

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

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# Introduction

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## Dictionary v3.0.0 Documentation v2.1.0

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

## *How to use the documentation*

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 three document sections, each with a different purpose.<sup>1</sup>

*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.

*Reference* 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**

Tutorials and videos are being developed. Tutorials will help newcomers get started. They will be lessons on how to:

- Describe a protocol using protocol tables.
- Make wide names and report templates using wide names.

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<sup>1</sup>David Laing and Divio's Grand Unified Theory of Documentation.

## *Introduction*

## **Quick start**

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

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

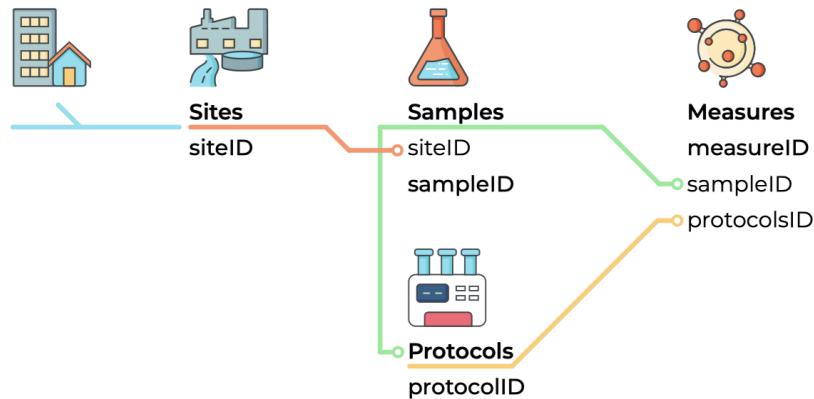


Figure 1.: **Figure 1 - Key ODM tables for recording data**

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

## **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 [OSF.io](#). 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[(tables.qmd#samples)]] for the table.

<https://vimeo.com/802349692>

## *Introduction*

### **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 airport template](#) is a hybrid template that exemplifies this (found in the “Airports” folder).

(Video)

## **4. Next steps**

In addition to recording measures from samples, you can also record measures for a specific site, such as wastewater flow rate (flowRate), or the population served by the site, such as the Covid-19 hospitalization rate for a wastewater treatment plant’s wasteshed or municipality. **Figure 2** illustrates the these three types of measurements: **sample**, **site**, and **population**.

The “who, where, and why” of these measurements is stored in contact tables, while the “how,” which refers to the measurement protocol or method, is stored in the protocols tables.

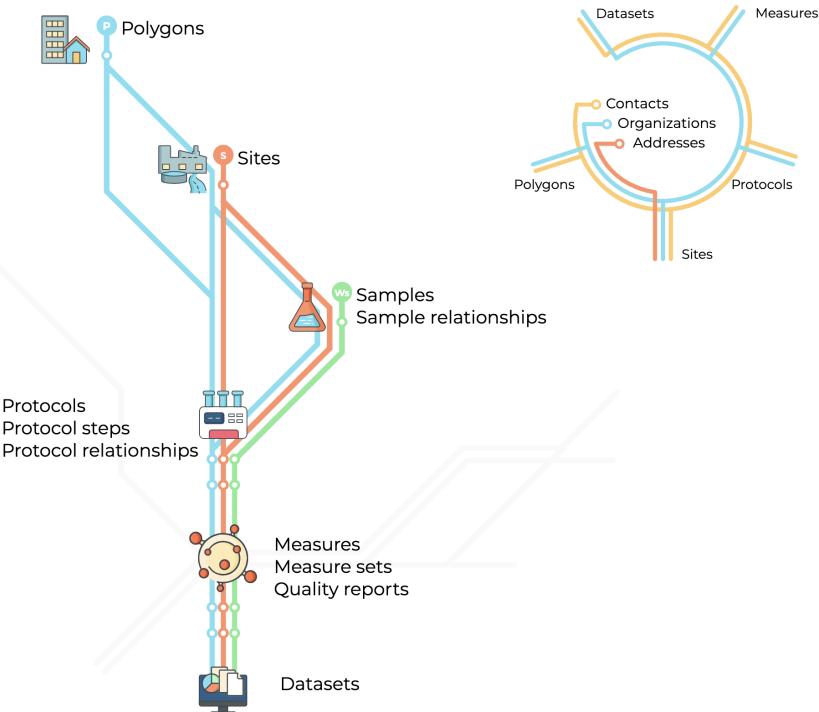


Figure 2.: **Figure 2 - ODM tables and ‘subway’ lines for storing measures**

## 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

New names:

