(hpv). Human Papiloma Virus (HPV) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet

Group: papillomavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* mea-

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA

Parts

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

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData

Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(idbaUD). A sequencing software that is an iterative assembler optimized for metagenomics and complex genomic datasets. *Part Type:* cate-

Parts

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/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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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: active. Last updated: 2.0.0.

NA

(indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occasionally 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(infPump). A facility that transports 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*

Parts

Scale: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

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

NA

(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 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.

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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. *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*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(insType). Type of instrument used to perform the measurement. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: insType-
Set *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: active. Last updated: 2.0.0.

NA

(intAMRGrp). The group for measures and methods pertaining to integrase-
related anti-microbial resistance. *Part Type*: groups *Domain*: bio *Speci-*
ment ID: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*:
intAMRGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*:
NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeU-
nitAggScale *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: active.
Last updated: 2.1.0.

NA

(integer). The data type for integers. Only used for the dictionary entries
of parts. *Part Type*: dataTypes *Domain*: naDomain *Speciment ID*: naSpec-
imenSet *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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

Class: naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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 metadata for a languageID. *Part Type*: attributes *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:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(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 metadata 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:* **deprecated**. First released: deprecated. Last updated: 3.0.0.

NA

(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 metadata 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: active. Last updated: 3.0.1.

NA

(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 metadata 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:* **deprecated**. First released: deprecated. Last updated: 3.0.0.

NA

(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 differentiate between variants of languages and language families, such as historical vs. revived versions of languages. Part of the metadata 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:*

Parts

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**.
First released: deprecated. Last updated: 3.0.0.

NA

(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 *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *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: active. Last updated: 3.0.0.

NA

(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 *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(jn17V). The JN.1.7 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet

Parts

Compartment Set: anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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/klebgonomics/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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*:

Parts

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

Parts

NA

(1455s). The FLiRT/SLip variant mutation L455S. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: any-CompartmentSet *Group*: flirtSLipGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(1981f). 1981f 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(1a). 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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. *Part Type:* categories

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.1.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(lambda). 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(lang). Language code for translation purposes. Specifies the language 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes. Part of the metadata 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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:*

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(IBC). 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: active. Last updated: 2.0.0.

NA

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

NA

(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:* quantAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Parts

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

NA

(IDC). 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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://choosealicense.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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(licSet). The set to describe valid categorical values for the licensing fields for measures or datasets. *Part Type:* mmaSets *Domain:* naDomain *Specimen 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: active. Last updated: 2.2.0.

NA

(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 *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(listeria). Listeria *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* listeriaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category*

Parts

Set ID: NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

Unit Set: geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*

Parts

Scale: quantAggrScale *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(low). A marker for low severity *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet

Parts

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

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(lp81V). The LP.8.1 variant of SARS-CoV-2, a Omicron subvariant of JN.1, and FLiRT variant. *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(IPGC). Only captured a small/low percentage of the genome. *Part Type*: qualityIndicators *Domain*: naDomain *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.3.0.

NA

(lppa24s). Omicron Variant LPPA24S mutation *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*:

seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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://choosealicense.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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(ItcfO). 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: active. Last updated: 2.0.0.

NA

(ItDpcr). 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: active. Last updated: 2.0.0.

NA

(luminWWExtract). luminultra wastewater extraction kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

Parts

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

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(manufacturer). Manufacturer of 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:* 100 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(maxValue). The maximum value of a part. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass

Parts

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

NA

(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:* standard-Conc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *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: active. Last updated: 3.0.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(measureSetRepID). Unique identifier that links together a group of related measures. *Part Type:* attributes *Domain:* naDomain *Speciment ID:*

Parts

naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *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: active. Last updated: 2.0.0.

NA

(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 variants 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(mega). Sequencing software that provides tools for sequence alignment and consensus sequence extraction. *Part Type:* categories *Domain:* naDo-

main *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*:

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(mes). The abbreviated short name used to reference the The attribute to describe a part type of measures. All measures have 'partType' = "measure-

Parts

ments". 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: active. Last updated: 2.2.2.

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(metaPhlAn). Software tool that profiles microbial communities and can provide resistance gene insights. Also used for deduplication. *Part Type:*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:*

Parts

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

NA

(mfMgcl2SS). Membrane filtration with addition of 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(mgPO₄3L). milligrams orthophosphate per liter (mg PO₄3-/L) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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

NA

(minLength). The maximum value of 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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA exclusive 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(mmaSet). The set for a measure, method, or attribute. Only applicable for categorical fields, and the categories that populate them. The use has been extended to include 'partType' values as well, to codify instances where a categorical variable takes any part of a certain part type. Examples of the part type use case include 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 *Specimen 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: active. Last updated: 2.0.0.

NA

(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 *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*:

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(mpn100mL). most probable number per 100 milliliter (MPN/100 mL) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment*

Parts

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: active. Last updated: 3.0.0.

NA

(mpnmL). most probable number per milliliter (MPN/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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* <https://doi.org/10.1016/j.jviromet.2010.07.012> *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum*

Parts

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

NA

(mpxCII). The virus known as Mpox, previously also known as Monkey Pox, Clade I virus type. *Part Type:* measurements *Domain:* bio *Specimen 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(mpxCIII). The virus known as Mpox, previously also known as Monkey Pox, Clade II virus type. *Part Type:* measurements *Domain:* bio *Specimen 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal

Parts

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

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.3.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(mr). The abbreviated short name used to reference the The table that contains information and details about a given measure table *Part Type*: short-Name *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*:

Parts

naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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/ms-pl/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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 *Specimen 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: active. Last updated: 3.0.0.

NA

(mumps). Mumps *Part Type:* measurements *Domain:* bio *Specimen 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: depreciated. Last updated: 2.3.0.

NA

(mutationPanel). Measures and methods related to a panel or list of more than one mutation from the same sequence read. *Part Type:* classes

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA
Maximum Length: NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: NA *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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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 differentiate between the ‘name’ field in different tables, please use

Parts

attribute-specific widenames per widenname 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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/wdecoester/NanoPlot> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(natName). The native name of the language, i.e. what the language is called by its speakers. Part of the metadata 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: active. Last updated: 3.0.1.

NA

(naUnit). Not applicable 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: active. Last updated: 3.0.1.

NA

(naUnitSet). Not applicable for unit sets. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartment

Parts

mentSet *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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(ncbiNom). Nomenclature 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

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(ncovtools). Tools and plots for performing 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

Length: 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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. *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(nh3nh4). Ammonia and Ammonium combined concentration, as Nitrogen *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:*

Parts

standardConc Nomenclature: standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

Length: 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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-

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(norovirus). 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*:

seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(nsp15). SARS-CoV-2 nsp15 Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet

Parts

mentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: GENEPIO:0100171 Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 3.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 3.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*:

Parts

NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(ntcFlag). quality indicator for when there is observed amplicification 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: depreciated. Last updated: 3.0.0.

NA

(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*: NA *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

Parts

NA

(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 *Specimen 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:* NA *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: active. Last updated: 3.0.0.

NA

(nwss). NWSS header *Part Type:* attributes *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *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: active. Last updated: 2.0.0.

NA

(nwssForm). Dataset was originally recorded and/or stored in the US-CDC's NWSS format. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(off11). 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/off-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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(omicr1). Omicron B.1.1.529 *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(omicr2). Omicron BA.2 *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(omicr275). Omicron BA.2.75 *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(omicr4). Omicron BA.4 *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(omicr5). Omicron BA.5 *Part Type*: measurements *Domain*: bio *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(omicronGrp). A group of measures/methods related to the SARS-CoV-2 Omicron Variant. *Part Type*: groups *Domain*: bio *Specimen ID*: saSpecimenSet *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*:

Parts

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

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(opWa). An outdoor accumulation 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(orBoo). “OR” aggregation. If any value in the aggregation is “TRUE” then the OR aggregation is also “TRUE”. If all values in the aggregation

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum*

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:*

seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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 Refer-*

Parts

ence: GENEPIO:0100177 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: GENEPIO:0100179 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: GENEPIO:0100180 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(organism). Organism class Identify class = 'organism' for when a part identifies an organism and partType = 'groups'. Individual 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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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

Parts

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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(organizationsRequired). Specifies the columns required in a Organizations table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpec-

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(orgTypeSet). The set for storing organization types. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-CompartmentSet *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(orthoGrp). A group of measures/methods related to orthopox viruses (excluding variola 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: active. Last updated: 2.2.0.

NA

(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:*

Parts

<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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

Set: anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

Length: 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(p681r). Delta Variant p681r 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*

Type: varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.2.

NA

(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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(papillomavirusGrp). A group of measures/methods related to papillomaviruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* papillomavirusGrp *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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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

Parts

Class: naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

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: 1000 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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 duplicates. partIDs are short. partIDs that are constructed by different part attributes can be up to 28 characters (check max), but each part attribute should be 1 to 5 characters. partIDs are machine readable, but a knowledgeable user can understand what they represent. partID are used, for example, as a header in an Excel input table. Numbers are allowed but there are no other special characters other than ‘.’ ‘.’ is a reserved character that is used to generate a partID using a component or table attributes. A partID for a subComponent is automatically generated using attributes of a component. For example, the partID for the component ‘SARS-CoV-2’ is ‘covid’. ‘Covid’ can have many subComponents including different groups (Covid-19-al, Covid-19-va, covid-pr (allele, variant or protein) or units and aggregations (i.e. covid-al-N1-mean-cpl representing covid allele N1, mean observation of viral copies per litre of effluent). A similar approach to naming subComponent is used for naming parts in a reportTable. *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(partsOrder). Order of headers in the Parts table. *Part Type:* table-Support *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

Parts

Type: integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(partsRequired). Required headers in the Parts table. *Part Type:* table-Support *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(partTypes). Part types describe the purpose or use of the part. Environment data has three main part types: measure (i.e. covN1 viral measures, wastewater 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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(pCode). The zip code or postal code for a given address, specifying a specific 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: active. Last updated: 2.0.0.

NA

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

Parts

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(pcrSeq). Specifies the PCR selection method for sequencing, ie. that a pre-determined primer was used. Primer should be specified if this is selected.

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

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

NA

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

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

Unit Set: percentUnitSet *Aggregation Scale:* quantAggScale *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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

NA

(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 *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *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/ref-seq/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: active. Last updated: 3.0.0.

NA

(ph). pH measurement *Part Type*: measurements *Domain*: che *Specimen 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*: NA *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

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*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*:

Parts

NA *Minimum Length*: 0 *Maximum Length*: 75 *Part Status*: active. First released: active. Last updated: 2.1.0.

NA

(phos). Total phosphorous *Part Type*: measurements *Domain*: phy *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(phostot). Total phosphates *Part Type*: measurements *Domain*: phy *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(phred). PHRED Quality Score For Sequencing *Part Type*: measurements *Domain*: bio *Specimen 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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal
Maximum Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum*

Parts

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

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(pmmovGrp). A group of measures/methods related to the Pepper Mild Mottle Virus (PMMoV). Used to describe the organism information for

Parts

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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.2.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(polygonRelationshipsOrder). Specifies the order of the columns in the polygon relationships table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Parts

Group: naGroup *Class:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.1.

NA

(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:* NA *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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(polySiSpecimenSet). A specimen set that includes 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: active. Last updated: 3.0.0.

NA

(polySpecimenSet). A specimen set that includes 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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

Parts

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA

Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a single 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(poPolySpecimenSet). A specimen set that includes population or polygon specimen. *Part Type*: specimenSets *Domain*: naDomain *Specimen 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: active. Last updated: 3.0.0.

NA

(popServ). An measure of a site, which specifies the population of/population served by a given site. *Part Type*: measurements *Domain*: phy *Specimen 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.3.0.

NA

(popServRange). Population served by a site, when reported as an interval. *Part Type*: measurements *Domain*: phy *Specimen 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*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*:

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active.
 Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(poSiSpecimenSet). A specimen set that includes 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: active. Last updated: 2.0.0.

NA

(poSpecimenSet). A specimen set that includes 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: active. Last updated: 2.0.0.

NA

(postgresql). The licensing for the measure or data set is managed under the PostgreSQL License. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *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: active. Last updated: 2.2.0.

NA

(pp). Percent positive of sample measures. Can use for Moore swabs, etc. *Part Type:* units *Domain:* bio *Specimen 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: active. Last updated: 2.0.0.

NA

(ppm). Parts per million. *Part Type:* units *Domain:* phy *Specimen ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

Parts

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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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 *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

Parts

Maximum Value: NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *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: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

Parts

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(predicted). Predicted data, data generated by predictive models or algorithms, 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(preQC). A QC pipeline tool for sequencing data that evaluates data quality before assembly, particularly for large genomes. *Part Type:* categories

Parts

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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(pretreat). Was the sample chemically treated in anyway with the addition of stabilizers or other Pretreatment 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:* 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: active. Last updated: 2.0.0.

NA

(primClar). A large settling tank that removes solids and floating materials from wastewater before secondary treatment. *Part Type:* categories

Parts

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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(private). The measure or data set is private data - not for dissemination. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.2.

NA

(procGrp). A group of measures/methods related to processing samples for analysis. *Part Type:* groups *Domain:* allDo *Speciment ID:* siSaSpecimenSet

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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*: **deprecated**. First released: deprecated. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(prop). Proportion as a percent 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:*

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(protocolIDContainer). Unique identifier for the protocol and the steps and other protocols that make it up. Protocol ID Container in populated 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: active. Last updated: 2.0.0.*

NA

(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*

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. *Part Type:* tables *Domain:* naDo-

main 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but prior 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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.

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:* 1000 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(purposeSet). Purpose set for a sample or measure. *Part Type:* mmaSets
Domain: naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-CompartmentSet
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: active. Last updated: 2.0.0.

Parts

NA

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active.
 Last updated: 3.0.0.

NA

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

NA

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

Parts

NA

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(q954h). q954h 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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

Parts

NA

(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*: 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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(qf1). A flag to indicate there is a quality concern, not otherwise specified.
Part Type: qualityIndicators *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. *Part Type:* categories *Domain:* naDomain *Specimen 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: active. Last updated: 2.0.0.

NA

(qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. *Part Type:* categories *Domain:* naDomain *Specimen ID:*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 2.0.0.*

NA

(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: active. Last updated: 2.0.0.*

NA

(qiAllprep). qiagen allprep dna/rna kit *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: procGrp Class: pcr Nomenclature: pcr Ontology Refer-*

ence: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: 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: depreciated. Last updated: 3.0.1.

NA

(qiaampDSP). 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: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(qualAggScale). The qualitative aggregation scale. *Part Type:* aggregation-Scales *Domain:* naDomain *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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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

Parts

Class: naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData

Parts

Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(ranSeq). Specifies the random selection method for sequencing No primer set should be used if this is selected. *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: active.
Last updated: 2.0.0.

NA

(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*:
quantAggrScale *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:
active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjunctiion 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*

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(rdrpIP2). IP2 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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(rdpIP4). IP4 rdp 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(recomb). A catch-all measure for viruses of non-specified and recombinant lineages, defined as those viruses 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:* NA *Reference Link:*

NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(redundans). A sequencing software that is a genome assembler that reduces redundancy, useful for fragmented 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/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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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 technical 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(relDateEnd). The end date of the relevancy period of a measure - mostly for time-varying 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: active. Last updated: 2.3.0.

NA

(relDateStart). The start date of the relevancy period of a measure - mostly for time-varying 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: active. Last updated: 2.3.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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:* 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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

Parts

NA

(repOrg1). The primary or most responsible authority for routine 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 organization. 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: active. Last updated: 2.0.0.

NA

(repOrg2). The secondary, additional or alternative authority for routine 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 organization. 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 the 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.*

NA

(reportDate). The date a measure was reported. This date is the first date the laboratory or entity reported the measure findings to the public health or other entity 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: active. Last updated: 2.0.0.*

Parts

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(res). An artificial body of water, often contained by a dam, constructed for the purpose of water storage. *Part Type*: categories *Domain*: naDo-

Parts

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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

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

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(resFinderDtbse). nomenclature 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 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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(restrict). Missing data is withheld because it is restricted access. Missing value indicator for data that has been classified as restricted, 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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 *Nomen-*

Parts

clature: 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: active. Last updated: 3.0.0.

NA

(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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.2.0.*

NA

(rickettsiaGrp). A group of measures/methods related to rickettsia 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: active. Last updated: 2.2.0.*

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

Length: 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(rppw). Raw wastewater sample post-pasteurization *Part Type*: categories
Domain: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: na-
CompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass
Ontology Reference: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Ag-*
gregation Scale: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*
Type: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*:
NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First
released: active. Last updated: 2.0.0.

NA

(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: active. Last
updated: 3.0.0.

NA

(rsvAB). Human Respiratory Syncytial Virus Type A (RSV A) and Type
B (RSV B). *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpec-
imenSet *Compartment Set*: anyCompartmentSet *Group*: rsvGrp *Class*:
organism *Nomenclature*: organism *Ontology Reference*: NCIT:C184696
Category Set ID: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeU-
nitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData

Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.3.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.3.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.3.

Parts

NA

(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: active. Last updated: 2.1.2.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.1.2.

NA

(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*: NA *Reference Link*: NA
Data Type: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA
Maximum Length: NA *Part Status*: active. First released: active. Last updated: 2.1.3.

NA

(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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(s373p). s373p omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

Parts

anyCompartmentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(s375f). s375f omicron-variant mutation gene target Part Type: measurements Domain: bio Specimen 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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(s477n). s477n omicron-variant mutation gene target Part Type: measurements Domain: bio Specimen 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: NA Reference Link: NA Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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

Parts

Unit Set: geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

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

NA

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

NA

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

NA

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

NA

(safv5). Strain 5 of the saffold virus (SAFV-5) *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*: NA *Reference Link*: NA
Data Type: seeUnitData *Missingness Set*: genMissingnessSet *Minimum*

Parts

Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA
Maximum Length: NA *Part Status:* active. First released: active. Last updated: 3.0.1.

NA

(safv6). Strain 6 of the saffold virus (SAFV-6) *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:* NA *Reference Link:* NA
Data Type: seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal
Maximum Value: seeUnitVal *Minimum Length:* NA *Maximum Length:* NA
Part Status: active. First released: active. Last updated: 3.0.1.

NA

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

NA

(safv8). Strain 8 of the saffold virus (SAFV-8) *Part Type:* measurements
Domain: bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

mentSet Group: scaffoldGrp Class: organism Nomenclature: organism
 Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet
 Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA
 Data Type: seeUnitData Missingness Set: genMissingnessSet Minimum
 Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA
 Maximum Length: NA Part Status: active. First released: active. Last
 updated: 3.0.1.

NA

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

NA

(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:

Parts

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: active. Last updated: 3.0.1.

NA

(salinity). Measurement of salinity/salt content *Part Type*: measurements
Domain: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: water-
CompartmentSet *Group*: miscMeas *Class*: standardConc *Nomenclature*:
standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*:
salinityUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Refer-*
ence 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:
active. Last updated: 3.0.0.

NA

(salinityUnitSet). Unit set for salinity measurements. *Part Type*: unitSets
Domain: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: any-
CompartmentSet *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 *Maxi-*
imum Value: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*:
active. First released: active. Last updated: 3.0.0.

NA

(salmonella). Salmonella *Part Type*: measurements *Domain*: bio *Speci-*
ment 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: 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: active. Last updated: 2.0.0.

NA

(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. *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: active. Last updated: 2.0.0.*

NA

(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*

Parts

Length: 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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. *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: active. Last updated: 2.0.0.

NA

(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

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(sampleTypeOther). Description for other type of method not listed in collection. *deprecated*. *Part Type*: methods *Domain*: naDomain *Specimen 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*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(samRmdup). A deduplication method that identifies and removes PCR duplicates based on alignment data. *Part Type*: categories *Domain*: naDomain *Specimen 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: active. Last updated: 3.0.0.

NA

(samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. *Part Type*: categories *Domain*: naDomain *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software

Parts

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: active. Last updated: 3.0.0.

NA

(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:* NA *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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.2.2.*

NA

(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: active. Last updated: 2.0.0.*

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(scf). A measurment for specifying the frequency 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.1.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(schoolClos). Temporary shutdown of educational institutions to prevent 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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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

Parts

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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

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

NA

(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*

Parts

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

NA

(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 minimum 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: integer *Missingness*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(seqContam). Sequence is contaminated. *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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(seqQCSet). The category set of valid input 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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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:*

Parts

sequence *Ontology Reference*: NA *Category Set ID*: seqSelSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:*

Parts

<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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum*

Parts

Length: 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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. *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

Parts

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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(setsOrder). Specifies the order of the columns in the Sets table. *Part Type:* table *Support Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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: active. Last updated: 2.0.0.

NA

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

Parts

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(shedSet). The set for all valid values of sampleshed. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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: active. Last updated: 2.0.0.

NA

(shigella). Shigella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* shigellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category*

Parts

Set ID: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale
Quality Set: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

Minimum Value: NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(shrtNameSet). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). *Part Type:* shortSets

Domain: naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-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:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.2.2.

NA

(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:*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(siSaSpecimenSet). A specimen set that includes 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: active. Last updated: 2.0.0.

NA

(siSpecimenSet). A specimen set that includes 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: active. Last updated: 2.0.0.

NA

(sistr). Salmonella In Silico Typing Resource (SISTR). Used for in silico serotyping of Salmonella enterica based on whole-genome sequencing.

Parts

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: active. Last updated: 3.0.0.

NA

(sit). A measure made on a compartment or property at a site. An example is the wastewater flow rate, taken at a wastewater 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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type of region is represented by the base sew-

Parts

ershed. 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information 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: active. Last updated: 2.0.0.

NA

(sitesOrder). Specifies the order of the columns 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:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

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

NA

(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

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(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 *Specimen 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: active. Last updated: 3.0.0.

NA

(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 *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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*:

Parts

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: active. Last updated: 3.0.0.

NA

(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*: <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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.

NA

(solidDry). 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: active. Last updated: 2.3.0.*

NA

(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: standard-Conc 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: active. Last updated: 2.2.0.*

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(specimenSet). An identification 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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(speed). Measures and methods relating to speed. *Part Type:* classes *Domain:* phy *Specimen 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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(speedUnitSet). Unit set for reporting speeds (centrifugation speed, etc.) *Part Type:* unitSets *Domain:* naDomain *Specimen 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: active. Last updated: 2.2.0.

NA

(spg). A buffer solution/medium that stabilizes viruses, including in wastewater samples, by preventing RNA degradation. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass

Parts

Ontology Reference: NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* see-UnitAggScale *Quality Set:* NA *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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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

Parts

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

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(srst2). Software tool for analyzing antimicrobial resistance using short read sequences. *Part Type:* categories *Domain:* naDomain *Specimen 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: active. Last updated: 3.0.0.

NA

(ssake). A sequencing software that is a simple de novo assembler for highly overlapping short reads. *Part Type:* categories *Domain:* naDomain *Specimen 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(standardConc). Measures and methods relating to standard concentrations. *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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

Parts

NA

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.1.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

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

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(stepID). The unique identifier for a specific protocol step. Protocol Steps are the component parts of a larger protocols, the latter being linked to

Parts

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: active. Last updated: 2.0.0.

NA

(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 ‘protocolID-Sub’ 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: active. Last updated: 2.0.0.

NA

(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 ‘protocolID-Sub’ 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: active. Last updated: 2.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

NA

(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*

Parts

Type: varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*:

Parts

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

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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*: NA *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(su). The abbreviated short name used to reference the Summary sheet of the dictionary.xlsx 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: **deprecated**. First released: deprecated. Last updated: 3.0.0.*

NA

(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: active. Last updated: 3.0.0.*

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

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

NA

(sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Aggregation for a population or disease measure to

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(summary). Summary sheet of the dictionary.xlsx 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(surfSw). Surface swab. *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA
Reference Link: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA
Maximum Length: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA
Maximum Length: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(tableSupport). Parts designed to support the metadata definition of tables 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: active. Last updated: 2.0.0.

NA

(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 apply 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: active. Last updated: 3.0.1.

NA

(taiforestV). Orthoebolavirus taiense (formerly Tai Forest ebolavirus) is a rare viral species that causes Tai 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.1.

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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

Parts

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

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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:* NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(thermMag). Nucleic acid extraction performed using the thermo magmax microbiome ultra nucleic acid isolation kit. *Part Type:* categories *Domain:*

Parts

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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(tHub). A transport 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 *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(timeClass). Measures and methods relating to time. *Part Type:* classes *Domain:* allDo *Specimen 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:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

NA

(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 *Specimen*

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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*: 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: depreciated. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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

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:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(trizolRNA). trizol and RNA purification kit *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Parts

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

NA

(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: active. Last updated: 2.2.3.

NA

(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: active. Last updated: 2.3.0.

NA

(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: active. Last updated: 3.0.0.

NA

(ts). Total solids concentration *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: waterQualityGrp *Class*: standardConc *Nomenclature*: standard-Conc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 3.0.1.

NA

(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:*

Parts

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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(turb). A measure for the turbidity of water, or a liquid sample, quantifying 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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

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

NA

(turbidityUnitSet). Unit set for turbidity measurements. *Part Type*: unit-Sets *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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum*

Parts

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

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(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:*

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: depreciated. Last updated: 2.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*

Parts

Set: naUnitSet *Aggregation Scale:* 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*:

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:*

Parts

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

NA

(unlicense). The licensing for the measure or data set is managed under The Unlicense. *Part Type*: categories *Domain*: naDomain *Specimen ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *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: active. Last updated: 2.2.0.

NA

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

NA

(untreat). A quality which denotes an absence of purposeful intervention or processes on an item. *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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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*

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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum*

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

NA

(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:* 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: active. Last updated: 3.0.0.

NA

(validationStudy). A meature 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: active. Last updated: 2.0.0.

NA

(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:*

Parts

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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData

Parts

Missingness Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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:* NA
Reference Link: NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA
Maximum Length: NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: 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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness*

Parts

Set: genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: depreciated. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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

Parts

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

NA

(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:* NA *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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: 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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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*: 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: active. Last updated: 2.2.0.

NA

(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*

Parts

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

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

Parts

NA

(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: depreciated. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.3.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(weath). A measure for weather captured through qualitative categories; part of a larger suite of weather measures that may be useful when col-

Parts

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*: 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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

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

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(wideNamesRequired). Column for indicating which fields in the wide names table are mandatory. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

Parts

Group: naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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*

Parts

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.2.

NA

(wrongStorage). Sample was stored inappropriately. *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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal

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

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(wtfpl). The licensing for the measure or data set is managed under the Do What The Fck You Want To Public License. *Part Type:** categories *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:* <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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: proc-Grp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: GENE-PIO: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: active. Last updated: 3.0.0.

NA

(wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: proc-Grp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: GENE-PIO: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*

Parts

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

NA

(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: active. Last updated: 3.0.0.*

NA

(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: active. Last updated: 3.0.0.*

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

Parts

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(wwPriSed). Wastewater 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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:*

Parts

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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 2.0.0.

NA

(wwtpMuC). Municipal wastewater treatment plant for combined sewage *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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: active. Last updated: 3.0.0.

NA

(xecV). The XEC variant of SARS-CoV-2, a subvariant of the Omicron strain. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpeci-

menSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA

Parts

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

NA

(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: active. Last updated: 2.0.0.

NA

(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:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* genMissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 3.0.0.

NA

(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: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: genMissingnessSet
Minimum Value: seeUnitVal *Maximum Value*: seeUnitVal
Minimum Length: NA *Maximum Length*: NA *Part Status*: active.
 First released: active. Last updated: 2.2.0.

NA

(zlib). The licensing for the measure or data set is managed under the zLib License.
Part Type: categories *Domain*: naDomain *Speciment ID*:

Parts

naSpecimenSet *Compartment Set*: naCompartmentSet *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: active. Last updated: 2.2.0.

NA

(zo). The abbreviated short name used to reference the Look up table for the possible sub-national region or zone inputs. *table Part Type*: short-Name *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.2.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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: active. Last updated: 2.1.0.

NA

(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:*

Parts

NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.1.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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:* 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: active. Last updated: 2.2.0.

NA

(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: active. Last updated: 2.0.0.

NA

(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:* 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: active. Last updated: 2.0.0.

NA

(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:* **deprecated**. First released: deprecated. Last updated: 3.0.1.

Sets

Dictionary v3.0.1 Documentation v2.1.1

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.

NA

(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.

NA (`andBoo`). “AND” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (`cuCo`). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gmnn). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (orBoo). “OR” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (otherDep). Other aggregation method. Add description to aggregationOther Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA

(aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative.

NA (naAggrScale). Not application for aggregation sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (qualAggScale). The qualitative aggregation scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (quantAggScale). The "quantAggScale" aggregation scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean.

booleanAggrSet

(booleanAggrSet)Aggreagation set for boolean. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (andBoo). “AND” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orBoo). “OR” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

linearAggrSet

(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.

NA (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

logAggrSet

(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.

NA (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gmn). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

naAggrSet

(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.

NA (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

otherAggrSet

(otherAggrSet)Aggregation set used for unitless measures. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gmN). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

Sets

NA (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.

NA (upperCI95). Specifies the the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean.

NA (booleanAggrSet). Aggreagation set for boolean. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (naAggrSet). Not application for aggregation sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (otherAggrSet). Aggregation set used for unitless measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(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 surveillance data. The other two components are measures and methods.

NA (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.

NA (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.

NA (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.

NA (addressID). A unique identifier for an address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (aliasIDDep). Alias id Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (aDate). Date the measurement was performed in the lab. Status: depreciated. First released: 1.0.0. Last updated: 2.1.0.

NA (aDateEnd). Date the measurement or analysis was completed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (aDateStart). Date the measurement or analysis was started. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (charLength). The number of characters used for the wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (domain). Domain is the highest level of describing of a measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (contactID). A unique identifier for a given contact person. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (cphid). Unique identifier for the table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (aggregationSet). The aggregation set for a unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (custodyCont). A unique identifier for data custodians. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (descr). A detailed description of a measure, method, or attribute. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (source). The database or table sourced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (custodyID). The data custodian of a database. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (specimenSet). An identification 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.

NA (compartmentSet). An identification 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.

NA (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.

Sets

NA (capitalEndonym). The name locals use for their country's capital. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (capitalExonym). The English name foreigners use for the country's capital. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (funderCont). A unique identifier for a funder. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (wideMeasure). Unique identifier for a measure in a wide table only. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (addL2). Line 2 (the unit number) for a given address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (collDate). Sample collection date, where time is reported in a separate field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (collNumPer). Composite collection number.period. Status: deprecated. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (collType). The type of collection. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (columnNameDep). Name for the column Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (wideProtocol). Unique identifier for a protocol in a wide table only. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (wideAttribute). Unique identifier for an attribute in a wide table only. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (method). A procedure for collecting a sample or performing a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (contactName). Contact person or group, for the lab. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (mmaSet). The set for a measure, method, or attribute. Only applicable for categorical fields, and the categories that populate them.

Sets

The use has been extended to include ‘partType’ values as well, to codify instances where a categorical variable takes any part of a certain part type. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (unitSet). An identification 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.

NA (funderID). The funding agency of the dataset. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (countryEndonym). The name locals use for their country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (countryExonym). The English name foreigners use for the country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (cphDate). date of reporting for covid-19 measure. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (instrumentID). A unique identifier for an instrument. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (labID). Unique identifier for a laboratory. Status: depreciated. First released: 1.0.0. Last updated: 2.1.0.

NA (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.

NA (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.

NA (datasetDate). Specifies the date a given dataset was created. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lang). Language code for translation purposes. Specifies the language 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.

NA (missingnessSet). Missingness sets for measures, methods or attributes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (dateDep). Date Status: depreciated. First released: 1.0.0. Last updated: 3.0.0.

NA (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 differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname rules (see PHES-ODM documentation for more details). Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (detailsDep). More details on the existing confidentiality requirements of this measurement. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (enaMap). ENA header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (enaNotes). ENA notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (epiWeek). The number of the epi week in which a sample was collected, or to which a measure would apply. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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 date resolves the possible ambiguity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (epiYear). The year in which the epi week is occurring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (measureRepID). Unique identifier for a measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (fileLocation). The location of the file containing the geometry of the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (firstName). Specifies the first name of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (fraction). Fraction of the sample that is analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (reportTableName). The report table that the wide name calls from. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (reportTableInput). The short name for the listed source table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (license). The license of a dataset. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (partTypeName). The part type being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (measureSetRepID). Unique identifier that links together a group of related measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (siteType). Type of site or institution where sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (geoType). Type of geography that is represented by the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (geoWKT). Well-known text of the polygon Status: active. First released: 1.0.0. Last updated: 3.0.1.

NA (hostVersion). The version of the data repository or hosting platform being used. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (insType). Type of instrument used to perform the measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

Sets

NA (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: deprecated. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (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: deprecated. First released: 2.0.0. Last updated: 3.0.0.

NA (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 differentiate between variants of languages and language families, such as historical vs. revived versions of languages. Status: deprecated. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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: deprecated. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (parDatasetID). The datasetID that is a parent to another datasetID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lastName). Specifies the last name of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (li). Link to an external reference that describes the geometry of the polygon. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (parent). If this sample has been pooled into one big sample for analysis this indicates the sample of the larger pooled sample. Status: deprecated. First released: 1.1.0. Last updated: 2.0.0.

Sets

NA (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.

NA (manufacturer). Manufacturer of an instrument. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (compartmentName). The compartment referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (measureLic). Specifies the access and use licensing for a given single measurement. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (compartmentInput). The partID for the compartment being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (specimenName). The specimen referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (specimenInput). The partID for the specimen being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (model). Model number or version of the instrument. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (nameEngl). English-language name of a given country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (nameOfficial). Official english-language name of a given state. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (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.

NA (ncbi). NCBI header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ncbiNotes). NCBI notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (norman). NORMAN header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (normanNotes). Norman notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (stepVer). Specifies the version of a given protocol step. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (nwss). NWSS header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nwssNotes). NWSS notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (nwssProcess). NWSS process Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (polygonIDSubject). The polygon ID subject in a polygon relationship. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orgLevel). The geographic level of an organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orgSector). The sector of an organization Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orgType). Specifies the type or purpose of a given organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (origin). An attribute of a sample specifying the origin. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (polygonID). Unique identifier for the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (polygonIDObject). The polygon ID Object in a polygon relationship. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (polygonRelID). Unique identifier for each row in the polygon relationships table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (email). Contact e-mail address, for the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (repOrg1). The primary or most responsible authority for routine surveillance reports or findings, or where the site is located. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (fractionName). The fraction analyzed referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fractionInput). The partID for the fraction being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pCode). The zip code or postal code for a given address, specifying a specific geographic area. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (actionType). The type of public health action being taken. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (phage). PHAGE header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (phageNotes). PHAGE notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (phone). International dialing code for the country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (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.

NA (poLic). The license for the availability of the polygon shapefile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (protocolID). A unique identifier for a given protocol. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (stepID). The unique identifier for a specific protocol step. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (action). The specific public health action or designation being taken or applied. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (ptDescDep). If preTreatment then describe the treatment that was performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (purpose). The reason the measure or sample was taken. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (phActionID). Unique identifier for public health actions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (recDate). The date the sample was received at the laboratory for analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qualityReportID). A unique identifier for a given quality report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (relationshipID). Attribute for specifying the relationship between a sample subject and object. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (actionDT). The date and Time of the public health action. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (reportDate). The date a measure was reported. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (measureName). The measure referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (measureInput). The partID for the measure being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (repType). Attribute 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.

NA (coPhone). Contact phone number, for the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sampleID). Unique identifier for a sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (saMaterial). Type of sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sampleIDObject). Populated by **sampleID** - this specifies the object of a sample relationship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sampleIDSubject). Populated by **sampleID** - this specifies the subject of a sample relationship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (repOrg2). The secondary, additional or alternative authority for routine surveillance reports or findings, or where the site is located. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (setID). The unique identifier of a value set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721) Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (siteID). Unique identifier for the location where a sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (severity). An indicator of the severity or seriousness of a quality flag. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (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.

NA (relDateStart). The start date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000) Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (geoEPSG). The unique EPSG code specifying a given geospatial area. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (methodName). The method referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (role). Specifies the organizational role of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (protocolVersion). Specifies the version of a method set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (specimen). The substance or thing upon which the observation was made. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (methodInput). The partID for the method being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (unitName). The unit referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (equation). The equation used in the calculation/data treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (value). Value of a measure, observation or attribute. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

Sets

NA (unit). The units of a measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (lastEdited). The date the entry was last updated. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (unitInput). The partID for the unit being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (aggregationName). The aggregation referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (uSiteMeasureID). Unique identifier for each measurement for a site. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

NA (utc). UTC – Time zone. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (utcDST). Time zone during Daylight Saving Time. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (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.

NA (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.

NA (version1Category). ODM V1 category Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Location). ODM V1 location Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Table). ODM V1 table Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1to2Changes). Changes for part between ODM v1 and V2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Variable). ODM V1 variable Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (aggregationInput). The partID for the aggregation being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (index). Index number in case the measurement was taken multiple times. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Sets

NA (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.

NA (attributeName). The attribute referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (attributeInput). The partID for the attribute being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (wSphere). World Sphere header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wSphereNotes). W-Sphere notes Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (zoneName). The english-language name for a given country sub-domain. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (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.

NA (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.

NA (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.

NA

(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 wastewater treatment plant, airplane holding tank, wastewater pumping station, etc. Each of these site types is recorded as a category that can be identified in categorySetID = sTypeCatSets

NA (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 microbial 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.

NA (aas). Atline analyzer with sampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (abricate). Software tool for screening bacterial genomes against multiple resistance databases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (active). Indicator that a part is in current use. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (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.

NA (admRegLevel). Administrative regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (aff30). 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.

NA (aft). Sample was collected in the afternoon, sometime after lunch. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (afu). Air filter as part of filtration or circulating unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (agri). Agricultural activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (airpln). Airplane sample shed category type Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (airport). Airport sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (aloh3). Alo3 precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (amiconUf). Amicon ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (amiMP96). Nucleic 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.

NA (amp). Specifies the amplicon strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (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.

NA (anneal). Describes the annealing and/or extension cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (aradb). An archive for antibiotic resistance genes and associated information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (areaPr). An area proportional sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (argAnnotSoft). Software annotation tool for antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (articV4). Artic V4 sequencing primer for VOCs and VOIs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with 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.

NA (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.

NA (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.

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

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produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (bacCul). Growing a bacterial culture to test for bacterial presence. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (bacMet). Database of antibacterial biocide and metal resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bact16sABIRev). Bacteroides 16S reverse primer (BacR287) (ABI)
Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bagFilt). Sample was collected using bag-mediated filtration. Status:
active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (bamUtil). A deduplication method that removes duplicate reads
directly from BAM files. Status: active. First released: 3.0.0. Last updated:
3.0.0.

NA (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.

NA (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.

NA (bayesSmooth). This data treatment smooths the measurement value
using bayesian smoothing techniques. Status: active. First released: 3.0.0.
Last updated: 3.0.0.

NA (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.