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## Dictionary v3.0.0 Documentation v2.1.0

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 measures 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.<sup>2</sup> It also adopts an

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<sup>2</sup>[FAIR Principles](#).

## *Background*

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 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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## *Getting to know the ODM*

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*Getting to know the ODM*

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*Getting to know the ODM*

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* `` -> `...404`
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## *Getting to know the ODM*

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* `` -> `...405`  
* `` -> `...406`  
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* `` -> `...418`
```

Dictionary v3.0.0 Documentation v2.1.0

## **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.

## *“Sets” and the rationale behind sets*

See the [parts reference document](#) for more details.

The are additional part types to support the dictionary including:

- Aggregations
- Aggregation scales
- Categories
- Classes
- Compartments
- Dictionary support
- Domains
- Groups
- Missingness
- Nomenclature
- Quality indicators
- Specimens
- Tables
- Units

For information and details about all the part types, please see the [parts reference document](#).

## **“Sets” and the rationale behind sets**

“Sets” are a way of grouping together different possible categorical inputs within the ODM. The purpose behind sets is to group options together so that users only need to check a few options from a drop-down menu, rather than scroll through a long list. Sets are also designed so that a single part can be used in multiple sets, which avoids the need to create multiple versions of this part for these different use contexts. For example, if you’re taking a measure of concentration, that measure will likely populate the unit choice drop-down list with units from the “standard concentration unit set”. Units in this set include Milligrams per litre, parts per million,

## *Getting to know the ODM*

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
- Quality sets
- Specimen sets

Details about these sets are their similar - but unique - applications can be found in the [parts reference document](#). Importantly, “category sets” are not considered a “set” like these others. See the section below for an explanation of this difference.

### **Why category sets are treated differently**

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. Category sets are, however, an exception to this rule because the categories that make up a category set are 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 category 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). Category sets are also a distinct part type, and more information about them can be found in the [parts reference document](#).

## *The “what” and “why” of Specimen IDs*

### **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 person measure, ie. a measure of something at the level of an individual person, such as a blood pressure reading; or a population measure, ie. an aggregate measure of a population, such as the number of confirmed cases of a given illness. While there is currently nothing in version 2.0 of the ODM with uses the person specimen ID explicitly, it has been included to allow for the possibility of storing individual-level data in a future version. The reason specimen IDs were created was so that there could be a single manner in which measures and methods are recorded, regardless of the level at which they were performed, while still maintaining the possibility to collect site, sample, and population measures as a distinct types of metadata.

### **The “what” and “why” of Groups and Classes**

Groups and classes, similar to sets, are ways of grouping together different measures within the ODM. Given that the ODM aims to be as robust as possible and has a very long list of possible measures, groups and classes were designed to give shorter lists of measures in the drop down lists by specifying details about the kind of measure that a user is recording. Groups and classes can work together to further specify what kinds of measures are being reported. For example, the group `sarsCov2` contains many measures, but by specifying that the class is an `allele` or `variant`, the list of possible measures is pared down. Alternatively, class can be said to be non-applicable, paring down the measures in the `sarsCov2` group to only be unspecified measures of the quantity of the virus.

## **Tables and table types within the ODM**

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

### **Program description tables**

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

### **Results tables**

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

### **Look-up tables**

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