NA (bbmap). BBMap. A general-purpose read mapper. High-sensitivity
aligner for DNA and RNA reads. Best for: Error-prone reads from platforms

Sets

like Nanopore or PacBio. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (bbMP96). Nucleic 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.

NA (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.

NA (bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (beeExtractFloc). Beef extract flocculation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (bioanalsys). 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (blasr). BLASR (Basic Local Alignment with Successive Refinement). A long-read specific mapper. Optimized for PacBio data. Best for: High-

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quality long-read alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (bow). An outdoor accumulation 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municipal sewer lines, allowing drainage into the main sewer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (builLev). Surveillance is done only at the level of a single building. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (busStat). A terminal where buses arrive and depart. Status: active. First released: 2.2.3. Last updated: 2.2.3.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (cardDtbse). Database that provides high-quality reference sequences for resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (caSmooth). This data treatment smooths the measurement value using central average smoothing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (ccbynca40). 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.

NA (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.

NA (ccc). Acute care hospitals, or complex continuing 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.

Sets

NA (cdc). Child day care facility. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (cdcCovEIDTFor). Sarbeco_E forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovEIDTProbe). Sarbeco_E probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovEIDTRev). Sarbeco_E reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN1IDTFor). 2019-nCoV_N1 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN1IDTProbe). 2019-nCoV_N1 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN1IDTRev). 2019-nCoV_N1 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN2IDTFor). 2019-nCoV_N2 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN2IDTProbe). 2019-nCoV_N2 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN2IDTRev). 2019-nCoV_N2 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN3IDTFor). 2019-nCoV_N3 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN3IDTProbe). 2019-nCoV_N3 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN3IDTRev). 2019-nCoV_N3 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (census). Government or other agency census for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (centriconUf). Centricon ultrafiltration. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ceres). Ceres nanotrap. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (cK). Composite key for a table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

NA (clari). Clarified sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (communitLev). Surveillance is done at the level of an entire community. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (comp). A composite sample, usually generated by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (comp3). A grab-composite sample composed of 3 separate grab samples. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (comp3dep). A grab-composite sample composed of 3 separate grab samples. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (corFcil). Correctional facility Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (cosca). COSCa passive sampling device. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (count). A count of residents for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

Sets

NA (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.

NA (countryLevel). Countries or sovereign states Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (countyLevel). Districts, counties, regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (day7Smooth). This data treatment smooths the measurement value across 7-days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ddbj). DNA Data Bank of Japan (DDBJ) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (denat). Describes the denaturation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (deprecated). 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.

NA (derived). Derived data, data that has undergone aggregation, standardization, adjustment, or any cleaning prior to reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (desk). Desk, table, countertop or other flat working surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (deso). Dewatered solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (development). Indicator that a part is under development use. See `partID = status` Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (discover). 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.

NA (dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (dorm). Higher education dormitory or residential building Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (dpcr). Describes a PCR analysis done using digital PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (edFac). A school or other educational facility not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (education). A measure or sample taken for education or training. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (elutionBuff). Elution buffer is used to resuspend material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (emergSurv). A targeted surveillance strategy which is considered important and/or urgent. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ena). European Nucleotide Archive (ENA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (enaForm). Dataset was originally recorded and/or stored in ENA format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (enviroInst). Local probe instruments 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.

NA (epiDate). Episode date is the earliest of onset, test or reported date. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (esp). exclusions based sample preparation (ESP) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (estimate). Estimated data, data that should be understood to be an estimation, possibly not taken directly from sample measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (estuary). Estuary, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (eve). Sample was collected in the evening, late in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (extract4s). Nucleic acid extraction performed using the 4s method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (faeces). Fecal matter. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (fiNa). Used to categorize a sample that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (fK). Foreign key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (floor). Floor of a building or room. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (flowInst). Flow meter instruments; used to measure wastewater flow rates to enable standardization of sample data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (flowPr). A flow proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

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NA (flowStand). This data treatment standardizes the measurement value to flow rates. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (fluidPcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (countLevel). Specifies that a sewershed/site represents an entire nation or country. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (freyja). Freyja Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (genBank). GenBank Archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (github). GitHub external data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

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NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (grb). A single large representative grab sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (gromstole). Gromstole 1.0 Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (gsa). Genome Sequence Archive (GSA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (hcAct). Healthcare activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (hcf). A building for the provision of healthcare, not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (header). Header for a table. Also known as a table variable or entity relationship 'attribute'. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (healthAdm). Health administrative or planning organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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NA (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.

NA (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.

NA (hFr). An indicator in wide-names to show that information on the fraction analyzed is found under a separate header. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (high). Indicates a very severe quality issue, likely meaning the data should not be reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (hlthReg). Health region served by the sewer network Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (hma). Handheld measurement analyzer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (hollowFiberUF). Hollow fiber dead end ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (horGrb). Instrument 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.

NA (hosptl). Hospital Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (htSite). Holding tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (husb). Animal husbandry occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (hySel). Selection by hybridization in array or solution for genomic target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (idbaUD). A sequencing software that is an iterative assembler optimized for metagenomics and complex genomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occasionally services, and making them into products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (indus). Industrial activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (infPump). A facility that transports raw wastewater from collection systems to treatment plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (innovaprepUF). Innovaprep ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (instituLev). Surveillance is done at the level of an entire institution. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (lab). Laboratory for environmental testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (lagoon). Lagoon system for extensive wastewater treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (lake). Lake, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (landTH). A transport hub is a place where passengers and cargo are exchanged between land-based vehicles and/or between land-based

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transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

NA (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.

NA (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.

NA (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.

NA (less10). Fewer than 10 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less100). Between 10 and 100 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less100k). Between 10,000 and 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less10k). Between 1,000 and 10,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less1k). Between 100 and 1,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less1mil). Between 100,000 and 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (liquid). The liquid or supernatant is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (low). A marker for low severity Status: active. First released: 2.0.0. Last updated: 2.0.0.

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NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (luminWWExtract). luminultra wastewater extraction kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (lysi). Lysis buffer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (mall). A large commercial complex with multiple retail stores, services, and restaurants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (manComp). Specifies a composite sample where the sub-samples were collected manually. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (mateLay). Specifies the mate pair layout for a sequencing method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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NA (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.

NA (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.

NA (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.

NA (megares). A comprehensive database of antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (memMgCl3). membrane filtration with addition of mgcl3 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (metaPhlAn). Software tool that profiles microbial communities and can provide resistance gene insights. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mfAcidmgcl2). Membrane filtration with acidification and mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfMgcl2). Membrane filtration with addition of mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfNoAmend). Membrane filtration with no amendment Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfSampleAcid). Membrane filtration with sample acidification Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (mhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (mid). A marker for med-level severity, where there are some concerns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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

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1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (moorSw). Moore swab passive sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (more1mil). More than 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (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.

NA (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (mspsDep). Moore swab passive sample. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (mSwrPpl). Major sewer pipeline Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (muCoMat). Murine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (multiComLev). The scope of the surveillance covers multiple communities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (municipalLevel). Municipalities or communes Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (muniLevel). Specifies that a sewershed/site represents an entire municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (nac). Denotes a no amplification control replicate sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

Sets

NA (ncbiForm). Dataset was originally recorded and/or stored in NCBI format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (ncovtools). Tools and plots for performing QC on coronavirus sequencing results. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (neighborLevel). Local administrative units or neighborhoods Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (ngsInst). Next generation sequencer instruments and platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (night). Sample was collected at night, between sunset and sunrise. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (noliquid). No liquid concentration, liquid recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (none). No sample storage medium used Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (norm). The purpose of a measure or sample is for normalization. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (normanForm). Dataset was originally recorded and/or stored in Norman format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (новоalign). 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.

NA (новоPlasty). 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.

NA (nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ntc). Denotes a non-template control sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ntp). Denotes a sample replicate/control with no target present. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (nww). Non-wastewater, coming from any kind of water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ocean). Ocean, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (oColDep). Other type of collection method. Add description to collectionOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (office). A workplace where administrative, managerial, or clerical tasks are performed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (off11). 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.

NA (ola). Offline laboratory analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (onse). Online sensor Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (opt). Denotes a sample control or replicate used for optical calibration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (opWa). An outdoor accumulation 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.

NA (orb). Individual residential buildings or institutions not captured in other categories Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (osf). Open Science Foundation project/data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (otco). Other type of collection method. Add description to collectionOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (other). Other Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (otsisaDep). Other type of site. Add description to typeOther. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (otsisiDep). Other site type. Add description to typeOther Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (pAct). Describes the polymerase activation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pairLay). Specifies the paired layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (pceDep). Effluent obtained after primary clarifiers. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (pcs). Sludge produced by primary clarifiers. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (pEfflu). Effluent obtained after primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (peg). Peg precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (phAdvise). A public health action type wherein a public health advisory is disseminated to the public. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (pharmPl). An industrial building in which pharmaceutical drugs are synthesised and processed on an industrial scale. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (phenCl). Nucleic acid extraction performed using phenol chloroform. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (phi6Mat). Pseudomonas virus phi6 is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (phyloPhIA). 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.

NA (phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (pK). Primary key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

Sets

NA (pmmvABIFor). PMMV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pmmvABIProbe). PMMV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pmmvABIRev). PMMV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pogr). Raw wastewater after a treatment plant's headworks. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (policy). Describes organizations whose core focus is on policy or political activity. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (predicted). Predicted data, data generated by predictive models or algorithms, not taken directly from sample measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (private). The measure or data set is private data - not for dissemination. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

Sets

NA (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.

NA (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.

NA (promAuto). Nucleic acid extraction performed using the promega automated tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (promegaLVTNA). promega wastewater large volume tna capture kit Status: depreciated. First released: 2.2.0. Last updated: 3.0.1.

NA (promHt). Nucleic acid extraction performed using the promega ht tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (promManu). Nucleic acid extraction performed using the promega manual tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (provisional). A provisional or interm report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (pSludge). Sludge produced by primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (pstGrit). Raw wastewater after a treatment plant’s headworks (post grit or removal of large solids at a treatment plant but prior to a primary clarifier) Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (pubHealth). Public health agency. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (puroMat). Puro Virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

Sets

NA (qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qiAllprep). qiagen allprep dna/rna kit Status: depreciated. First released: 2.2.0. Last updated: 3.0.1.

NA (qiaampDSP). qiagen qiaamp dsp viral rna mini kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (qiaSeqFX). QIAseq FX DNA Library Kit by Qiagen. A library 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.

NA (qpcr). Real-time PCR, also called ‘quantAggScale’ PCR. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (qualityControl). A measure or sample taken for the purpose of quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (rainDpccr). Describes a PCR analysis done using Raindance’s digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (rainy). Qualitative category for the weather measure, specifying a rainy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (ranSeq). Specifies the random selection method for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (raw). Raw data, without adjustment or additional treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (raws). Raw wastes water sample Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rawWW). Wastewater without any form of treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rawWWdown). Downstream from a site. See partType = rawWWup. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjutiion 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.

NA (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.

NA (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.

NA (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.

NA (regular). A measure or sample taken for surveillance or epidemiology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (repGrab). A single large representative grab sample. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (research). Describes organizations whose focus is on research generation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (researchPurp). Purpose of sampling/measure is for research. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (resFinderDtbse). nomenclature from the National Center for Biotechnology Information Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (retPond). Retention pond Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rev). A review of records for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (river). River, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (road). A paved or unpaved pathway designed for vehicular and pedestrian travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (rppw). Raw wastewater sample post-pasteurization Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rt). Describes the reverse transcription cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (rural). Rural populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (samConc). Sample concentrate. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (sce). Effluent obtained after secondary clarifiers. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (school). A school serving students in the kindergarten to 12th grade range Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (sciencellRNA). sciencell viral rna isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (scsDep). Sludge produced by secondary clarifiers. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

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NA (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.

NA (sea). Sea, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (sEfflu). Effluent obtained after secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (septage). Wastewater from within a septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (septTnk). Septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (serDil). Describes a serial dilution process for standard curve generation for PCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (serialDilution). The serial dilution method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (seseDep). Sediments obtained in sewer. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (ship). A cruise ship or other ship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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NA (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.

NA (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.

NA (sinLay). Specifies the single layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (skimMilkFloc). Skimmed milk flocculation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (snowy). Qualitative category for the weather measure, specifying a snowy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

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NA (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.

NA (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.

NA (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (solid). The solids or pellet is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (spike). The spike matrix and recovery method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (sra). Sequence Read Archive (SRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (sSludge). Sludge produced by secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sss). Other type of social services shelter Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment to reduce the organic content and remove pathogens

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from wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (stateProvLevel). Departments, states, or provinces Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (std). Denotes a standard sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (stormy). Stormy weather Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (subSamp). A general replicate type for a subsample not otherwise defined. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (suburban). Suburban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (surface). Surface other than floor or desk. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (surfSw). Surface swab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (swgTrck). Sewage truck Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

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NA (swrSed). Sediments obtained in sewer Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (swrSet). Sewer catchment area. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (synthetic). A synthetic or artificially generated sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (terminal). Airport terminal sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (tesDate). Date that the covid-19 test was performed. Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (tHub). A transport 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.

NA (timePr). A time proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (timeStand). This data treatment standardizes the measurement value against time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (tradSero). Traditional Serotyping methods used for serotyping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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NA (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.

NA (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.

NA (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.

NA (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (treeTime). A lineage or clade analysis software tool for phylogenetic analysis, often for molecular clock dating and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (triturator). The location where wastewater transportation vehicles unload wastewater. Status: active. First released: 2.2.3. Last updated: 2.2.3.

NA (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.

NA (trizolEtOH). trizol, garnet bead beating, alcohol precipitation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (trizolRNA). trizol and RNA purification kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (uGene). Sequencing software that offers alignment and consensus sequence generation features. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (unique). A unique sample, not duplicated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (unkn). Denotes an unknown sample replicate type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (untracent). Ultracentrifugation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (upstream). A general site type for upstream wastewater sampling sites. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (urban). Urban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (validationStudy). A measure or sample taken for a validation study. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (volPr). A volume proportional sample generally collected by an autosampler. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (vsvABIFor). VSV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vsvABIProbe). VSV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vsvABIRev). VSV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (watConcBuff). water concentrating buffer (R2042-1) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (water). Non-wastewater, coming from any kind of water body. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (wSphereForm). Dataset was originally recorded and/or stored in wSphere format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwCominuated). wastewater comminution process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwDry). Wastewater sludge drying occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwFilt). Wastewater filtration occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwGrit). Wastewater grit removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwMic). Wastewater microbial treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwPriSed). Wastewater primary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwScreen). Wastewater screening process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwtp). A general site type for wastewater treatment plants. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (wwtpInd). Industrial wastewater treatment plant Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (wwtpMuC). Municipal wastewater treatment plant for combined sewage Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wwTrt). Wastewater treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (zenodo). Zenodo open data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

Sets

NA (zymo1035). zymo quick-rna viral kit #r1035 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (zymo1041). zymo quick-rna viral 96 kit #r1041 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (zymoWatRNA). zymo environ water rna kit (cat. r2042) Status: deprecated. First released: 2.2.0. Last updated: 3.0.1.

NA (FALSE). Boolean data type = FALSE Status: active. First released: 1.0.0. Last updated: 2.3.0.

NA (TRUE). Boolean data type = TRUE Status: active. First released: 1.0.0. Last updated: 2.3.0.

NA (overlap). Locations/polygon have overlapping portions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (neighbour). Locations/polygon are neighbouring eachother. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (cali). Purpose of calibrating a machine, method, or other. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA

(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.

NA (allele). Measures and methods related to alleles. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (bactFung). Measures and methods relating to bacteria. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (capacity). Measures and methods relating to capacity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (conductivity). Measures and methods related to conductivity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (database). Measures and methods related to databases and data repositories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dilution). Measures and methods relating to dilutions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (disease). Measure and methods related to disease or infection in humans. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (flowClass). Measures and methods related to flow. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (gas). Measures and methods relating to gas and gases. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (humid). Measures and methods related to humidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lookup). Tables to describe and support the ODM dictionary. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mutation). Measures and methods related to mutations. Status: depreciated. First released: 2.0.0. Last updated: 2.3.0.

NA (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.

NA (naClass). Class is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (organism). Organism class Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (outbreak). Measures and methods relating to public health outbreaks. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

NA (pcr). Measures and methods relating to qPCR. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pHClass). Measures and methods relating to pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (physical). Measures and methods related to generic physical properties. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (popClass). Measures and methods relating to population (ie. Measures of population, location). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (precipitation). Measures and methods related to precipitation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (programDescr). Tables used to describe surveillance and testing programs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (protein). Measures and methods related to proteins. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (results). Tables used to record samples, measures and quality reports. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sequence). Measures and methods related to genetic sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (software). Measures and methods related to software. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (speed). Measures and methods relating to speed. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (standardConc). Measures and methods relating to standard concentrations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (standardCurve). Measures and methods relating to generating or recording a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (temperature). Measures and methods related to temperatures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (timeClass). Measures and methods relating to time. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (turbidity). Measures and methods relating to water and wastewater turbidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (variant). Measures and methods relating to variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (weather). Measures and methods relating to weather. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(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.

NA (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA

(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.

airCompartmentSet

(airCompartmentSet)A compartment set for measures and methods in the air compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

airSurfaceCompartmentSet

(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.

NA (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

airWaterCompartmentSet

(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.

NA (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

anyCompartmentSet

(anyCompartmentSet)A compartment set for measures and methods in any compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

humanCompartmentSet

(humanCompartmentSet)A compartment set for measures and methods in the human compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

naCompartmentSet

(naCompartmentSet)Compartment not applicable. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

surfaceCompartmentSet

(surfaceCompartmentSet)A compartment set for measures and methods in the surface compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

surfaceWaterCompartmentSet

(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.

NA (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

waterCompartmentSet

(waterCompartmentSet)A compartment set for measures and methods in the water compartment. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

NA (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.

Sets

wideCompartmentSet

(wideCompartmentSet)Compartment set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 3.0.0.

NA (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA

(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.

NA (airCompartmentSet). A compartment set for measures and methods in the air compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (`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.

NA (`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.

NA (`anyCompartmentSet`). A compartment set for measures and methods in any compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (`humanCompartmentSet`). A compartment set for measures and methods in the human compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (`naCompartmentSet`). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (`surfaceCompartmentSet`). A compartment set for measures and methods in the surface compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (`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.

NA (`waterCompartmentSet`). A compartment set for measures and methods in the water compartment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (`wideCompartmentSet`). Compartment set for wide names. Status: active. First released: 2.2.0. Last updated: 3.0.0.

NA

(dataTypes). The data type for a part. Data types used in the ODM include: varchar, boolean, float, category, date, time, datetime, url, email. dataType corresponds to 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 identified within the part entry. TBA: dataType for dictionary.

NA (blob). The data type for Binary Large Object (BLOB) data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (boolean). The data type for boolean/binary data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (categorical). The data type for categorical data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (date). The data type for date data (does not include time). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (datetime). The data type for date and time data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (float). The data type for float data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (integer). The data type for integers. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA

NA (varchar). The data type for variable character data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(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.

NA (airportLists). Parts lists used to generate airport and airplane data entry templates. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (airportTemplate). The input template for airport and airplane surveillance in the EU. Status: active. First released: 2.0.0. Last updated: 2.1.0.

NA (lists). Parts lists for template dropdowns and other documentation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (summary). Summary sheet of the dictionary.xlsx file. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(dictSets). Sets used to describe and group dictionary tables.

airportSheetSet

(airportSheetSet)Worksheets in the full airport surveillance template (list + template). 'ODM_template-planes_{version}.xlsx Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (airportLists). Parts lists used to generate airport and airplane data entry templates. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (airportTemplate). The input template for airport and airplane surveillance in the EU. Status: active. First released: 2.0.0. Last updated: 2.1.0.

contactTableSet

(contactTableSet)Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). 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.