## *Measures, Methods, and Attributes: Key parts*

### **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 `measureID`, 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 `unitID` and `aggregationID` 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 (`methodID`) 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 `methodSteps` table can be populated by one of the inputs from the category set associated with that `methodID`. This provides a higher level of detail for a given method. For example, the `methodID` 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 present in both the `samples` and `measures` tables. This field serves to highlight whether or not there is a quality issues with the sample or the measure. 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.

## **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.

## *Dates within the ODM*

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

## **Dates within the ODM**

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

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

## **Translation and language capabilities**

The default language of the ODM is English, but French translations of all descriptive elements of the data model dictionary are also available. 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 (`languageLUs`), the translation look-up table (`translationLUs`), and the parts table (`partsLUs`). 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.

## *Recording protocols*

- 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.

## Getting to know the ODM

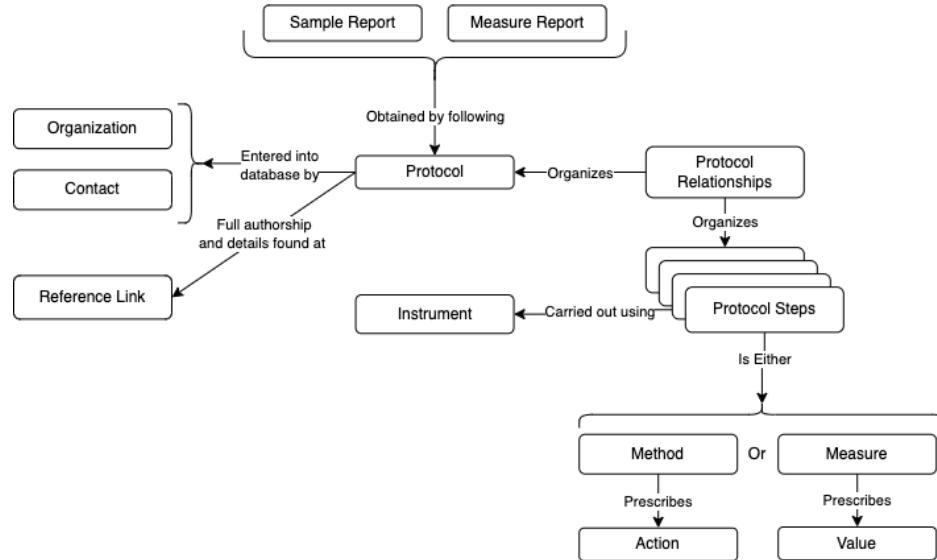


Figure 3.: Figure A: Main entities and relationships used to represent protocols

## Recommended formula for user-generated IDs

There are 13 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:

*Recommended formula for user-generated IDs*

User ID	Formula	Example
Address ID	country code + province code + 2-3 letters of municipality + row	caOnOtt002
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
Polygon ID	orgID + siteID	caOnOtt002Uni-CaOnOttOtt
Protocol ID	first 5 letters of name + protocolVersion	pmmov1
Protocol report ID	orgID + last 3 letters of part ID of method/measure	caOnOtt002Uni-Ion
Step ID	quality flag part ID + either the measure report ID, the sample ID, or measure set report ID that the quality report is for	flagJcaOnOt-tOttawa-site1202008021000covN1002
Measure report ID	sampleID + part ID of measure + row number	caOnOt-tOtt20200802Covn1002
Measure set report ID	Report ID of first measure in the set + # measures in the set	caOnOt-tOtt20200801Covn1002003
Sample ID	siteID + collDT/collDTEnd (not including time) + index (if applicable)	caOnOt-tOtt20200801
Site ID	country code (ISO) + province code (ISO) + first 2-3 letters of municipality + 3 first letters of site name	caOnOttOtt

To go into greater detail, the *Address ID* uses the recipe country code + province code + 2-3 letters of municipality + row. So it's built using pieces of the metadata fields for the given address' entry in the addresses table, and the row it occupies in that table. For example, the ID for an

## *Getting to know the ODM*

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.

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

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

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

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

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.

### *Recommended formula for user-generated IDs*

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.

*Quality ID* ia generated using the recipe of part ID for the given quality flag + either the measure report ID, the sample ID, or measure set report ID for which the quality report is being generated. Generating an example, if we are reporting the qulaity flag J - Weak signal extrapolation (partID = flagJ) for a measure report with the ID caOnOttOttawa-site1202008021000covN1002, we get the quality ID of flagJcaOnOttOttawasite1202008021000covN1002.

The *Measure Report ID* is built using sampleID + part ID of measure + row number. For example, taking a measure of the SARS-CoV-2 N1 gene region (partID = covN1) from a sample with the ID caOnOttOtt20200801, recorded in the second row of the table, we get the measure report ID of caOnOttOtt20200802Covn1002.

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

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

### *Getting to know the ODM*

Lastly, 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.

## **Questions and online community**

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

# How to use the ODM

New names:

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* `` -> `...108`  
* `` -> `...109`  
* `` -> `...110`  
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*How to use the ODM*

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*How to use the ODM*

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*How to use the ODM*

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* `` -> `...363`  
* `` -> `...364`  
* `` -> `...365`  
* `` -> `...366`  
* `` -> `...367`  
* `` -> `...368`  
* `` -> `...369`  
* `` -> `...370`
```

*How to use the ODM*

```
* `` -> `...371`  
* `` -> `...372`  
* `` -> `...373`  
* `` -> `...374`  
* `` -> `...375`  
* `` -> `...376`  
* `` -> `...377`  
* `` -> `...378`  
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* `` -> `...399`  
* `` -> `...400`  
* `` -> `...401`  
* `` -> `...402`  
* `` -> `...403`  
* `` -> `...404`
```

## *How to use the ODM*

```
* `` -> `...405`  
* `` -> `...406`  
* `` -> `...407`  
* `` -> `...408`  
* `` -> `...409`  
* `` -> `...410`  
* `` -> `...411`  
* `` -> `...412`  
* `` -> `...413`  
* `` -> `...414`  
* `` -> `...415`  
* `` -> `...416`  
* `` -> `...417`  
* `` -> `...418`
```

Dictionary v3.0.0 Documentation v2.1.0

## **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](#) section). 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

### *1) How to use templates*

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** and **Measure report** tables are used for day-to-day reporting. You can record information about a sample in the **Sample report** table. Measures (or measurements) are recorded in the **Measure report** table. A measure is “measurement or observation of any substance including a biological, physical or chemical substance”.
- There are three optional tables that support the reporting of samples and measures:
  - **Sample relationships** is used only when you have samples that are pooled or split.
  - **Measure set report** can be used to link measures together.
  - **Quality reports** 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** and **Sample report** tables).
- Typically, there is a one time initial setup where you will need to enter information into the **Sites**, **Address**, **Organization**, and **Contact** tables.
  - **Sites** is mandatory and records information about where testing is performed.
  - **Address**, **Organization**, and **Contact** provide the contact information for sites and entities such as laboratories.
- There are optional supporting tables, such as **Protocols** and **Instrument**, where you can use the templates to record information about how samples are taken and how measures are reported. You

## *How to use the ODM*

only need to complete these tables once and then update them as needed.

- `Protocol steps` and `Protocol relationships` tables are used alongside +

	A	B
1	Frog	Chair
2	Frog	Table
3	Cat	Sofa
4	Dog	Sofa

- Other supporting tables include `Polygon`, which stores information about the sample shed, and `Dataset`, which stores information about the data custodian and owner of the data.