NA (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.

NA (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.

NA (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information 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.

crosswalkTableSet

(crosswalkTableSet) Tables used to translate to and from other environmental dictionaries and models. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (enaMap). ENA header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (enaNotes). ENA notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ncbi). NCBI header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ncbiNotes). NCBI notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (norman). NORMAN header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (normanNotes). Norman notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nwss). NWSS header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nwssNotes). NWSS notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (nwssProcess). NWSS process Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (phage). PHAGE header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (phageNotes). PHAGE notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Category). ODM V1 category Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Location). ODM V1 location Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Table). ODM V1 table Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1to2Changes). Changes for part between ODM v1 and V2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (version1Variable). ODM V1 variable Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wSphere). World Sphere header Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wSphereNotes). W-Sphere notes Status: active. First released: 1.0.0. Last updated: 2.0.0.

dictionaryRefTableSet

(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. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

erdTableSet

(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. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (addresses). The table that contains information about addresses. Addresses can be recorded for sites, organizations or contacts (individuals). 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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 variants 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.

NA (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.

NA (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.

NA (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.

NA (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.

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NA (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.

NA (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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information 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.

NA (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.

NA (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.

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NA (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.

fullDictionarySheetSet

(fullDictionarySheetSet)Worksheets in the full Excel dictionary. The full dictionary is ODM_full-dictionary.xlsx </br> Status: active. First Released: 2.0.0. Last updated: 2.0.0. ****NA**** (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. </br>Status: active. First released: 2.3.0. Last updated: 2.3.0. ****NA**** (addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). 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. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. ****NA**** (calculations). Table for recording data on data treatments and calculations applied to measurements and reported values. </br>Status: active. First released: 2.3.0. Last updated: 2.3.0. ****NA**** (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. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. ****NA**** (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions

field. </br>Status: active. First released: 2.1.0. Last updated: 2.1.0. **NA** (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. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. **NA** (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. </br>Status: active. First released: 1.0.0. Last updated: 2.0.0. **NA** (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. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. **NA** (lists). Parts lists for template dropdowns and other documentation. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. **NA** (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. </br>Status: active. First released: 1.0.0. Last updated: 2.0.0. **NA** (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 variants that are identified in a single sample. The short name for the table (partID) can be found in the instructions field. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. **NA** (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions

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field. </br>Status: active. First released: 1.0.0. Last updated: 2.0.0. **NA** (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. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. **NA** (phActions) Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. </br>Status: active. First released: 3.0.0. Last updated: 3.0.0. **NA** (polygons) Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. </br>Status: active. First released: 2.3.0. Last updated: 2.3.0. **NA** (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. </br>Status: active. First released: 1.0.0. Last updated: 2.0.0. **NA** (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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation rotation speed is described as a measure. The short name for the table (partID) can be found in the instructions field. </br>Status: active. First released: 2.0.0. Last updated: 2.0.0. **NA** (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. </br>Status: active.

First released: 2.0.0. Last updated: 2.0.0.
****NA**** (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. </br>Status: active. First released: 1.0.0. Last
 updated: 2.0.0. ****NA**** (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.
 </br>Status: active. First released: 2.0.0. Last updated:
 2.0.0. ****NA**** (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. </br>Status: active. First
 released: 2.0.0. Last updated: 2.0.0. ****NA****
 (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 relation-
 ships' (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.

NA (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.

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NA (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information 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.

NA (summary). Summary sheet of the dictionary.xlsx file. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

listSet

(listSet)PartTypes that contain categories, sets, or lists. Used to generate documentation. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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 surveillance data. The other two components are measures and methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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 wastewater treatment plant, airplane holding tank, wastewater 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.

NA (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.

NA (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.

NA (compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment.

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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.

NA (dataTypes). The data type for a part. Data types used in the ODM include: varchar, boolean, float, category, date, time, datetime, url, email. dataType corresponds to 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 identified within the part entry. TBA: dataType for dictionary. Status: active. First released: 2.0.0. Last updated: 3.0.1.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA exclusive sets, or general all-purpose sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (nomenclatures). A classification system to report the measure class. See `partID = nomenclatureID`. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (partTypes). Part types describe the purpose or use of the part. Environment data has three main part types: measure (i.e. covN1 viral measures, wastewater 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.

NA (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.

NA (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.

NA (specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See

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partID = specimenID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

otherReportTableSet

(otherReportTableSet) Additional tables that form the full data model. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

protocolTableSet

(protocolTableSet)Tables holding information on the methods used for sample collection or measurement. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation 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.

NA (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.

NA (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the

Sets

table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

regularReportTableSet

(regularReportTableSet)Tables used for daily reporting of new measurements and information on sample collection. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

templateSheetSet

(templateSheetSet)Worksheets in the full generic ODM surveillance template (all tables). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (addresses). The table that contains information about addresses. Addresses can be recorded for sites, organizations or contacts (individuals). 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (lists). Parts lists for template dropdowns and other documentation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (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 variants 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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

NA (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.

NA (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information 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.

NA (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.

NA (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.

NA

(domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature).

NA (allDo). Domain that specifies that it could apply to all domains; biological, chemical, and physical. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (bio). A living organism or biological substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (che). A chemical compound. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (naDomain). Not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (phy). A physical property or object not characterized by life or chemistry. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(exceptions). An exception part type for use in creating wide names that do not follow the general structure.

NA

(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.

NA (acinetobacterGrp). A group of measures/methods related to acinebac-
ter bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (adenovirusGrp). A group of measures/methods related to Aden-
oviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (anaplasmaGrp). A group of measures/methods related to anaplasma
bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (astrovirusGrp). A group of measures/methods related to astroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (babesiaGrp). A group of measures/methods related to babesia parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bacteroidesGrp). A group of measures/methods related to bacteroides bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bactMisc). A group of measures/methods related to miscellaneous bacteria. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (betaCoronaGrp). A group of measures/methods related to beta coronaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (brucellaGrp). A group of measures/methods related to brucella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (campGrp). A group of measures/methods related to campylobacter bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cAurisGrp). A group of measures/methods related to *Candida auris*. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (chikungunyaGrp). A group of measures/methods related to chikungunya virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (chlamydiaGrp). A group of measures/methods related to chlamydia bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (clostridiumGrp). A group of measures/methods related to clostridium bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (colGrp). A group of measurement-like attributes related to sample collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (cryptosporidiumGrp). A group of measures/methods related to cryptosporidium parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (diphtheriaGrp). A group of measures/methods related to the diphtheria bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ecoliGrp). A group of measures/methods related to Escherichia coli bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (enterovirusGrp). A group of measures/methods related to enteroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (flavivirusGrp). A group of measures/methods related to flaviviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (fluAGrp). A group of measures/methods related to Influenza A viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fluBGrp). A group of measures/methods related to Influenza B viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fluGrp). A group of measures/methods related to general influenza viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (gonococcusGrp). A group of measures/methods related to gonococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (haemophilusGrp). A group of measures/methods related to haemophilus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hepGrp). A group of measures/methods related to hepatitis viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (herpesGrp). A group of measures/methods related to herpes viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hivGrp). A group of measures/methods related to Human Immunodeficiency Virus (HIV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hrvGrp). A group of measures/methods related to rhinoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (klebsiellaGrp). A group of measures/methods related to klbsiella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (legionellaGrp). A group of measures/methods related to legionella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (listeriaGrp). A group of measures/methods related to listeria bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (malariaGrp). A group of measures/methods related to plasmodium parasites or malaria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (measGrp). A group of measures that cannot be otherwise categorized. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (measlesGrp). A group of measures/methods related to the measles virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (metaboliteGrp). A group of measures/methods related to metabolites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (miscAttr). A group of miscellaneous measurement-like attributes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (miscMeas). A group of measures that cannot be otherwise categorized. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (mpoxGrp). A group of measures/methods related to Mpox (formerly “Monkey Pox”). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (mpvGrp). A group of measures/methods related to metapneumoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (mumpsGrp). A group of measures/methods related to the mumps virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (mycoplasmaGrp). A group of measures/methods related to mycoplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (naGroup). Used when there is no group; ie. group is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (norogIGrp). A group of measures/methods related to norovirus GI. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (norogIIGrp). A group of measures/methods related to norovirus GII. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (norogrps). A group of measures/methods related to noroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (orthoGrp). A group of measures/methods related to orthopox viruses (excluding variola viruses). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (papillomavirusGrp). A group of measures/methods related to papillomaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (parafluGrp). A group of measures/methods related to parainfluenza viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (phageGrp). A group of measures/methods related to bacteriophages. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (polioGrp). A group of measures/methods related to polioviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (popGrp). A group of measures/methods related to population-level factors. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (procGrp). A group of measures/methods related to processing samples for analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pseudomonasGrp). A group of measures/methods related to pseudomonas bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (rickettsiaGrp). A group of measures/methods related to rickettsia parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (rotavirusGrp). A group of measures/methods related to rotaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (rsvGrp). Human Respiratory Syncytial virus (RSV). Status: active. First released: 2.0.0. Last updated: 2.1.2.

NA (rubellaGrp). A group of measures/methods related to the rubella virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (salmonellaGrp). A group of measures/methods related to salmonella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (sapovirusGrp). A group of measures/methods related to sapoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (shigellaGrp). A group of measures/methods related to shigella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (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.

NA (staphGrp). A group of measures/methods related to staphylococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (strepGrp). A group of measures/methods related to streptococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (treponemaGrp). A group of measures/methods related to treponema bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (trichomonasGrp). A group of measures/methods related to trichomonas bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (tuberculosisGrp). A group of measures/methods related to tuberculosis. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (tularemiaGrp). A group of measures/methods related to Francisella tularensis. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ureaplasmaGrp). A group of measures/methods related to ureaplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (varicellaGrp). A group of measures/methods related to varicella viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vibrioGrp). A group of measures/methods related to vibrio bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (virusMisc). A group of measures/methods related to miscellaneous viruses. Status: depreciated. First released: 1.0.0. Last updated: 2.2.0.

NA (vsvGrp). A group of measures/methods related to Vesicular Stomatitis Virus (VSV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (waterQualityGrp). A group of measures/methods related to water quality. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (yersiniaGrp). A group of measures/methods related to yersinia bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ebolaGrp). A group of measures/methods related to Orthobolaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (hantaGrp). A group of measures/methods related to Orthohantaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (aichivAGrp). A group of measures/methods related to human aichiviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (kobuGrp). A group of measures/methods related to kobuviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (bocaparvGrp). A group of measures/methods related to bocaparvoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (circoGrp). A group of measures/methods related to circoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (cosaVGrp). A group of measures/methods related to cosaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (deltaretroGrp). A group of measures/methods related to deltaretroviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Sets

NA (eeevGrp). A group of measures/methods related to eastern equine encephalitis viruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (erythroparvoGrp). A group of measures/methods related to erythroviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (giardiaGrp). A group of measures/methods related to Giardia. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (gammaretroGrp). A group of measures/methods related to gammaretroviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (lymphocryptoGrp). A group of measures/methods related to lymphocryptoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (mastadenoGrp). A group of measures/methods related to human mastadenoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (parechoGrp). A group of measures/methods related to parechoviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (picobirnaGrp). A group of measures/methods related to picobirnaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (polyomaGrp). A group of measures/methods related to polyomaviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (hhvGrp). A group of measures/methods related to roseoloviruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (saliGrp). A group of measures/methods related to salivirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (saffoldGrp). A group of measures/methods related to saffold virus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (tanapoxGrp). A group of measures/methods related to tanapox viruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (ttvGrp). A group of measures/methods related to torque teno viruses. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA

(measurements). The attribute to describe a part type of measures. All measures have **partType** = “measure”. mes

NA (a1306s). a1306s delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (a1918v). a1918v delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (a2710t). a2710t omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (a63t). a63t omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (a67v). a67v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (a67vDel69Del70). Omicron Variant a67v mutation mutation, and del 69 and del70 mutations co-occurring Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

Sets

NA (acinetobacter). Acinetobacter Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (adenovirusF40). Adenovirus (F40/41) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (adv40). Adenovirus serotype 40. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (adv41). Adenovirus serotype 41. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (advF41Fibre). Human Adenovirus Group F41 Fiber gene target Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (airTemp). Environmental temperature. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (alkaline). Measure of alkalinity Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (ambigNs). The number of ambiguous bases (Ns) normalized per 100 kilobasepairs (kbp). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ampSize). The length of the amplicon generated by PCR amplification. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (aPhagocytophilum). Anaplasma phagocytophilum Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (astrovirus). Astrovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (babesia). Babesia Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bBurgdorferi). Borrelia burgdorferi Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bcov). Measure of the amount of bovine coronavirus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (beta). B.1.351 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (blaCMY). Cephamycin Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (blaCTXM1). CTX-M Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (blaIMP). Imipenemase (IMP) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (blaKPC). Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (blaNDM). New-Delhi Metallo- (NDM) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (blaOXA48). OXA-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (blaSHV). SHV-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (blaTEM). TEM-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (bod5t). 5 day total biochemical oxygen demand. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (brsv). Bovine respiratory syncytial virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (brsvN). bovine respiratory syncytial virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (brucella). Brucella Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (caff). Caffeine (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (camp). *Campylobacter*. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (cAuris). The yeast species *Candida auris*, or *C. auris*. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (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.

NA (cbp). Carbapenemase-encoding genes. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (cDiff). *Clostridium difficile* Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cDip). *Corynebacterium diphtheriae* Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (centSpeed). Centrifugation speed Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (chikv). Chikungunya virus (CHIKV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (chlamydia). *Chlamydia* Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cJejuni). *Campylobacter jejuni* gene target/measurement Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (co2). A measure of an amount or concentraion of carbon dioxide. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (cod). Chemical oxygen demand. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (colis). Colistin-resistant bacteria. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (conc). Measurement of concentration (generalized) - designed for describing protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (concVol). The total volume of a sample after the concentration step. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cond). Measurement of conductivity of sample or site. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (cov). Covid-19 infection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (cov2Me). Measure the amount of SARS-CoV-2 virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (covB117). Variant B.1.1.7 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (covB135). Variant B.1.351 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (covE). SARS-CoV-2 E gene. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (covM). SARS-CoV-2 M gene (orf5) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (covN1). SARS-CoV-2 nucleocapsid gene, allele 1. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (covN2). SARS-CoV-2 nucleocapsid gene, allele 2. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (covN200). SARS-CoV-2 nucleocapsid gene, amino acids 199-202. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (covN3). SARS-CoV-2 nucleocapsid gene, allele 3. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (covP1). Variant P.1 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (covRdrp). SARS-CoV-2 RdRp gene. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (covS). S sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (covUTR5). SARS-COV-2 5' UTR Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cPerfringens). Clostridium perfringens Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cra). crAssphage virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (crea). Creatinine (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cryptosporidium). Cryptosporidium Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (cVDPV2). Circulating vaccine-derived poliovirus type 2 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (d339h). The FLiRT/SLip variant mutation D339H. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (d377y). d377y delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (d3g). d3g omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (d63g). d63g delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (d796y). d796y omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (d950n). d950n delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ddcovE). ddcov__e sars-cov-2 mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ddcovN). ddcov__n sars-cov-2 mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (del142144). Omicron Variant 142-144 Deletion mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (del143). 143 or 145 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (del156157). Delta Variant 156-157 Deletion mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (del157). 157 or 158 deletion delta-variant gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (del2084). 2084 or 2084 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (del212). 212 or 212 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (del3133). Omicron Variant 142-14431-33 Deletion mutation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (del3674). 3674 or 3676 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (del6970). 69 or 70 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (delta). B.1.617.2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (den1). Dengue virus, Type 1, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (den2). Dengue virus, Type 2, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (den3). Dengue virus, Type 3, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (den4). Dengue virus, Type 4, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dengue). Dengue virus, general measurement Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

Sets

NA (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.

NA (dilFact). Specifies the extent to which a sample or aliquot was diluted prior to analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (dillute). Exact concentration or dillutions for generating a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (dissOxy). Measure of dissolved oxygen in liquid medium Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (dnvE). Dengue Type 2-specific gene taget. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dnvNS5). Dengue Type 1-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dnvprM). Dengue Type 3 and 4-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (e156g). e156g delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (e484a). e484a omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (eaec). Enteraggregative Escherichia coli (EAEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ebv). Epstein–Barr virus (EBV), formerly known as Human gamma-herpesvirus 4 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (ehec). Enterohemorrhagic Escherichia coli (EHEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (eiec). Enteroinvasive Escherichia coli (EIEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (enterovirus). Enterovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (envRnF). Rainfall, i.e. amount of precipitation in the form of rain. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (envSnwD). Total depth of snow on the ground. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (envSnwF). Snowfall, i.e. amount of precipitation in the form of snow. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (epec). Enteropathogenic Escherichia coli (EPEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (eSarbec). Sarbecovirus-specific E sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (esbl). Extended-spectrum beta-lactamase-encoding genes. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (estFreqReads). Estimated frequency of reads in a sequencing assay Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (etec). Enterotoxigenic Escherichia coli (ETEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (exoNnsp14). SARS-CoV-2 exoN gene (nsp14) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (expec). Extraintestinal pathogenic Escherichia coli (ExPEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (exvol). Extraction volume of sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (f456l). The FLiRT/SLip variant mutation F456L. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fColiphage). Male-specific (F+) coliphage - general Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fDNA). F+ DNA coliphage Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fecalCol). Measure of prevalence of fecal coliform bacteria Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (finVol). The final volume of a testing solution or sample. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (flowVol). Volume of influent. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (flu). General influenza virus measure Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (fluA). Influenza A virus. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (fluA1). Influenza virus A1 type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (fluA2). influenza virus A2 type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (fluB). Influenza virus B type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (fRNABact). A measure for amount of F-Specific RNA bacteriophages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (fRNAColi). F+ RNA coliphage Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (frnaG2). A measure for amount of G2 F-Specific RNA bacteriophages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (fTularensis). Francisella tularensis Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (g215c). g215c delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (g339d). g339d omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (g496s). g496s omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (g662s). g662s delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gam). P.1 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (hDucreyi). Haemophilus ducreyi Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hel). SARS-CoV-2 hel gene (nsp13) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (hepA). Hepatitis A Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hepB). Hepatitis B Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hepC). Hepatitis C Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hepE). Hepatitis E Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hepGRna). Measure of the amount Hepatitis G Armored RNA. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (hf183). Human-Specific HF183 Bacteriodes 16S rRNA Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hiao5). A serotonin metabolite used for normalizing wastewater surveillance signal. Analysis of 5-HIAA is done in clinical settings to assess the possibility of carcinoid syndrome in patients, and used in wastewater analysis to estimate human population numbers. Studies have shown that 5-HIAA can be quantified 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.

NA (hInfluenzae). Haemophilus influenzae Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hiv). Human Immunodeficiency Virus (HIV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (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.

NA (hmpv). Human Metapneumovirus (HMPV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hpiv). Human Parainfluenza Virus (HPIV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hvp). Human Papiloma Virus (HPV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hrv). Human Rhinovirus (HRV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hrvA). Human Rhinovirus (HRV) A Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hrvB). Human Rhinovirus (HRV) B Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hrvC). Human Rhinovirus (HRV) C Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (hsv). Herpes Simplex Virus Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (i1566v). i1566v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (i3758v). i3758v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (i82t). i82t delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ibu). Ibuprofen (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (indusIn). Percentage of total wastewater input coming from industrial sources. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (ins214epe). Omicron Variant ins214epe Insertion mutation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (integraseCl1). Integrase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ip2ip4). Combined ip2 and ip4 sars-cov-2 gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (k856r). k856r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (klebsiellaPneu). Klebsiella pneumoniae Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (l24s). Omicron Variant l24s mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (l452r). l452r delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (l455s). The FLiRT/SLip variant mutation L455S. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (l981f). l981f omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (lambda). C.37 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (legionella). Legionella Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (listeria). Listeria Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (lod). Limit of detection, ie. the minimum level of a genetic target. Status: active. First released: 1.1.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (lppa24s). Omicron Variant LPPA24S mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (mcr11). The MCR-1.1 colistin anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (measles). Measles Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (measOth). Other measure, not otherwise specified in measures. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (meOthDe). Description of other measure (measOtherDesc). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (mGenitalus). Mycoplasma genitalus Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (mhv). A measure for amount of murine hepatitis viurs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (mpox). The virus known as Mpox, previously also known as Monkey Pox. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (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.

NA (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.

NA (mpxCII). 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.

NA (mpxCIII). 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.

NA (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.

NA (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.

NA (mpxF3L). Human MPox Virus (hMPXV) Clade I gene target, F3L Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (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.

NA (mpxG2RWA). Human MPox Virus (hMPXV) Clade II gene target, measured with G2R_WA primers and probe to detect Clade II viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (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.

NA (mrsa). Methicillin-resistant Staphylococcus aureus (MRSA) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ms2Col). Measure of the amount of ms2 coliphage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mTuberculosis). Mycobacterium tuberculosis Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (mu). B.1.621 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (muCo). Measure of the amount of murine coronavirus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mumps). Mumps Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (n). N sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (n1n2). Combined N1 and N2 sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (n211i). Omicron Variant n211i mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (n679k). Omicron Variant n679k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (n856k). Omicron Variant n856k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (n969k). Omicron Variant n969k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (nBPSeq). The number of total base pairs generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nContig). The number of contigs (contiguous sequences) in a sequence assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nGonorrhoeae). Neisseria gonorrhoeae Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (nh3nh4). Ammonia and Ammonium combined concentration, as Nitrogen Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nH4N). Ammonium nitrogen concentration, as N. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (niid19). niid_2019-ncov_n sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noro). Norovirus. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (noroG1). Norovirus genogroup 1 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noroG2). Norovirus genogroup 2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nSarbec). Sarbecovirus-specific N sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nsp1). SARS-CoV-2 nsp1 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (nsp10). SARS-CoV-2 nsp10 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp11). SARS-CoV-2 nsp11 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp15). SARS-CoV-2 nsp15 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp16). SARS-CoV-2 nsp16 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp2). SARS-CoV-2 nsp2 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp3). SARS-CoV-2 nsp3 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp4). SARS-CoV-2 nsp4 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp5). SARS-CoV-2 nsp5 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp6). SARS-CoV-2 nsp6 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp7). SARS-CoV-2 nsp7 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp8). SARS-CoV-2 nsp8 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nsp9). SARS-CoV-2 nsp9 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (nUniRead). The number of unique reads generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (oc43). Measure of the amount of coronavirus OC43. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (omicr1). Omicron B.1.1.529 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (omicr2). Omicron BA.2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (omicr275). Omicron BA.2.75 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (omicr4). Omicron BA.4 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (omicr5). Omicron BA.5 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ophos). Ortho-phosphate concentration. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (orf10). SARS-CoV-2 orf10 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf14). SARS-CoV-2 orf14 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf1a). ORF1a sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orf1ab). ORF1ab sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (orf1b). ORF1b sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orf3a). SARS-CoV-2 orf3a Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf3b). SARS-CoV-2 orf3b Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf6). SARS-CoV-2 orf6 (ns6) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf7a). SARS-CoV-2 orf7a Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf7b). SARS-CoV-2 orf7b (ns7b) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf8). SARS-CoV-2 orf8 (ns8) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf9b). SARS-CoV-2 orf9b Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orf9c). SARS-CoV-2 orf9c Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (p100l). Delta Variant p100l mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (p13L). Omicron Variant p13l mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (p2046l). Delta Variant p2046l mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (p2287s). Delta Variant p2287s mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (p3395h). Omicron Variant p3395h mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (p681r). Delta Variant p681r mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (percNLength). The percentage of the assembly that consists of ambiguous bases (Ns). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ph). pH measurement Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (phagetype). The phagotyping results from an organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (phi6). Measure of the amount of pseudomonas virus phi6. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (phos). Total phosphorous Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (phostot). Total phosphates Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (phred). PHRED Quality Score For Sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (plasmodium). Plasmodium Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (popAreaType). Type of populated area being sample (ie. urban, rural) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (popDensity). Measure of population density of a site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (popServRange). Population served by a site, when reported as an interval. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ppmv). Pepper mild mottle virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (precip). General measure of precipitation, type not specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (preSampWeath). Weather leading up to, but not including, the day of sampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (pseudomonas). Pseudomonas Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (puro). Measure of the amount of puro virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pv2). Poliovirus type 2 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (q19e). q19e omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (q493r). q493r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (q498r). q498r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (q954h). q954h omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (r203m). r203m delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (r346t). The FLiRT/SLip variant mutation R346T. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (rdrpIP2). IP2 rdrp sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (rdrpIP4). IP4 rdrp sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (recomb). A catch-all measure for viruses of non-specified and recombinant lineages, defined as those viruses 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.

NA (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.

NA (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.

NA (rickettsia). Rickettsia Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (rnaseP). Ribonuclease P (RNase P) (usually measured as a human fecal indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (rotavirus). Rotavirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (rsvAMe). Human Respiratory Syncytial Virus Type A (RSV A). Status: active. First released: 2.1.0. Last updated: 2.1.3.

NA (rsvB). Human Respiratory Syncytial Virus Type B (RSV B). Status: active. First released: 2.1.0. Last updated: 2.1.3.

NA (rsvMe). Human Respiratory Syncytial virus (RSV), generic measure. Status: active. First released: 2.0.0. Last updated: 2.1.2.

NA (rsvN). Human Respiratory syncytial Virus, N-gene region. Status: active. First released: 2.1.3. Last updated: 2.1.3.

NA (rubella). Rubella Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (s2083i). s2083i omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (s371l). s371l omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (s373p). s373p omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (s375f). s375f omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (s477n). s477n omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (salinity). Measurement of salinity/salt content Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (salmonella). Salmonella Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (samVol). The volume of a given sample. Status: active. First released: 2.2.0. Last updated: 3.0.0.

NA (sapovirus). Sapovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (serovar). The serovar of the organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (settsol). Amount of settled solids from a wastewater sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (shaker). The speed/aggitation level for a shaker plate/shaker platform. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (shigella). Shigella Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (spikeGene). SARS-CoV-2 Spike gene (orf2) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (stec). Shiga-toxin-producing Escheria coli (STEC). Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (sTemp). Temperature that the sample is stored at in Celsius. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (strainID). The strain identifier for a given organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (stercobilin). Stercobilin is a tetrapyrrolic bile pigment and is one end-product of heme catabolism. It is the chemical responsible for the

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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.

NA (stoTim). Length of time that a sample was in storage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (strepPneu). Streptococcus pneumoniae Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (suc). Sucralose (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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 whole municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (t19r). t19r delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (t3646a). t3646a delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (t547k). t547k omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (t9i). t9i omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (taqpatN). TaqPath N sars-cov-2 mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (taqpatS). TaqPath N sars-cov-2 mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (tds). Total dissolved solids Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (temp). Temperature of the sample measured in degrees Celcius
Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (tempVol). The volume of DNA or RNA template used for PCR.
Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (tetW). The tetW tetracycline anti-microbial resistance gene target.
Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (tn). Total nitrogen concentration, as N. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (tPallidum). Treponema pallidum Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ts). Total solids concentration Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (tss). Total suspended solids Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (tssConc). Total suspended solids concentration of the wastewater.
Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (turb). A measure for the turbidity of water, or a liquid sample, quantifying 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.

NA (tVaginalis). Trichomonas vaginalis Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (tWeighE). The weight of the tube used for analysis while empty.
Status: active. First released: 2.0.0. Last updated: 2.0.0.

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NA (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.

NA (ureaplasma). Ureaplasma Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (v1104l). The FLiRT/SLip variant mutation V1104L Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (v2930l). v2930l delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (vanAA). The VanA-A vancomycin anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vanc). Vancomycin resistant bacteria. Status: active. First released: 2.1.0. Last updated: 2.1.0.

NA (varicella). Varicella Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vibrio). Vibrio Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vol). Total volume of water or sludge sampled. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (vss). Volatile suspended solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (vtec). Verotoxin-producing *Escherichia coli* (VTEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (watTemp). Temperature of the wastewater. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (westNile). West Nile Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (wt214). Delta Variant wt214 gene target Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (y505h). y505h omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (yEnterocolitica). *Yersinia enterocolitica* Status: active. First released: 2.2.0. Last updated: 2.2.0.

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NA (zika). Zika Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (sudanV). Sudan virus (species Orthoebolavirus sudanense) causes Sudan virus disease. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

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NA (doby). 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.

NA (aivA). Measures of Aichivirus A, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis in human or animal hosts. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (aivB). Measures of Aichivirus B, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis in human or animal hosts. Also called Bovine kobuvirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (aivC). Measures of Aichivirus C, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis in human or animal hosts. Also called Porcine kobuvirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (aivD). Measures of Aichivirus D, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis in human or animal hosts. Also called kagovirus from black cattle. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (aivE). Measures of Aichivirus E, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis in human or animal hosts. Also called Rabbit picornavirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (aivF). Measures of Aichivirus F, the species of aichivirus in the Kobuvirus genus, and picornavirus family. Typically a cause of gastroenteritis in human or animal hosts. Also called bat kobuvirus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (cacipacore). Orthoflavivirus cacipacoreense, causative agent of the rare Cacipacore virus Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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

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circovirus type 1 (PCV1) is not linked with a disease. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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 Multi-systemic Wasting Syndrome (PMWS), a new emerging and multifactorial disease in swine. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (cosaV). Cosavirus is a genus of viruses in the order Picornavirales, in the family Picornaviridae. Human serve as natural hosts. There are 5 species of enteric viruses in this genus. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

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NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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

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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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (saliA). Salivirus A (Salivirus aklassse) 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.

NA (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.

NA (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.

NA (safv2). Strain 2 of the saffold virus (SAFV-2) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (safv3). Strain 3 of the saffold virus (SAFV-3) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (safv4). Strain 4 of the saffold virus (SAFV-4) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (safv5). Strain 5 of the saffold virus (SAFV-5) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (safv6). Strain 6 of the saffold virus (SAFV-6) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (safv7). Strain 7 of the saffold virus (SAFV-7) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (safv8). Strain 8 of the saffold virus (SAFV-8) Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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.

Sets

NA (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.

NA (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.

NA

(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

NA (amrSoft). Software use to analyse bacterial genomes and genes for anti-microbial resistance (AMR). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (bactMeth). Description of the bacterial testing/detection method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (conSeqSoft). Software use to run consensus sequence on sequencing analyses. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dedup). Sequencing and PCR deduplication method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dehost). Sequencing and PCR dehosting method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (extraction). Description of the nucleic acid extraction method. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (inhibMeth). Description of the method used to evaluate molecular inhibition. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (methodConc). Description of the method to concentrate a wastewater sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (pcrAct). Describes a given PCR cycle for delineating more method information. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pcrmeth). Description of the PCR method. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (popAs). Method for assessing the population count for a site/polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (qaqc). Quality assurance and quality control method. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (qcMethod). Method for sequencing quality control or assessment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (rawSeqProc). The software/library/pipeline used to process the raw sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (resuspension). Describes the method used for resuspending material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (retainedElement). The element retained after centrifugation, filtration, solid separation, etc. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (sampleTypeOther). Description for other type of method not listed in collection. depreciated. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (seqLay). The layout of genetic material used in sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seqQC). The quality control pipeline for sequencing or PCR data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (seqSel). The primer sequence selection method used in sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seqStrat). The sequencing strategy used for an analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seroMeth). The method used to determine the serovar. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (shipOnIce). Was the sample kept cool while being shipped to the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (solidSep). Process used to separate solid and liquid phases of the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (spikeMat). Material into which the recovery efficiency control target is spiked. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (stdCurveMet). Describes the specific approach used for calculating a standard curve. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (stoMed). The medium used to store a sample before final analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (tyOtDep). Description for other type of sample not listed in Status: deprecated. First released: 1.0.0. Last updated: 2.0.0.

NA

(missingness). The part type for missingness values. Only used for the dictionary entries of parts.

NA (dnc). A missingness value for when data was not measured or collected; an analysis not run, etc. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA

NA (restrict). Missing data is withheld because it is restricted access. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA exclusive sets, or general all-purpose sets.

genMissingnessSet

(genMissingnessSet)The general set for missingness values. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (restrict). Missing data is withheld because it is restricted access. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

geoRefMissingnessSet

(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.

NA (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.

nrNAMissingnessSet

(nrNAMissingnessSet)Not reported, Not applicable missing set. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA exclusive sets, or general all-purpose sets.

NA (genMissingnessSet). The general set for missingness values. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nrNAMissingnessSet). Not reported, Not applicable missing set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA

(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.

actionTypeSet

(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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

allActionsSet

(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.

NA (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.

NA (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.

NA (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

Sets

NA (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

allStandardSet

(allStandardSet)Set of valid input values for the standard field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (bayesSmooth). This data treatment smooths the measurement value using bayesian smoothing techniques. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (caSmooth). This data treatment smooths the measurement value using central average smoothing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (day7Smooth). This data treatment smooths the measurement value across 7-days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (flowStand). This data treatment standardizes the measurement value to flow rates. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (timeStand). This data treatment standardizes the measurement value against time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

amrClassSet

(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.

NA (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.

NA (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

amrSoftSet

(amrSoftSet)The valid set of AMR analysis software categories. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (abricate). Software tool for screening bacterial genomes against multiple resistance databases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (argAnnotSoft). Software annotation tool for antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (metaPhlAn). Software tool that profiles microbial communities and can provide resistance gene insights. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

Sets

NA (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

bactMethSet

(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.

NA (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.

NA (bacCul). Growing a bacterial culture to test for bacterial presence. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

booleanSet

(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.

NA (FALSE). Boolean data type = FALSE Status: active. First released: 1.0.0. Last updated: 2.3.0.

NA (TRUE). Boolean data type = TRUE Status: active. First released: 1.0.0. Last updated: 2.3.0.

calcTypeSet

(calcTypeSet)The set of valid inputs for the calculation type field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

cladeAnSet

(cladeAnSet) Valid category set for lineage or clade analysis software types. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (phyloPhlAn). 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.

NA (phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

collAppxSet

(collAppxSet)The category set of valid inputs for the collGenT attribute field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (aft). Sample was collected in the afternoon, sometime after lunch. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (eve). Sample was collected in the evening, late in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (night). Sample was collected at night, between sunset and sunrise. Status: active. First released: 3.0.0. Last updated: 3.0.0.

collectSet

(collectSet)Methods for collection samples. Sample collection methods include water, air, and surface. See the attribute **Compartment set** of the sample collection method. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (areaPr). An area proportional sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (bagFilt). Sample was collected using bag-mediated filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (comp). A composite sample, usually generated by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (cosca). COSCa passive sampling device. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (flowPr). A flow proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (grb). A single large representative grab sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (manComp). Specifies a composite sample where the sub-samples were collected manually. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (moorSw). Moore swab passive sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (surfSw). Surface swab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (timePr). A time proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (volPr). A volume proportional sample generally collected by an autosampler. Status: active. First released: 2.0.0. Last updated: 2.0.0.

conSeqSoftSet

(conSeqSoftSet) The valid set of consensus sequencing software categories. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (uGene). Sequencing software that offers alignment and consensus sequence generation features. Status: active. First released: 3.0.0. Last updated: 3.0.0.

contMeasImpSet

(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.

NA (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.

NA (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.

NA (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.

NA (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

dataRepoSet

(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.

NA (ardb). An archive for antibiotic resistance genes and associated information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (bacMet). Database of antibacterial biocide and metal resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cardDtbase). Database that provides high-quality reference sequences for resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ddbj). DNA Data Bank of Japan (DDBJ) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ena). European Nucleotide Archive (ENA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (genBank). GenBank Archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (github). GitHub external data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gsa). Genome Sequence Archive (GSA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (megares). A comprehensive database of antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (osf). Open Science Foundation project/data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (resFinderDtbse). nomenclature from the National Center for Biotechnology Information Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (sra). Sequence Read Archive (SRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (zenodo). Zenodo open data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

dedupSet

(dedupSet)The valid set of deduplication method categorical inputs. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (bamUtil). A deduplication method that removes duplicate reads directly from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

dehostSet

(dehostSet)The valid set of dehosting method categorical inputs. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (metaPhlAn). Software tool that profiles microbial communities and can provide resistance gene insights. Status: active. First released: 3.0.0. Last updated: 3.0.0.

extractSet

(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.

NA (amiMP96). Nucleic 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.

NA (bbMP96). Nucleic 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.

NA (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.

NA (esp). exclusions based sample preparation (ESP) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (extract4s). Nucleic acid extraction performed using the 4s method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (luminWWExtract). luminultra wastewater extraction kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (phenCl). Nucleic acid extraction performed using phenol chloroform. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (promAuto). Nucleic acid extraction performed using the promega automated tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (promHt). Nucleic acid extraction performed using the promega ht tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (promManu). Nucleic acid extraction performed using the promega manual tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

Sets

NA (qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qiaampDSP). qiagen qiaamp dsp viral rna mini kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (sciencellRNA). sciencell viral rna isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (trizolEtOH). trizol, garnet bead beating, alcohol precipitation Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (trizolRNA). trizol and RNA purification kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (zymo1035). zymo quick-rna viral kit #r1035 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (zymo1041). zymo quick-rna viral 96 kit #r1041 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

fractionSet

(fractionSet)set for the fraction of the sample (solid, liquid, etc.). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

geoTypeSet

(geoTypeSet)set for different type of geographic components. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (hlthReg). Health region served by the sewer network Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (swrSet). Sewer catchment area. Status: active. First released: 1.0.0. Last updated: 2.0.0.

gteSet

(gteSet)The set for valid inputs for the Genomic Target Enrichment method. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (hySel). Selection by hybridization in array or solution for genomic target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

inhibitionSet

(inhibitionSet)Category set for inhibition methods. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (serialDilution). The serial dilution method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (spike). The spike matrix and recovery method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

insTypeSet

(insTypeSet)List of instruments that are used for measures and methods Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (aas). Atline analyzer with sampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

Sets

NA (enviroInst). Local probe instruments 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.

NA (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.

NA (flowInst). Flow meter instruments; used to measure wastewater flow rates to enable standardization of sample data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (hma). Handheld measurement analyzer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (ngsInst). Next generation sequencer instruments and platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ola). Offline laboratory analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (onse). Online sensor Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

libraryKitSet

(libraryKitSet)The valid set of categorical values for sequencing library preparation kits. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (ligaseDep). Ligase-Dependent Library Prep Kits by Lucigen/Episentre. 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.

NA (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.

NA (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.

NA (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.

NA (qiaSeqFX). QIAseq FX DNA Library Kit by Qiagen. A library 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.

NA (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.

NA (sureSelectXTs2). 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.

NA (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.

NA (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.

Sets

NA (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.

licSet

(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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (off11). 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.

Sets

NA (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.

NA (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.

NA (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.