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

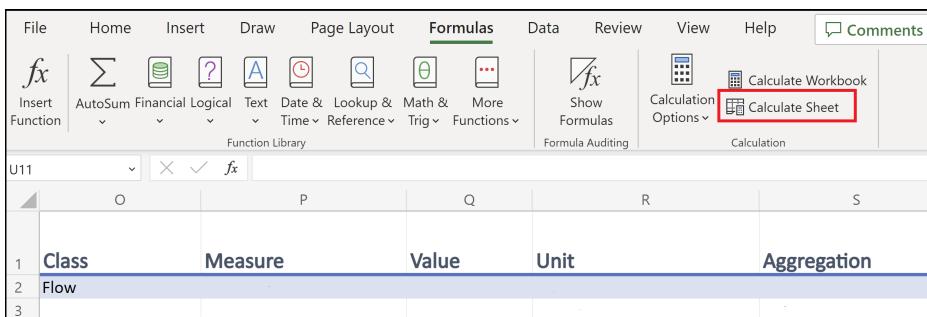
- **Identifier and unique identifier (red):** In these fields you will create a value that will be used to identify something. For instance, `Sample ID` is used to identify each unique sample. An identifier can be repeated between entries, while an unique identifier cannot. There is usually only one unique identifier per template, and they correspond to the name of the template. For example, `Measure ID` for the `Measure report` template, and `Contact ID` for the `Contact` template.
- **Drop-down and conditional drop-down menus (green):** These fields have a drop-down menu which contain the values that you can either select **or** type in. In conditional drop-down menus, the values depend on what you entered in a previous field.

## 1) How to use templates

- **Date fields (purple):** Dates are entered in these fields and must be in the form of the [ISO 8601](#) format: yyyy-mm-dd. All date 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.



The screenshot shows the Microsoft Excel ribbon with the 'Formulas' tab selected. Below the ribbon, there is a toolbar with various function icons. On the far right of the ribbon, under the 'Calculation' group, there are two buttons: 'Calculate Workbook' and 'Calculate Sheet'. The 'Calculate Sheet' button is highlighted with a red box. Below the ribbon, there is a small preview of a worksheet with columns labeled O, P, Q, R, S. The first row contains headers: Class, Measure, Value, Unit, and Aggregation. The second row contains data: Flow. The formula bar at the top shows 'U11' and an fx icon.

## *How to use the ODM*

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** (or **measures** Excel tab) and **Measure set report** (or **measureSets** tab) templates. In the **Measure report** 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** and **Measure set report** 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 template**

#### **1. Mandatory fields**

## *Quick Start*

- **Report ID:** Unique identifier for the **Measure report** 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.
- **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”).
- **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.

### 2. Examples

*Image will be added*

## **Measure Sets Template**

### 1. Mandatory fields

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

### 3. Examples

*Image will be added.*

*How to use the ODM*

## Detailed description

### Measures template

#### 1. Columns A to H

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

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

- These are identifier fields.
- Report ID (column A) is the unique identifier for this template, and it cannot be repeated. You can think of each Report ID as representing a unique measure. The field can be any combination of letters or words up to 30 characters.
- You can repeat the other fields between entries (if needed). For instance, if you enter two different measures from the same sample, then the Sample ID (column C) will be the same.
- You may have already created these identifiers in another template. For instance, you may have created Sample ID in the Sample report template.

##### ii) Column D

- Purpose has a drop-down menu. If you are unsure what to put, select Regular.

#### 2. Columns I to M

## Detailed description

	I	J	K	L	M
1	Analysis date start	Analysis date end	Report Date	Specimen	Fraction analyzed
2					
3					

i) Columns I to K

- These are date fields where you can enter the dates associated with your measure in the format yyyy-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

ii) Columns L and M

- **Specimen** and **Fraction analyzed** have drop-down menus. In general both fields are optional, but both are recommended (see next point for the exception).
- **Specimen** is mandatory when the data you are entering has more than one type of specimen. When there is only one specimen, the **Dataset** table records the specimen type. For example, if your **Measure report** table includes only wastewater sample measures, you can indicate this information in the **Dataset** table.
- **Fraction analyzed** applies only for water and wastewater samples. You should record the fraction for all samples if the compartment type is water or wastewater.

### 3. Columns N to S

	N	O	P	Q	R	S
1	Group	Class	Measure	Value	Unit	Aggregation
2						
3						

i) Columns N and O

## How to use the ODM

- **Group** and **Class** help organize the **Measure** field by making specific measures easier to find (see the example in the next section). Both fields have a drop-down menu and are optional.
- Leave these fields **blank** if you do not use them.