NA (private). The measure or data set is private data - not for dissemination. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

matCharSet

(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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

methodConcSet

(methodConcSet)A set a concentration methods. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (aloh3). Aloh3 precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (amiconUf). Amicon ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (beeExtractFloc). Beef extract flocculation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (centriconUf). Centricon ultrafiltration. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ceres). Ceres nanotrap. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (hollowFiberUF). Hollow fiber dead end ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (innovaprepUF). Innovaprep ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (memMgCl3). membrane filtration with addition of mgcl3 Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (mfAcidmgcl2). Membrane filtration with acidification and mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfMgcl2). Membrane filtration with addition of mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfNoAmend). Membrane filtration with no amendment Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfSampleAcid). Membrane filtration with sample acidification Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noliquid). No liquid concentration, liquid recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (peg). Peg precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (skimMilkFloc). Skimmed milk flocculation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (untracent). Ultracentrifugation Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (watConcBuff). water concentrating buffer (R2042-1) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

ogFormSet

(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.

NA (enaForm). Dataset was originally recorded and/or stored in ENA format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ncbiForm). Dataset was originally recorded and/or stored in NCBI format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (normanForm). Dataset was originally recorded and/or stored in Norman format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (wSphereForm). Dataset was originally recorded and/or stored in wSphere format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

orgLevelSet

(orgLevelSet)Categories of organization levels. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sets

NA (admRegLevel). Administrative regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (countryLevel). Countries or sovereign states Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (countyLevel). Districts, counties, regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (municipalLevel). Municipalities or communes Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (neighborLevel). Local administrative units or neighborhoods Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (stateProvLevel). Departments, states, or provinces Status: active. First released: 2.0.0. Last updated: 3.0.0.

orgSectorSet

(orgSectorSet) Categories of organization sectors. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (fiNa). Used to categorize a sampled that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (healthAdm). Health administrative or planning organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lab). Laboratory for environmental testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (policy). Describes organizations whose core focus is on policy or political activity. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (pubHealth). Public health agency. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (research). Describes organizations whose focus is on research generation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

orgTypeSet

(orgTypeSet)The set for storing organization types. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (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.

NA (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.

originSet

(originSet)The set for storing the valid categorical values of sample origin. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (derived). Derived data, data that has undergone aggregation, standardization, adjustment, or any cleaning prior to reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (synthetic). A synthetic or artificially generated sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

outbreakSet

(outbreakSet)set for the valid values of the outbreak measure. Status: active. First Released: 2.0.0. Last updated: 3.0.0.

NA (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

pcrActSet

(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.

NA (anneal). Describes the annealing and/or extension cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (denat). Describes the denaturation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pAct). Describes the polymerase activation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (rt). Describes the reverse transcription cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

pcrSet

(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.

NA (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.

Sets

NA (ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (dpcr). Describes a PCR analysis done using digital PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (fluidpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qpcr). Real-time PCR, also called 'quantAggScale' PCR Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (rainDpcr). Describes a PCR analysis done using Raindance's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

phAdviseSet

(phAdviseSet) A set of valid categories for the public health action field, where the action type is 'public health advisory'. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

polyRelSet

(polyRelSet)Value set for polygon relationships. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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

Sets

(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.

NA (neighbour). Locations/polygon are neighbouring eachother. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (overlap). Locations/polygon have overlapping portions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

popAreaSet

(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.

NA (rural). Rural populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (suburban). Suburban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (urban). Urban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

popIntSet

(popIntSet)The collection of categorical inputs for population interval measures. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (less10). Fewer than 10 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less100). Between 10 and 100 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA

NA (less100k). Between 10,000 and 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less10k). Between 1,000 and 10,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less1k). Between 100 and 1,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (less1mil). Between 100,000 and 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (more1mil). More than 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

popMetSet

(popMetSet)The set for valid inputs for the population assessment method. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (census). Government or other agency census for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (count). A count of residents for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (rev). A review of records for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

presampSet

(presampSet)The set of valid input values for reporting pre-sampling activity. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

Sets

NA (agri). Agricultural activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (hcAct). Healthcare activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (husb). Animal husbandry occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (indus). Industrial activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwCominuated). wastewater comminution process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwDry). Wastewater sludge drying occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwFilt). Wastewater filtration occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwGrit). Wastewater grit removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwMic). Wastewater microbial treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwPriSed). Wastewater primary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwScreen). Wastewater screening process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (wwTrt). Wastewater treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

primerSet

(primerSet)The set for genetic primers used in sequencing or PCR assays. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (articV4). Artic V4 sequencing primer for VOCs and VOIs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (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.

NA (articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with 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.

NA (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.

NA (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.

NA (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.

NA (bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (bact16sABIRev). Bacteroides 16S reverse primer (BacR287) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovEIDTFor). Sarbeco_E forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovEIDTProbe). Sarbeco_E probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovEIDTRev). Sarbeco_E reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN1IDTFor). 2019-nCoV_N1 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN1IDTProbe). 2019-nCoV_N1 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN1IDTRev). 2019-nCoV_N1 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN2IDTFor). 2019-nCoV_N2 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN2IDTProbe). 2019-nCoV_N2 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN2IDTRev). 2019-nCoV_N2 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN3IDTFor). 2019-nCoV_N3 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN3IDTProbe). 2019-nCoV_N3 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (cdcCovN3IDTRev). 2019-nCoV_N3 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (pmmvABIFor). PMMV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pmmvABIProbe). PMMV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (pmmvABIRev). PMMV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vsvABIFor). VSV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

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NA (vsvABIProbe). VSV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (vsvABIRev). VSV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

protocolRelSet

(protocolRelSet)set for valid values of relationshipID in the protocolRelationships table. Use only for protocolRelationships table relationshipID. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

purposeSet

(purposeSet)Purpose set for a sample or measure. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (cali). Purpose of calibrating a machine, method, or other. Status: active. First released: 3.0.1. Last updated: 3.0.1.

NA (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.

NA (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.

NA (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.

NA (education). A measure or sample taken for education or training. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (emergSurv). A targeted surveillance strategy which is considered important and/or urgent. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (norm). The purpose of a measure or sample is for normalization. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (provisional). A provisional or interm report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (qualityControl). A measure or sample taken for the purpose of quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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NA (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.

NA (regular). A measure or sample taken for surveillance or epidemiology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (researchPurp). Purpose of sampling/measure is for research. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (validationStudy). A measure or sample taken for a validation study. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. Status: active. First released: 3.0.0. Last updated: 3.0.0.

rawSeqProcSet

(rawSeqProcSet) The category set of valid input 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (dada2). A sequencing data processing application that is primarily used in amplicon sequencing for error correction and generating amplicon

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sequence variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and

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single-cell workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

readMapperSet

(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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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

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genome or transcriptome assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

relSet

(relSet)set for valid values of relationshipID across all fields and tables. Status: active. First Released: 2.2.3. Last updated: 2.2.3.

NA (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.

NA (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.

NA (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.

NA (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.

NA (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

replicateSet

(replicateSet)The set for storing valid categorical values of replicate type. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (nac). Denotes a no amplification control replicate sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

Sets

NA (nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ntc). Denotes a non-template control sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ntp). Denotes a sample replicate/control with no target present. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (opt). Denotes a sample control or replicate used for optical calibration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (std). Denotes a standard sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (subSamp). A general replicate type for a subsample not otherwise defined. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (unique). A unique sample, not duplicated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (unkn). Denotes an unknown sample replicate type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

resusSet

(resusSet)The set to describe valid categorical values for the resuspension method. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

NA (elutionBuff). Elution buffer is used to resuspend material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

retElSet

(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.

NA (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.

NA (liquid). The liquid or supernatant is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (solid). The solids or pellet is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

sampleMatSet

(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.

Sets

NA (afu). Air filter as part of filtration or circulating unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (desk). Desk, table, countertop or other flat working surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (faeces). Fecal matter. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (floor). Floor of a building or room. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (nww). Non-wastewater, coming from any kind of water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pEfflu). Effluent obtained after primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pSludge). Sludge produced by primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but prior to a primary clarifier) Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rawWW). Wastewater without any form of treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rawWWdown). Downstream from a site. See partType = rawWWup. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

NA (rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjunction 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.

NA (sEfflu). Effluent obtained after secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (septage). Wastewater from within a septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (sSludge). Sludge produced by secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (surface). Surface other than floor or desk. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (swrSed). Sediments obtained in sewer Status: active. First released: 1.0.0. Last updated: 2.0.0.

sampleRelSet

(sampleRelSet)set for valid values of relationshipID in the sampleRelationships table. Use only for sampleRelationships table relationshipID. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (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.

NA (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.

NA (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

scriptSet

(scriptSet)The set for script versions Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (freyja). Freyja Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gromstole). Gromstole 1.0 Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

seqAssSet

(seqAssSet) The valid set of categorical values for sequence assembly software methods. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (discover). 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.

NA (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.

Sets

NA (idbaUD). A sequencing software that is an iterative assembler optimized for metagenomics and complex genomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

seqLaySet

(seqLaySet)The set for the layout of genetic material used in sequencing
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sets

NA (mateLay). Specifies the mate pair layout for a sequencing method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pairLay). Specifies the paired layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sinLay). Specifies the single layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

seqQCSet

(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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (ncovtools). Tools and plots for performing QC on coronavirus sequencing results. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

seqSelSet

(seqSelSet)The set for the selection method used in sequencing Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (ranSeq). Specifies the random selection method for sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

seqStratSet

(seqStratSet)The set for the sequencing strategy used for an analysis Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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 microbial 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.

NA (amp). Specifies the amplicon strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

Sets

seroMethSet

(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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (pathogenwatch). Pathogenwatch. Focus: Integrates MLST, serotyping, and resistance typing with a user-friendly interface. Applications: Primarily used for *Salmonella* and *Escherichia coli*. Features: Combines

Sets

typing results with interactive visualization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (tradSero). Traditional Serotyping methods used for serotyping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

setTypeSet

(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.

NA (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.

NA (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.

NA (dictSets). Sets used to describe and group dictionary tables. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA exclusive sets, or general all-purpose sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

sevSet

(sevSet)A set for severity indicators. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (low). A marker for low severity Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mid). A marker for med-level severity, where there are some concerns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

shedSet

(shedSet)The set for all valid values of sampleshed. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

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NA (airpln). Airplane sample shed category type Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (airport). Airport sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (busStat). A terminal where buses arrive and depart. Status: active. First released: 2.2.3. Last updated: 2.2.3.

NA (ccc). Acute care hospitals, or complex continuing 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.

NA (cdc). Child day care facility. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (corFcil). Correctional facility Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (dorm). Higher education dormitory or residential building Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (edFac). A school or other educational facility not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (farm). An agricultural area, building, 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.

NA (fiNa). Used to categorize a sampled that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (hcf). A building for the provision of healthcare, not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (hosptl). Hospital Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (hotel). A building which 1) contains multiple dwellings of pre-furnished accommodation 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.

NA (indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occasionally services, and making them into products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (ltcfO). Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or

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assisted living facilities. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mall). A large commercial complex with multiple retail stores, services, and restaurants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (office). A workplace where administrative, managerial, or clerical tasks are performed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (orb). Individual residential buildings or institutions not captured in other categories Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (pharmPl). An industrial building in which pharmaceutical drugs are synthesised and processed on an industrial scale. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (road). A paved or unpaved pathway designed for vehicular and pedestrian travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (school). A school serving students in the kindergarten to 12th grade range Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ship). A cruise ship or other ship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sss). Other type of social services shelter Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (terminal). Airport terminal sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (tHub). A transport 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.

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NA (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.

NA (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.

NA (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.

NA (uCampus). University or college campus - comprising an entire campus or part of a campus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (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.

siteLevelSet

(siteLevelSet) The category set containing all valid entries for the siteLevel field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (countLevel). Specifies that a sewershed/site represents an entire nation or country. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (muniLevel). Specifies that a sewershed/site represents an entire municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

siteTypeSet

(siteTypeSet)set for the type of sampling site. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

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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.

NA (bow). An outdoor accumulation 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.

NA (bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municipal sewer lines, allowing drainage into the main sewer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (estuary). Estuary, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (htSite). Holding tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (lagoon). Lagoon system for extensive wastewater treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (lake). Lake, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (mSwrPpl). Major sewer pipeline Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ocean). Ocean, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (opWa). An outdoor accumulation 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (retPond). Retention pond Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (river). River, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (sea). Sea, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (septTnk). Septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (swgTrck). Sewage truck Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (triturator). The location where wastewater transportation vehicles unload wastewater. Status: active. First released: 2.2.3. Last updated: 2.2.3.

NA (upstream). A general site type for upstream wastewater sampling sites. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Sets

NA (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.

NA (wwtp). A general site type for wastewater treatment plants. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (wwtpInd). Industrial wastewater treatment plant Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (wwtpMuC). Municipal wastewater treatment plant for combined sewage Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only Status: active. First released: 2.0.0. Last updated: 2.0.0.

solidSeparationSet

(solidSeparationSet)set for the separation of solids. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

spikeMatSet

(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.

NA (clari). Clarified sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (deso). Dewatered solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (lysi). Lysis buffer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (raws). Raw wastes water sample Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (rppw). Raw wastewater sample post-pasteurization Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (samConc). Sample concentrate. Status: active. First released: 1.0.0. Last updated: 2.0.0.

spikeTargetSet

(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.

Sets

NA (bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (mlhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (muCoMat). Murine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (puroMat). Puro Virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

statusSet

(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.

NA (active). Indicator that a part is in current use. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (deprecated). 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.

NA (development). Indicator that a part is under development use. See partID = status Status: active. First released: 2.0.0. Last updated: 2.0.0.

stdCurveSet

(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.

Sets

NA (serDil). Describes a serial dilution process for standard curve generation for PCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

stoMedSet

(stoMedSet)The set of valid categorical inputs for the stoMed field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (none). No sample storage medium used Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (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.

NA (vtm). A buffer solution/medium that preserves viral samples during transport, commonly used for wastewater viral studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

survAlertSet

(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.

NA (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

survLevelSet

(survLevelSet) The list of valid categories for the survLevel measure. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (builLev). Surveillance is done only at the level of a single building. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (communitLev). Surveillance is done at the level of an entire community. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (instituLev). Surveillance is done at the level of an entire institution. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (multiComLev). The scope of the surveillance covers multiple communities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

tableSet

(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. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (cK). Composite key for a table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

NA (fK). Foreign key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (header). Header for a table. Also known as a table variable or entity relationship 'attribute'. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (pK). Primary key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

tempSet

(tempSet)The organizing set for templates. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

NA (dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

threatDesSet

(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.

NA (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.

NA (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.

NA (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.

NA (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.

valTreatSet

(valTreatSet)Valid set of values for the value treatment set. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (raw). Raw data, without adjustment or additional treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

weathSet

(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.

NA (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.

NA (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.

Sets

NA (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.

NA (rainy). Qualitative category for the weather measure, specifying a rainy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (snowy). Qualitative category for the weather measure, specifying a snowy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (stormy). Stormy weather Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

wideFractionSet

(wideFractionSet)Fraction set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

NA (hFr). An indicator in wide-names to show that information on the fraction analyzed is found under a separate header. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA

(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.

NA (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.

NA (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.

NA (allStandardSet). Set of valid input values for the standard field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (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.

NA (amrSoftSet). The valid set of AMR analysis software categories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (calcTypeSet). The set of valid inputs for the calculation type field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cladeAnSet). Valid category set for lineage or clade analysis software types. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (collAppxSet). The category set of valid inputs for the collGenT attribute field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (collectSet). Methods for collection samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (conSeqSoftSet). The valid set of consensus sequencing software categories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (dedupSet). The valid set of deduplication method categorical inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (dehostSet). The valid set of dehosting method categorical inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (fractionSet). set for the fraction of the sample (solid, liquid, etc.). Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (geoTypeSet). set for different type of geographic components. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gteSet). The set for valid inputs for the Genomic Target Enrichment method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (inhibitionSet). Category set for inhibition methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (insTypeSet). List of instruments that are used for measures and methods Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (libraryKitSet). The valid set of categorical values for sequencing library preparation kits. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (methodConcSet). A set a concentration methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (orgLevelSet). Categories of organization levels. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orgSectorSet). Categories of organization sectors. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (orgTypeSet). The set for storing organization types. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (originSet). The set for storing the valid categorical values of sample origin. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (outbreakSet). set for the valid values of the outbreak measure. Status: active. First released: 2.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (phAdviseSet). A set of valid categories for the public health action field, where the action type is 'public health advisory'. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (popIntSet). The collection of categorical inputs for population interval measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (popMetSet). The set for valid inputs for the population assessment method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (presampSet). The set of valid input values for reporting pre-sampling activity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (primerSet). The set for genetic primers used in sequencing or PCR assays. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (protocolRelSet). set for valid values of relationshipID in the protocolRelationships table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (purposeSet). Purpose set for a sample or measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (rawSeqProcSet). The category set of valid input 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.

NA (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.

NA (relSet). set for valid values of relationshipID across all fields and tables. Status: active. First released: 2.2.3. Last updated: 2.2.3.

NA (replicateSet). The set for storing valid categorical values of replicate type. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (resusSet). The set to describe valid categorical values for the resuspension method. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

Sets

NA (sampleRelSet). set for valid values of relationshipID in the sampleRelationships table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (scriptSet). The set for script versions Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seqAssSet). The valid set of categorical values for sequence assembly software methods. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (seqLaySet). The set for the layout of genetic material used in sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (seqSelSet). The set for the selection method used in sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seqStratSet). The set for the sequencing strategy used for an analysis Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (sevSet). A set for severity indicators. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (shedSet). The set for all valid values of sampleshed. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (siteLevelSet). The category set containing all valid entries for the siteLevel field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (siteTypeSet). set for the type of sampling site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (solidSeparationSet). set for the separation of solids. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (stoMedSet). The set of valid categorical inputs for the stoMed field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (survLevelSet). The list of valid categories for the survLevel measure. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (tableSet). The set for valid inputs in table columns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (tempSet). The organizing set for templates. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

Sets

NA (valTreatSet). Valid set of values for the value treatment set. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (wideFractionSet). Fraction set for wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (polyRelSet). Value set for polygon relationships. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA

(nomenclatures). A classification system to report the measure class. See partID = nomenclatureID.

NA (icd). Classification system for diseases in humans. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (naNomenclature). Not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ncbiNom). Nomenclature from the National Center for Biotechnology Information Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (nextclade). Specifies variant or genetic nomenclature as set out by NextClade. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA

(partTypes). Part types describe the purpose or use of the part. Environment data has three main part types: measure (i.e. covN1 viral measures, wastewater 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.

NA (partTypes). Part types describe the purpose or use of the part. Environment data has three main part types: measure (i.e. covN1 viral measures, wastewater 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.

NA (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.

NA (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.

Sets

NA (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.

NA (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 surveillance data. The other two components are measures and methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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 wastewater treatment plant, airplane holding tank, wastewater 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.

NA (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.

NA (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.

NA (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.

NA (dataTypes). The data type for a part. Data types used in the ODM include: varchar, boolean, 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 identified within the part entry. TBA: dataType for dictionary. Status: active. First released: 2.0.0. Last updated: 3.0.1.

NA (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.

NA (dictSets). Sets used to describe and group dictionary tables. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA exclusive sets, or general all-purpose sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (nomenclatures). A classification system to report the measure class. See `partID = nomenclatureID`. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See `partID = specimenID`. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (tableSupport). Parts designed to support the metadata definition of tables in the parts table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA

(qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts.

NA (ampliArtifact). Sequence amplification artifacts detected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (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.

NA (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.

NA (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (frozen). Sample was frozen before analysis or processing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lAGC). Average coverage of the genome is low/poor. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (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.

NA (leaked). Sample leaked, some volume and material was lost. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lowCovMut). Low coverage of characteristic mutations. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Sets

NA (lowQualSeq). Low-quality sequence. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (lowSNRatio). Low signal-to-noise ratio. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (lowVol). Sample is low-volume, but was run regardless. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (IPGC). Only captured a small/low percentage of the genome. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (noLabel). Sample had no label Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noTime). Sample is missing the autosampler time; incomplete meta-data on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (ntcFlag). quality indicator for when there is observed amplicification in the non-template controls (NTCs) of a PCR reaction. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

NA (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

NA (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (seqContam). Sequence is contaminated. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (shortRead). Read lengths are shorter than expected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (spill). Sample contents spilled from container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wrongStorage). Sample was stored inappropriately. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wrongTemp). Sample was stored at an inappropriate temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set.

Sets

genQualitySet

(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.

NA (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (qf1). A flag to indicate there is a quality concern, not otherwise specified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

measQualitySet

(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.

NA (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.

NA (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.

NA (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.

NA (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (IBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (noTime). Sample is missing the autosampler time; incomplete meta-data on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

pcrQualitySet

(pcrQualitySet)Quality set for PCR measures. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

sampleQualitySet

(sampleQualitySet)Quality set for a sample. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA

NA (frozen). Sample was frozen before analysis or processing Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (leaked). Sample leaked, some volume and material was lost. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lowVol). Sample is low-volume, but was run regardless. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (noLabel). Sample had no label Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (noTime). Sample is missing the autosampler time; incomplete meta-data on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (spill). Sample contents spilled from container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wrongStorage). Sample was stored inappropriately. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wrongTemp). Sample was stored at an inappropriate temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

seqQualitySet

(seqQualitySet)Quality set for sequencing measures Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (ampliArtifact). Sequence amplification artifacts detected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

Sets

NA (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.

NA (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.

NA (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lAGC). Average coverage of the genome is low/poor. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (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.

NA (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.

NA (lowCovMut). Low coverage of characteristic mutations. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (lowQualSeq). Low-quality sequence. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (lowSNRatio). Low signal-to-noise ratio. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (lPGC). Only captured a small/low percentage of the genome. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (noTime). Sample is missing the autosampler time; incomplete meta-data on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (seqContam). Sequence is contaminated. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (shortRead). Read lengths are shorter than expected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

NA (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set.

NA (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.

Sets

NA (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.

NA (pcrQualitySet). Quality set for PCR measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sampleQualitySet). Quality set for a sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seqQualitySet). Quality set for sequencing measures Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(shortSets). Sets used to group together short names for tables or part types in ODM.

shrtNameSet

(shrtNameSet)The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). Status: active. First Released: 2.2.2. Last updated: 2.2.2.

NA (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.

NA (ad). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). Status: active. First released: 2.2.2. Last updated: 2.2.2.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA

(specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See `partID = specimenID`.

NA (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.

NA (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen.

anySpecimenSet

(anySpecimenSet) A specimen set that includes any specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (pop). A measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

naSpecimenSet

(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.

NA (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

polySiSpecimenSet

(polySiSpecimenSet) A specimen set that includes polygon or site specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

polySpecimenSet

(polySpecimenSet) A specimen set that includes only a polygon specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

poPolySpecimenSet

(poPolySpecimenSet) A specimen set that includes population or polygon specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

poSaSpecimenSet

(poSaSpecimenSet) A specimen set that includes population or sample specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

poSiSpecimenSet

(poSiSpecimenSet) A specimen set that includes population or site specimen.
 Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (pop). An measure or observation for a geographic area or population.
 Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (sit). A measure made on a compartment or property at a site. Status:
 active. First released: 2.0.0. Last updated: 2.0.0.

poSpecimenSet

(poSpecimenSet) A specimen set that includes only a population specimen.
 Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (pop). An measure or observation for a geographic area or population.
 Status: active. First released: 1.0.0. Last updated: 2.0.0.

saSpecimenSet

(saSpecimenSet) A specimen set that includes only a sample specimen.
 Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

siSaSpecimenSet

(siSaSpecimenSet) A specimen set that includes site or sample specimen.
 Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

siSpecimenSet

(siSpecimenSet)A specimen set that includes only a site specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

wideSpecimenSet

(wideSpecimenSet)Specimen set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen.

NA (anySpecimenSet). A specimen set that includes any specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (naSpecimenSet). A specimen set for when specimen/specimen set is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (polySiSpecimenSet). A specimen set that includes polygon or site specimen. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (polySpecimenSet). A specimen set that includes only a polygon specimen. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (poPolySpecimenSet). A specimen set that includes population or polygon specimen. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (poSaSpecimenSet). A specimen set that includes population or sample specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (poSiSpecimenSet). A specimen set that includes population or site specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (poSpecimenSet). A specimen set that includes only a population specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (saSpecimenSet). A specimen set that includes only a sample specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (siSaSpecimenSet). A specimen set that includes site or sample specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (siSpecimenSet). A specimen set that includes only a site specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (wideSpecimenSet). Specimen set for wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA

(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.

NA (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.

NA (addresses). The table that contains information about addresses. Addresses can be recorded for sites, organizations or contacts (individuals). 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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 variants 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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation 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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information 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.

Sets

NA (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.

NA (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.

NA (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.

NA

(units). The unit of the measurement. Every measurement must have a unit. Meaning, **units** are a mandatory field whenever a measurement is recorded.

NA (acti). Number of active cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (actiCaseOn). Number of active cases by onset date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (actiEp). Number of active cases by episode date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (actiRep). Number of active cases by report date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (actiTest). Number of active cases by test date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (cel). Degrees Celsius. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (cfu). Colony forming units Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cfu100). Colony forming units per 100 ml of filtered sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (cfugTS). colony forming units per grams total solids (CFU/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (cfumL). colony forming units per milliliter (CFU/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cm). Unit part for the SI unit of centimetres. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (conf). Number of confirmed cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (cpWell). Gene or variant copies per well. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ct). Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ctcq). cycle threshold (Ct) / quantification cycle (Cq) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (days). A unit for indicating a length of time in days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (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.

NA (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (fah). Unit for temperature, degrees Fahrenheit. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (fnu). formazin nephelometric unit (FNU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (foot). foot (ft) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gc). Gene or variant copies Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcDay). Unit of measurement of the number of gene copies per day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcL). Gene or variant copies per litre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcRx). Gene or variant copies per reaction in PCR Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gL). gram per liter (g/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gNgTS). nitrogen per total solids (gN/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gPergTS). Grams per total solids (g/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gPO43gTS). orthophosphate per total solids (gPO43-/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (grams). A unit of mass or weight. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (hosa). Hospital admissions or patients newly admitted to hospital. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (hosc). Hospital census or the number of people admitted with an ailment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (hours). A unit for indicating a length of time in hours. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (inch). inch (in) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (kgm3). Kilogram per cubic meter (kg/m^3) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (kgS). Kilograms per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (kl). Kilolitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (l). Litres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (lday). Unit of litres per day, usually for measuring flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (lhour). liter per hour (L/h) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (lmin). liter per minute (L/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (log10cpG). Unit for log10 copies per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

Sets

NA (log10cpL). Unit for log10 copies per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10cpml). Unit for log10 copies per millilitre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (log10gcngDNA). log10 gene copies per nanogram total DNA Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (log10ugG). Unit for log10 micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10ugL). Unit for log10 micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (lsec). liter per second (L/s) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (m3D). Cubic metres per day. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (m3H). Cubic metres per hour. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (m3min). cubic meter per minute (m^3/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (m3S). Cubic metre per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (meqL). Unit for alkalinity, miliequivalents per litre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (meter). meter (m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (mgLCaCO3). Unit for alkalinity, miligram per litre of calcium carbonate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mgPO43L). milligrams orthophosphate per liter (mg PO43-/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (minutes). A unit for indicating a length of time in minutes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ml). Millilitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (mmhocm). Millimho per centimeter (mmho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (months). A unit for indicating a length of time in months. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mpn100mL). most probable number per 100 milliliter (MPN/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (mpnmL). most probable number per milliliter (MPN/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mScm). MilliSiemens per centimeter (mS/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mvolt). milliVolt (mV) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (naUnit). Not applicable for units. Status: active. First released: 2.0.0. Last updated: 3.0.1.

NA (newVax). Population of newly vaccinated persons Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ngL). nanograms per liter (ng/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nM). the unit of nanomolar. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (peeps). Unit specifying a number of people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (personPerKm). Persons per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (personPerMile). Persons per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a single person would use. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pp). Percent positive of sample measures. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (pps). Percentage of total solids, for primary sludge. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (ppt). Parts per thousand. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (prop). Proportion as a percent of total. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (propV). Proportion of a variant as percent of total variants. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (psu). practical salinity unit (PSU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (resPerKm). Residents per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (resPerMile). Residents per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (seconds). The unit of time, seconds. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (sm). Siemens per meter (S/m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (test). Number of tests performed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ugG). Micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ugL). Micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ugmg). Concentration unit of micrograms per milligram. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (umhocm). Micromho per centimeter (mho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (unitless). A unit for unitless measures, like pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (uSCm). Micro-siemens per centimetre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (varFreq). A description of the frequency of a variants detected. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (ww). weight for weight (% w/w) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (years). A unit for indicating a length of time in years. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(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.

Sets

absHumidUnitSet

(absHumidUnitSet)Unit set for absolute humidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

alkalinitySet

(alkalinitySet)Unit set for alkalinity measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (meqL). Unit for alkalinity, miliequivalents per litre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

alleleUnitSet

(alleleUnitSet)Unit set for alleles. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (ct). Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (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.

NA (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

bacteriaUnitSet

(bacteriaUnitSet)Unit set for bacteria-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (cfu). Colony forming units Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cfu100). Colony forming units per 100 ml of filtered sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (cfugTS). colony forming units per grams total solids (CFU/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (cfumL). colony forming units per milliliter (CFU/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (mpn100mL). most probable number per 100 milliliter (MPN/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mpnmL). most probable number per milliliter (MPN/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

basePairSet

(basePairSet)Unit set for base-pair measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

capacityUnitSet

(capacityUnitSet)Unit set for capacity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a single person would use. Status: active. First released: 1.0.0. Last updated: 2.0.0.

conductivityUnitSet

(conductivityUnitSet)Unit set related to conductivity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (mmhocm). Millimho per centimeter (mmho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mScm). MilliSiemens per centimeter (mS/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (umhocm). Micromho per centimeter (mho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (uSCm). Micro-siemens per centimetre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

dissGasUnitSet

(dissGasUnitSet)Unit set for carbon dioxide concentrations measurements in water or air. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

electricPotentSet

(electricPotentSet)Unit set for measurements of electrical potential. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (mvolt). milliVolt (mV) Status: active. First released: 3.0.0. Last updated: 3.0.0.

flowUnitSet

(flowUnitSet)Unit set for volume flow measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (kgS). Kilograms per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (lday). Unit of litres per day, usually for measuring flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (lhour). liter per hour (L/h) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (lmin). liter per minute (L/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (lsec). liter per second (L/s) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (m3D). Cubic metres per day. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (m3H). Cubic metres per hour. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (m3min). cubic meter per minute (m^3/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (m3S). Cubic metre per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

geneticUnitSet

(geneticUnitSet)Unit set for genetic-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (cpWell). Gene or variant copies per well. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ct). Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (ctcq). cycle threshold (Ct) / quantification cycle (Cq) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (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.

NA (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (gc). Gene or variant copies Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcDay). Unit of measurement of the number of gene copies per day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcL). Gene or variant copies per litre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

NA (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.

NA (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (gcRx). Gene or variant copies per reaction in PCR Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (log10cpG). Unit for log10 copies per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10cpL). Unit for log10 copies per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10cpml). Unit for log10 copies per millilitre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (log10gcngDNA). log10 gene copies per nanogram total DNA Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (log10ugG). Unit for log10 micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (log10ugL). Unit for log10 micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (prop). Proportion as a percent of total. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (propV). Proportion of a variant as percent of total variants. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

humidUnitSet

(humidUnitSet)A unit set for all types of humidity measurements. Status: active. First Released: 3.0.1. Last updated: 3.0.1.

NA (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

naUnitSet

(naUnitSet)Not applicable for unit sets. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (naUnit). Not applicable for units. Status: active. First released: 2.0.0. Last updated: 3.0.1.

percentUnitSet

(percentUnitSet)Unit set for percentages. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

popDensUnitSet

(popDensUnitSet)Unit set for measures of population density of a site. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (personPerKm). Persons per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (personPerMile). Persons per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (resPerKm). Residents per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (resPerMile). Residents per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

populationUnitSet

(populationUnitSet)Unit set for hospital-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (acti). Number of active cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (actiCaseOn). Number of active cases by onset date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (actiEp). Number of active cases by episode date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (actiRep). Number of active cases by report date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (actiTest). Number of active cases by test date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (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.

NA (caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and this measure is most

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commonly reported and used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (conf). Number of confirmed cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (hosa). Hospital admissions or patients newly admitted to hospital. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (hosc). Hospital census or the number of people admitted with an ailment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (newVax). Population of newly vaccinated persons Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (peeps). Unit specifying a number of people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

NA (test). Number of tests performed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

NA (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.

NA (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.

Sets

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

NA (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.

precipitationUnitSet

(precipitationUnitSet)Unit set for percipitation measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (cm). Unit part for the SI unit of centimetres. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (foot). foot (ft) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (inch). inch (in) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (meter). meter (m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

relHumidUnitSet

(relHumidUnitSet)Unit set for relative humidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

salinityUnitSet

(salinityUnitSet)Unit set for salinity measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

NA (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gL). gram per liter (g/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (ppt). Parts per thousand. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (psu). practical salinity unit (PSU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ww). weight for weight (% w/w) Status: active. First released: 3.0.0. Last updated: 3.0.0.

specHumidUnitSet

(specHumidUnitSet)Unit set for specific humidity. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

speedUnitSet

(speedUnitSet)Unit set for reporting speeds (centrifugation speed, etc.)
Status: active. First Released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (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.

stdConcentrationUnitSet

(stdConcentrationUnitSet)Unit set for concentration measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gNgTS). nitrogen per total solids (gN/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gPergTS). Grams per total solids (g/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

Sets

NA (gPO43gTS). orthophosphate per total solids (gPO43-/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (kgm3). Kilogram per cubic meter (kg/m³) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (mgLCaCO3). Unit for alkalinity, miligram per litre of calcium carbonate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mgPO43L). milligrams orthophosphate per liter (mg PO43-/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (ngL). nanograms per liter (ng/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (nM). the unit of nanomolar. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (pps). Percentage of total solids, for primary sludge. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA

NA (ugG). Micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ugL). Micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (ugmg). Concentration unit of micrograms per milligram. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

temperatureUnitSet

(temperatureUnitSet)Unit set for temperature measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (cel). Degrees Celsius. Status: active. First released: 1.1.0. Last updated: 2.0.0.

NA (fah). Unit for temperature, degrees Fahrenheit. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

timeUnitSet

(timeUnitSet)The unit set for measures of time. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (days). A unit for indicating a length of time in days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (hours). A unit for indicating a length of time in hours. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (minutes). A unit for indicating a length of time in minutes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (months). A unit for indicating a length of time in months. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (seconds). The unit of time, seconds. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (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.

NA (years). A unit for indicating a length of time in years. Status: active. First released: 2.0.0. Last updated: 2.0.0.

turbidityUnitSet

(turbidityUnitSet)Unit set for turbidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (fnu). formazin nephelometric unit (FNU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (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.

NA (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.

unitlessUnitSet

(unitlessUnitSet) Unit set for measurements that does not have units. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (unitless). A unit for unitless measures, like pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

volumeUnitSet

(volumeUnitSet) Unit set of volume measurements. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

NA (grams). A unit of mass or weight. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (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.

NA (kl). Kilolitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (l). Litres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (ml). Millilitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

Sets

NA (pp). Percent positive of sample measures. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (varFreq). A description of the frequency of a variants detected. Status: active. First released: 2.0.0. Last updated: 2.0.0.

windSpeedUnitSet

(windSpeedUnitSet)Unit set for wind speed measurements. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

NA (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.

NA (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

(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.

NA (absHumidUnitSet). Unit set for absolute humidity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (alkalinitySet). Unit set for alkalinity measurements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (alleleUnitSet). Unit set for alleles. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (bacteriaUnitSet). Unit set for bacteria-related measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (basePairSet). Unit set for base-pair measurements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (capacityUnitSet). Unit set for capacity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (conductivityUnitSet). Unit set related to conductivity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (dissGasUnitSet). Unit set for carbon dioxide concentrations measurements in water or air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (electricPotentSet). Unit set for measurements of electrical potential. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (flowUnitSet). Unit set for volume flow measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (geneticUnitSet). Unit set for genetic-related measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (naUnitSet). Not applicable for unit sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

NA (percentUnitSet). Unit set for percentages. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (popDensUnitSet). Unit set for measures of population density of a site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (populationUnitSet). Unit set for hospital-related measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (precipitationUnitSet). Unit set for precipitation measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (relHumidUnitSet). Unit set for relative humidity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (salinityUnitSet). Unit set for salinity measurements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

NA (specHumidUnitSet). Unit set for specific humidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (speedUnitSet). Unit set for reporting speeds (centrifugation speed, etc.) Status: active. First released: 2.2.0. Last updated: 2.2.0.

NA (stdConcentrationUnitSet). Unit set for concentration measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (temperatureUnitSet). Unit set for temperature measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (timeUnitSet). The unit set for measures of time. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (turbidityUnitSet). Unit set for turbidity measurements. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA (unitlessUnitSet). Unit set for measurements that does not have units. Status: active. First released: 2.0.0. Last updated: 2.0.0.

NA

NA (volumeUnitSet). Unit set of volume measurements. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (windSpeedUnitSet). Unit set for wind speed measurements. Status: active. First released: 1.0.0. Last updated: 2.0.0.

NA (humidUnitSet). A unit set for all types of humidity measurements. Status: active. First released: 3.0.1. Last updated: 3.0.1.

Tables

Dictionary v3.0.1 Documentation v2.1.1

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).

i Data storage

While storing data in the full suite of 26 tables in the PHES-ODM ensures optimal interoperability 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 ouputputs) 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

Tables

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 list

addresses
calculations
contacts
countries
datasets
instruments
languages
measures
measureSets
organizations
parts
phActions
polygonRelationships
polygons
protocolRelationships
protocols
protocolSteps
qualityReports
sampleRelationships
samples
sets
sites
translations

Tables

wideNames

zones

accessions { #accessions } 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

accessNum (accessNum). The accession number for the data entry in the given data repository or hosting platform.Role: Header.Requirement: mandatory.Data type: varchar.

hostVersion (hostVersion). The version of the data repository or hosting platform being used.Role: Header.Requirement: optional.Data type: varchar.

lastEdited (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.

addresses

partID: addresses. The table that contains information about addresses. Addresses can be recorded for sites, organizations or contacts (individuals). 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

addL1 (addL1). Line 1 (the street name, number and direction) for a given address.Role: Header.Requirement: mandatory.Data type: varchar.

addL2 (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.

pCode (pCode). The zip code or postal code for a given address, specifying a specific geographic area.Role: Header.Requirement: optional.Data type: varchar.

lastEdited (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 attributes.Role: Header.Requirement: optional.Data type: varchar.

calculations

partID: calculations. Table for recording data on data treatments and calculations applied to measurements and reported values. cl

treatmentID (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 differentiate 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 (summary). Summary sheet of the dictionary.xlsx file.Role: Header.Requirement: optional.Data type: varchar.

order (order). The order a single calculation/data treatment takes within the full container pipeline/workflow.Role: Header.Requirement: recommended.Data type: integer.