### ii) Column P

- **Measure** is where you select what is being measured. A measure in ODM is a “measurement or observation of any substance including a biological, physical or chemical substance”.
- **Measure** has a conditional drop-down menu. If you chose to enter in a **Class** (column O), the drop down menu will contain the **Measures** found in that **Class**. As mentioned, you can also enter a value into **Group** to help organize everything. If you did not enter a value in column O, the menu will contain all possible measures.
- For example, to find the allele measures for SARS-CoV-2 you can start by selecting SARS-CoV-2 in the **Group** column. Next, you select **Alleles** in the **Class** field. Then, in the drop-down menu of the **Measure** field, you will see all the possible measures that contain SARS-CoV-2 allele regions.

	N	O	P	Q
1	Group	Class	Measure	Value
2	SARS-CoV-2	Alleles	BRSV-N	
3			SARS-CoV-2-E	
4			SARS-CoV-2-N1	
5			SARS-CoV-2-N2	
6			SARS-CoV-2-N3	
7			SARS-CoV-2-RdRp	
8			crAssphage-N	
9			PMMoV-CP	
10				
11				

### *Detailed description*

#### iii) Column Q

- **Value** is where you enter the value of your measure. For instance, if you recorded an **Environmental temperature** of 20 °C, you would enter “20”.
- Note: While the value you enter into this field can be of any data type, each measure is associated with a specific one. Data types for each measure can be found in the reference documentation. For example, the data type for **Environmental temperature** can be found [here](#).

#### iv) Column R

- **Unit** is where you enter the unit of your measure. This is a conditional drop-down menu field that lists all units that are valid for what was entered in the **Measure** field. For example, if selected **Environmental temperature** in the **Measure** field, the only unit displayed is **Celsius**.

#### v) Column S

- **Aggregations** is where you enter the aggregation of your value using a drop-down menu. For instance, does your value represent a mean, median, etc.
- What appears in this menu list depends on what you entered in the **Unit** field (column R).

## 4. Columns T to AB

	T	U	V	W	X	Y	Z	AA	AB
1	Nomenclature	Index	Measure license	Reportable	Organization ID	Contact ID	Reference link	Last edited	Notes
2									
3									

#### i) Columns U, V, Z and AB

- These are free-form fields.
- **Index** (column U) is used if you have multiple entries with the same values in most of the other fields; an example is when you make replicates of measures. If this is the case

## *How to use the ODM*

you can enter “1”, “2”, etc. in this field to differentiate them.

- **Measure license** (column V) refers to the access and use licensing of the measure that you are entering.

### ii) Column T and W

- These are fields which contain drop-down menus.
- **Reportable** (column W) is where you can indicate if the measure should not be used for regular reporting due to quality concerns. You can record more details of the quality concerns in the **Quality reports** template.

### iii) Column X and Y

- These are identifier fields that are used to indicate the organization and contact person associated with the entry.

### iv) Column AA

- **Last edited** is where you can indicate the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the entry was entered with no updates.

## **Measure set report template**

### 1. Columns A to G

	A	B	C	D	E
1	Report set ID	Protocol ID	Name	Organization ID	Contact ID
2					
3					

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

- These are identifier fields.

### *3) How to report samples and sample relationships:*

- Report Set ID (column A) is the unique identifier for this template, and cannot be repeated between entries. In essence, each value of Report set ID represents a unique measure set. This field can be any combination of letters or words up to 30 characters.
- For the rest, you can repeat the identifier between entries (if needed). For instance, if you are entering two different measure sets that came from the same organization, then the Organization ID (column D) will be the same.
- You may have already created these identifiers in another template. For instance you may have created Organization ID in the Organization template.

#### Columns C and G

- These are free form fields in which you can enter the indicated information. Name (column C) refers to the name that you have given to the measure set.

#### ii) Column F

- Last edited is a date field in which you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the entry was entered with no updates.

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

## *How to use the ODM*

`report` (or `samples` tab) template, each entry represents a sample. A sample is the wastewater that you collected so that measures can be made. Along the same lines, each entry in the `Sample relationships` (`orSampleRelationships`) 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.

## *Quick Start*

- **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

*Image will be added*

## **Sample Relationships Template**

### 1. Mandatory fields

- **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.
- **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

*Image will be added*

## Detailed Description

### Sample report template

#### 1. Columns A to G

	A	B	C	D	E	F	G
1	Sample ID	Protocol ID	Organization ID	Contact ID	Site ID	Purpose	Sample material
2							
3							

##### i) Columns A to E:

- These are identifier fields.
- Sample ID (column A) is the unique identifier for this template and cannot be repeated between entries. You can think of each Sample ID value as representing a unique sample. This field can be any combination of letters or words up to 30 characters.
- For the rest of the fields, you can repeat values between entries. For instance, if you are entering two different samples from the same site, then the Site ID (column E) will be the same.
- You may have already created these identifiers in another template. For instance you may have created Site ID in the Sites template.

##### ii) Columns F to G:

- These are fields that contain drop-down menus where you can enter information regarding the Purpose (column F) and Sample material (column G) of your sample.

## Detailed Description

### 2. Columns H to O

	H	I	J	K	L	M	N	O
1	Dataset ID	Sample origin	Replicate Type	Sample collection type	Collection period	Collection number	Collection number and period	Pooled
2								
3								

i) Columns H:

- **Dataset ID** is an identifier field for the dataset that your sample is associated with.

ii) Columns I to K, O:

- These fields contain drop-down menus and are related to various characteristics of your sample.
- **Sample collection type** (column K) refers to the collection technique you used to obtain the sample.
- **Pooled** (column O) refers to whether or not the sample that you are entering is made up of multiple child samples.

iii) Columns L to N:

- These are free form fields.
- **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 create Sample that you are entering.
- **Collection number and period** (column N) is a combination of the previous two fields.

### 3. Columns P to W

	P	Q	R	S	T	U	V	W
1	Collection date time	Collection date time start	Collection date time end	Date sample was sent	Date sample received	Reportable	Last edited	Notes
2								
3								

i) Columns P to T, V:

## *How to use the ODM*

- These are date fields that are related to your sample. These dates will be in the format yyyy-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.
- **Last edited** is where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the entry was entered with no updates.

### ii) Column U and W:

- **Reportable** (column U) is a drop-down menu field where you can indicate if the sample should not be used for regular reporting due to quality concerns. You can record more details of the quality concerns in the **Quality reports** table.
- **Notes** (column W) is a free form field where you can indicate anything of interest.

## **Sample relationships template**

### 1. Columns A to E

	A	B	C	D	E
1	Sample ID Subject	Relationship	Sample ID Object	Last Edited	Notes
2					
3					

### i) Columns A and C:

- These are identifier fields.

#### *4) How to record a protocol*

- Both of these identifiers are **Sample ID** values and represent samples. You would have created them previously in the **Sample report** template. Neither of them are unique identifiers and, thus, can be repeated between entries.

##### ii) Columns B:

- **Relationship** is a drop-down menu field where you can select the type of relationship between two samples. For instance, if Sample B was a child of Sample A, you would put the **Sample ID** of Sample A in the **Sample ID subject** field (column A), and the **Sample ID** of Sample B in **Sample ID object** field (column C). Then you would chose **Child relationship** from the menu in this column.

##### iii) Columns D and E:

- These are a date field (column D) and a free form field (column E) where you can enter in the indicated information.
- **Last edited** (column D) is where you can enter in the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the entry was entered with no updates.

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** (or **protocols**) template represents a unique protocol. A protocol is made up of protocol steps. In the **Protocol steps** (or

## *How to use the ODM*

`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.

## *Quick Start*

- **Aggregation:** Statistical measures used to report a measure (for example, “mean”). 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.

### 2. Examples

*Image will be added*

## **Protocols template**

### 1. Mandatory fields

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

### 2. Examples

*Image will be added*

## **Protocol relationships template**

### 1. Mandatory fields

- **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.
- **Relationship:** Describes the relationship between the subject and object.

## *How to use the ODM*

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

## **2. Examples**

*Image will be added*

## **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							

##### i) Column A and E:

- These are identifier fields.