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equation (equation). The equation used in the calculation/data treatment.Role: Header.Requirement: recommended.Data type: varchar.

refLink (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.

sourceCode (sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps.Role: Header.Requirement: recommended.Data type: varchar.

lastEdited (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.

contacts

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

firstName (firstName). Specifies the first name of a given contact.Role: Header.Requirement: optional.Data type: varchar.

lastName (lastName). Specifies the last name of a given contact.Role: Header.Requirement: optional.Data type: varchar.

email (email). Contact e-mail address, for the lab.Role: Header.Requirement: mandatory.Data type: varchar.

coPhone (coPhone). Contact phone number, for the lab.Role: Header.Requirement: optional.Data type: varchar.

role (role). Specifies the organizational role of a given contact.Role: Header.Requirement: optional.Data type: varchar.

lastEdited (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 attributes.Role: Header.Requirement: optional.Data type: varchar.

countries

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

isoCodeX (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.

numCode (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.

tld (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.

nameEngl (nameEngl). English-language name of a given country.Role: Header.Requirement: mandatory.Data type: varchar.

nameOfficial (nameOfficial). Official english-language name of a given state.Role: Header.Requirement: mandatory.Data type: varchar.

sovereignty (sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory.Role: Header.Requirement: mandatory.Data type: varchar.

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countryExonym (countryExonym). The English name foreigners use for the country.Role: Header.Requirement: mandatory.Data type: varchar.

capitalExonym (capitalExonym). The English name foreigners use for the country's capital.Role: Header.Requirement: mandatory.Data type: varchar.

countryEndonym (countryEndonym). The name locals use for their country.Role: Header.Requirement: mandatory.Data type: varchar.

capitalEndonym (capitalEndonym). The name locals use for their country's capital.Role: Header.Requirement: mandatory.Data type: varchar.

langScript (langScript). The language(s) and script(s) used for the country's capital endonyms.Role: Header.Requirement: mandatory.Data type: varchar.

phone (phone). International dialing code for the country.Role: Header.Requirement: mandatory.Data type: varchar.

utc (utc). UTC – Time zone.Role: Header.Requirement: mandatory.Data type: varchar.

utcDST (utcDST). Time zone during Daylight Saving Time.Role: Header.Requirement: mandatory.Data type: varchar.

datasets

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

datasetDate (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 differentiate 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.

descr (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

refLink (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.

originalFormat (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

lastEdited (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.

instruments

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

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other entity. Specific naming conventions vary by usecase and are user-generated. To differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname 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.

descr (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

refLink (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.

insTypeOth (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.

lastEdited (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.

languages

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

langFam (langFam). Specifies the language family of a given language for translation and language tracking purposes.Role: Header.Requirement: mandatory.Data type: varchar.

langName (langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes.Role: Header.Requirement: mandatory.Data type: varchar.

natName (natName). The native name of the language, i.e. what the language is called by its speakers.Role: Header.Requirement: mandatory.Data type: varchar.

iso6391 (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.

iso6392T (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.

firstReleased (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

lastUpdated (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

changes (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.

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measures

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 differentiate 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.

aDateStart (aDateStart). Date the measurement or analysis was started.Role: Header.Requirement: optional.Data type: datetime.

aDateEnd (aDateEnd). Date the measurement or analysis was completed.Role: Header.Requirement: mandatory.Data type: datetime.

epiWeekStart (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 (epiWeek). The number of the epi week in which a sample was collected, or to which a measure would apply.Role: Header.Requirement: optional.Data type: integer.

epiYear (epiYear). The year in which the epi week is occurring.Role: Header.Requirement: optional.Data type: integer.

relDateStart (relDateStart). The start date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons.Role: Header.Requirement: mandatory.If.Data type: datetime.

relDateEnd (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons.Role: Header.Requirement: mandatory.If.Data type: datetime.

reportDate (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.

valTreat (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: valTreat-Set

index (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

measureLic (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.

lastEdited (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

refLink (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.

Tables

measureSets

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 variants 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 differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname rules (see PHES-ODM documentation for more details).Role: Header.Requirement: optional.Data type: varchar.

lastEdited (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.

organizations

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 differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

descr (descr). A detailed description of a measure, method, or attribute. Role: Header. Requirement: optional. Data type: varchar.

orgType (orgType). Specifies the type or purpose of a given organization. Role: Header. Requirement: recommended. Data type: categorical. Measure, method or attribute set: orgTypeSet

orgLevel (orgLevel). The geographic level of an organization. Role: Header. Requirement: recommended. Data type: categorical. Measure, method or attribute set: orgLevelSet

orgSector (orgSector). The sector of an organization. Role: Header. Requirement: recommended. Data type: categorical. Measure, method or attribute set: orgSectorSet

lastEdited (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 attributes. Role: Header. Requirement: optional. Data type: varchar.

parts

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.

partType (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

partDesc (partDesc). The description of the part. Role: Header. Requirement: mandatory. Data type: varchar.

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partInstr (partInstr). Additional notes and instructions on how a part is used and/or defined.Role: Header.Requirement: optional.Data type: varchar.

fKAliasID (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

ontologyRef (ontologyRef). Ontology reference for a part.Role: Header.Requirement: optional.Data type: varchar.

latExp (latExp). LaTeX expression used to generate formulas, symbols, etc. Mainly relevant for units.Role: Header.Requirement: mandatoryIf.Data type: varchar.

aggregationScale (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

firstReleased (firstReleased). The version in which a part was first released.Role: Header.Requirement: mandatory.Data type: varchar.

lastUpdated (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

changes (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

protocolSteps (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.

protocolStepsRequired (protocolStepsRequired). Specifies the columns required in a Protocol Steps table.Role: Header.Requirement: optional.Data type: varchar.

protocolStepsOrder (protocolStepsOrder). Specifies the order of the columns in a Protocol Steps table.Role: Header.Requirement: optional.Data type: integer.

protocolRelationships (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 procedure) and measureIDs (a

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measure). An example of a method is centrifugation; where the centrifugation 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.

protocolRelationshipsRequired (protocolRelationshipsRequired). Specifies the columns required in the Protocol Organization table.Role: Header.Requirement: optional.Data type: varchar.

protocolRelationshipsOrder (protocolRelationshipsOrder). Specifies the order of the columns in the Protocol Organization table.Role: Header.Requirement: optional.Data type: integer.

measures (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.

measuresRequired (measuresRequired). Specifies the columns required in a Measures table.Role: Header.Requirement: optional.Data type: varchar.

measuresOrder (measuresOrder). Specifies the order of the columns in a Measures table.Role: Header.Requirement: optional.Data type: integer.

measureSets (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 variants 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.

measureSetsOrder (measureSetsOrder). Specifies the order of the columns in a Measure Sets table.Role: Header.Requirement: optional.Data type: integer.

measureSetsRequired (measureSetsRequired). Specifies the columns required in a Measure Sets table.Role: Header.Requirement: optional.Data type: varchar.

datasets (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.

datasetsRequired (datasetsRequired). Specifies the columns required in a Datasets table.Role: Header.Requirement: optional.Data type: varchar.

datasetsOrder (datasetsOrder). Specifies the order of the columns in a Datasets table.Role: Header.Requirement: optional.Data type: integer.

sites (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information changes often. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

sitesRequired (sitesRequired). Specifies the columns required in a Sites table.Role: Header.Requirement: optional.Data type: varchar.

sitesOrder (sitesOrder). Specifies the order of the columns in a Sites table.Role: Header.Requirement: optional.Data type: integer.

samples (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.

samplesRequired (samplesRequired). Specifies the columns required in a Samples table.Role: Header.Requirement: optional.Data type: varchar.

samplesOrder (samplesOrder). Specifies the order of the columns in a Samples table.Role: Header.Requirement: optional.Data type: integer.

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addresses (addresses). The table that contains information about addresses. Addresses can be recorded for sites, organizations or contacts (individuals). 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.

addressesRequired (addressesRequired). Specifies the columns required in a Addresses table. Role: Header. Requirement: optional. Data type: varchar.

addressesOrder (addressesOrder). Specifies the order of the columns in the Addresses table. Role: Header. Requirement: optional. Data type: integer.

contacts (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.

contactsRequired (contactsRequired). Specifies the columns required in a Contacts table. Role: Header. Requirement: optional. Data type: varchar.

contactsOrder (contactsOrder). Specifies the order of the columns in a Contacts table. Role: Header. Requirement: optional. Data type: integer.

organizations (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.

organizationsRequired (organizationsRequired). Specifies the columns required in a Organizations table. Role: Header. Requirement: optional. Data type: varchar.

organizationsOrder (organizationsOrder). Specifies the order of the columns in a Organizations table. Role: Header. Requirement: optional. Data type: integer.

phActions (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.

phActionsRequired (phActionsRequired). Required headers in the public health actions table.Role: Header.Requirement: mandatory.Data type: varchar.

phActionsOrder (phActionsOrder). Specifies the order of the columns in the public health actions table.Role: Header.Requirement: mandatory.Data type: integer.

calculations (calculations). Table for recording data on data treatments and calculations applied to measurements and reported values.Role: Header.Requirement: optional.Data type: varchar.

calculationsRequired (calculationsRequired). Required headers in the calculations table.Role: Header.Requirement: mandatory.Data type: varchar.

calculationsOrder (calculationsOrder). Specifies the order of the columns in the calculations table.Role: Header.Requirement: mandatory.Data type: integer.

instruments (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.

instrumentsRequired (instrumentsRequired). Specifies the columns required in the Instruments table.Role: Header.Requirement: optional.Data type: varchar.

instrumentsOrder (instrumentsOrder). Specifies the order of the columns in the Instruments table.Role: Header.Requirement: optional.Data type: integer.

polygonRelationships (polygonRelationships). Table for recording the relationships between polygons. The short name for the table (partID) can

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be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

polygonRelationshipsRequired (polygonRelationshipsRequired). Required headers in the polygon relationships table.Role: Header.Requirement: mandatory.Data type: varchar.

polygonRelationshipsOrder (polygonRelationshipsOrder). Specifies the order of the columns in the polygon relationships table.Role: Header.Requirement: mandatory.Data type: integer.

polygons (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.

polygonsRequired (polygonsRequired). Specifies the columns required in a Polygons table.Role: Header.Requirement: optional.Data type: varchar.

polygonsOrder (polygonsOrder). Specifies the order of the columns in a Polygons table.Role: Header.Requirement: optional.Data type: integer.

accessions (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.

accessionsRequired (accessionsRequired). Required headers in the accessions table.Role: Header.Requirement: mandatory.Data type: varchar.

accessionsOrder (accessionsOrder). Specifies the order of the columns in the accessions table.Role: Header.Requirement: mandatory.Data type: integer.

languages (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.

languagesRequired (languagesRequired). Required headers in the Languages table.Role: Header.Requirement: optional.Data type: varchar.

languagesOrder (languagesOrder). Specifies the order of the columns in the Languages table.Role: Header.Requirement: optional.Data type: integer.

translations (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.

translationsRequired (translationsRequired). Required headers in the Translations table.Role: Header.Requirement: optional.Data type: varchar.

translationsOrder (translationsOrder). Specifies the order of the columns in the Translation table.Role: Header.Requirement: optional.Data type: integer.

parts (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.

partsRequired (partsRequired). Required headers in the Parts table.Role: Header.Requirement: optional.Data type: varchar.

partsOrder (partsOrder). Order of headers in the Parts table.Role: Header.Requirement: optional.Data type: integer.

sets (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

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short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

setsRequired (setsRequired). Required headers in the Sets table.Role: Header.Requirement: optional.Data type: varchar.

setsOrder (setsOrder). Specifies the order of the columns in the Sets table.Role: Header.Requirement: optional.Data type: integer.

qualityReports (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.

qualityReportsRequired (qualityReportsRequired). Specifies the columns required in the Quality Reports table.Role: Header.Requirement: optional.Data type: varchar.

qualityReportsOrder (qualityReportsOrder). Specifies the order of the columns in the Quality Reports table.Role: Header.Requirement: optional.Data type: integer.

sampleRelationships (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.

sampleRelationshipsRequired (sampleRelationshipsRequired). Specifies the columns required in a Sample Relationships table.Role: Header.Requirement: optional.Data type: varchar.

sampleRelationshipsOrder (sampleRelationshipsOrder). Specifies the order of the columns in a Sample Relationships table.Role: Header.Requirement: optional.Data type: integer.

protocols (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.

protocolsRequired (protocolsRequired). Specifies the columns required in the Protocols table.Role: Header.Requirement: optional.Data type: varchar.

protocolsOrder (protocolsOrder). Specifies the order of the columns in the Protocols table.Role: Header.Requirement: optional.Data type: integer.

countries (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.

countriesRequired (countriesRequired). Required headers in the countries table.Role: Header.Requirement: optional.Data type: varchar.

countriesOrder (countriesOrder). Specifies the order of the columns in the countries table.Role: Header.Requirement: optional.Data type: integer.

zones (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.

zonesRequired (zonesRequired). Required headers in the zones table.Role: Header.Requirement: optional.Data type: varchar.

zonesOrder (zonesOrder). Specifies the order of the columns in the zones table.Role: Header.Requirement: optional.Data type: integer.

wideNames (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.

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wideNamesRequired (wideNamesRequired). Column for indicating which fields in the wide names table are mandatory.Role: Header.Requirement: optional.Data type: varchar.

wideNamesOrder (wideNamesOrder). Column for indicating the order of the fields in the wide names table.Role: Header.Requirement: optional.Data type: integer.

refLink (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.

dataType (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

minValue (minValue). The minimum value of part.Role: Header.Requirement: mandatoryIf.Data type: varchar.

maxValue (maxValue). The maximum value of a part.Role: Header.Requirement: mandatoryIf.Data type: varchar.

minLength (minLength). The maximum value of measure.Role: Header.Requirement: mandatoryIf.Data type: integer.

maxLength (maxLength). The maximum length of the value of a part or measure.Role: Header.Requirement: mandatoryIf.Data type: integer.

phActions

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

actionDT (actionDT). The date and Time of the public health action.Role: Header.Requirement: optional.Data type: datetime.

relDateStart (relDateStart). The start date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons.Role: Header.Requirement: optional.Data type: datetime.

relDateEnd (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons.Role: Header.Requirement: optional.Data type: datetime.

lastEdited (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.

polygonRelationships

partID: polygonRelationships. Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. por

lastEdited (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.

polygons

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

Tables

other entity. Specific naming conventions vary by usecase and are user-generated. To differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

descr (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

geoType (geoType). Type of geography that is represented by the polygon.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: geoTypeSet

geoEPSG (geoEPSG). The unique EPSG code specifying a given geospatial area.Role: Header.Requirement: mandatory.Data type: float.

geoWKT (geoWKT). Well-known text of the polygonRole: Header.Requirement: mandatory.Data type: varchar.

fileLocation (fileLocation). The location of the file containing the geometry of the polygon.Role: Header.Requirement: optional.Data type: varchar.

refLink (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.

poLic (poLic). The license for the availability of the polygon shapefile.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: licSet

lastEdited (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.

protocolRelationships

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 procedure) and measureIDs (a measure). An example of a method is centrifugation; where the centrifugation rotation speed is described as a measure. The short name for the table (partID) can be found in the instructions field. pr

lastEdited (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

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 differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname rules (see PHES-ODM documentation for more details).Role: Header.Requirement: optional.Data type: varchar.

summ (summ). Short description of the assay and how it is different from the other assay methods.Role: Header.Requirement: optional.Data type: varchar.

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refLink (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.

protocolVersion (protocolVersion). Specifies the version of a method set.Role: Header.Requirement: optional.Data type: integer.

lastEdited (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.

protocolSteps

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

summ (summ). Short description of the assay and how it is different from the other assay methods.Role: Header.Requirement: optional.Data type: varchar.

stepVer (stepVer). Specifies the version of a given protocol step.Role: Header.Requirement: optional.Data type: varchar.

refLink (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.

lastEdited (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 attributes. Role: Header. Requirement: optional. Data type: varchar.

qualityReports

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

qualityFlag (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 (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

lastEdited (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 attributes. Role: Header. Requirement: optional. Data type: varchar.

sampleRelationships

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

lastEdited (lastEdited). The date the entry was last updated. Role: Header. Requirement: optional. Data type: datetime.

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notes (notes). A note used to describe details that are not captured in other attributes. Role: Header. Requirement: optional. Data type: varchar.

samples

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

origin (origin). An attribute of a sample specifying the origin. Role: Header. Requirement: optional. Data type: categorical. Measure, method or attribute set: originSet

collPer (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.

collNum (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 sites. Role: Header. Requirement: optional. Data type: boolean.

collDT (collDT). For grab samples this is the date, time and timezone the sample was taken. Role: Header. Requirement: mandatory. Data type: datetime.

collDTStart (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.

collDTEnd (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.

collDate (collDate). Sample collection date, where time is reported in a separate field.Role: Header.Requirement: optional.Data type: date.

collAppxT (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

epiWeekStart (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 (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.

epiYear (epiYear). The year in which the epi week is occuring.Role: Header.Requirement: optional.Data type: integer.

sentDate (sentDate). Date that the sample was sent from the collection site to the lab.Role: Header.Requirement: optional.Data type: datetime.

recDate (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.

lastEdited (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.

Tables

sets

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

setType (setType). The type of set. i.e. quality set, aggregation set, unit set
Role: 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 (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

firstReleased (firstReleased). The version in which a part was first released.
Role: Header.Requirement: mandatory.Data type: varchar.

lastUpdated (lastUpdated). The version in which the part was last updated.
Role: Header.Requirement: mandatory.Data type: varchar.

changes (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 attributes.
Role: Header.Requirement: optional.Data type: varchar.

sites

partID: sites. The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the information changes often. The short name for the table (partID) can be found in the instructions field. si

sampleShed (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

siteLevel (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 differentiate between the **name** field in different tables, please use attribute-specific widenames per widenname rules (see PHES-ODM documentation for more details).Role: Header.Requirement: recommended.Data type: varchar.

descr (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

healthRegion (healthRegion). A free-text variable for listing the health region for a given site.Role: Header.Requirement: optional.Data type: varchar.

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geoLat (geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721)Role: Header.Requirement: mandatoryIf.Data type: float.

geoLong (geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000)Role: Header.Requirement: mandatoryIf.Data type: float.

geoEPSG (geoEPSG). The unique EPSG code specifying a given geospatial area.Role: Header.Requirement: mandatoryIf.Data type: float.

lastEdited (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.

translations

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.

partDesc (partDesc). The description of the part.Role: Header.Requirement: mandatory.Data type: varchar.

partInstr (partInstr). Additional notes and instructions on how a part is used and/or defined.Role: Header.Requirement: optional.Data type: varchar.

firstReleased (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

lastUpdated (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

changes (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.

wideNames

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.

charLength (charLength). The number of characters used for the wide names.Role: Header.Requirement: optional.Data type: integer.

descr (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: mandatory.Data type: varchar.

source (source). The database or table sourced for the wide name.Role: Header.Requirement: mandatory.Data type: varchar.

wideMeasure (wideMeasure). Unique identifier for a measure in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

wideProtocol (wideProtocol). Unique identifier for a protocol in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

wideAttribute (wideAttribute). Unique identifier for an attribute in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

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reportTableName (reportTableName). The report table that the wide name calls from.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: tables

partTypeName (partTypeName). The part type being used in a wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: partTypes

compartmentName (compartmentName). The compartment referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: compartments

specimenName (specimenName). The specimen referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: specimens

fractionName (fractionName). The fraction analyzed referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: fractionSet

measureName (measureName). The measure referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: measurements

methodName (methodName). The method referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: methods

unitName (unitName). The unit referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: categorical.Measure, method or attribute set: units

aggregationName (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.

attributeName (attributeName). The attribute referenced for the wide name.Role: Header.Requirement: mandatory.If.Data type: categorical.Measure, method or attribute set: attributes

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

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

zoneName (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.