### *Detailed Description*

- **Protocol step ID** (column A) is the unique identifier field for this template and cannot be repeated between entries. You can think of each **Protocol Step ID** value as representing a unique protocol step. This field can be any combination of letters or words up to 30 characters.
- **Protocol step source** (column E) specifies the protocol step that you used as a basis for the given protocol step (it will be a previous **Protocol step ID**).

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). The former is for when you are entering a method as a protocol step. The latter is when you are entering a measure as a protocol step. Leave the other field **blank**.

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 entering.
- **Protocol step version** (column F) specifies the version of a given protocol step.

## 2. Columns H to O

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

i) Columns H to J:

- These are identifier fields.
- You can repeat values between entries. For instance, if you are entering two different protocol steps from the same organization, then the **Organization ID** field (column H) will be the same.

## *How to use the ODM*

### ii) Column K:

- **Value** is a free form field where, if the protocol step is a measure, you can enter its value.

### 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 only applicable if the protocol step is a measure.
- **Aggregation** (column M) depends on what you entered in **Unit** (column L). This field is only applicable if the protocol step is a measure.

### iv) Columns N and O:

- These are a date field (column N) and a free form field (column O) where you can enter in the indicated information.
- **Last edited** (column N) is where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates. This date will be in the format yyyy-mm-dd. Including hours and minutes is optional, but all date-entries use the ISO 8601 format. 2022-01-01T06:11:54 or 2022-01-01T06:11:54+13:30.

## **Protocols template**

### 1. Columns A to F

	A	B	C	D	E	F
<b>Source</b>						
1	Protocol ID	Protocol ID	Dataset ID	Name	Summary	Reference link
2						
3						

### *Detailed Description*

#### i) Columns A to C:

- These are identifier fields.
- **Protocol ID** (column B) is the unique identifier for this template, and cannot be repeated between entries. In essence, each value of **Protocol ID** represents a unique protocol. This field can be any combination of letters or words up to 30 characters.
- For **Dataset ID**(column C), you can repeat between entries (if needed). For instance, if you are entering two different protocols from the same dataset, then the **Dataset ID** will be the same.
- You may have already created the **Dataset ID** values in the **Dataset** template.
- **Source Protocol ID** (column A) is where you can enter the **Protocol ID** of the protocol that served as the basis for the protocol that is currently being entered.

#### ii) Columns D to F:

- 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.

## 2. Columns G to K

G	H	I	J	K
Organization ID	Contact ID	Protocol Version	Last Edited	Notes

#### i) Columns G, H:

- These are identifier fields. You can repeat values between entries.

## *How to use the ODM*

### ii) Columns I, K:

- These are free form fields.
- **Protocol version** (column I) is where you can indicate the version of the protocol that you are entering.

### iii) Columns J:

- **Last edited** is a date field where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

## **Protocol relationships template**

### 1. Columns A to H

	A	B	C	D	E	F	G	H
1	Protocol ID Container	Protocol ID Object	Step ID Object	Relationship	Protocol ID Subject	Step ID Subject	Last Edited	Notes
2								
3								

### i) Columns A to C, E and F:

- These are identifier fields.
- All of these identifiers are either **Protocol ID** values or **Protocol Step ID** values, and represent protocols and protocol steps, respectively. This includes **Protocol ID Container** (column A), which is a **Protocol ID** that contains the relationships that you are entering in this template. Note that none of these fields are unique identifiers and, thus, they can be repeated between entries.
- You should only enter a value for one of the two **object** columns (column B and C); this depends on whether the object of the relationship that you are entering is a protocol

## *5) How to report metadata*

or a protocol step. The same is true for the two **subject** columns (column E and F).

- An example will be given in point (ii) below.

### ii) Columns D:

- **Relationship** contains a drop-down menu; it is where you can select the type of relationship that is being entered.
- For example, pretend you wanted to enter a relationship stating that Protocol step A takes place before Protocol step B in a particular protocol container. You would enter the relevant identifiers in the **Step ID Object** field (column B) and the **Step ID subject** field (column F). You would then select **Is Before** from the **Relationship** field. Finally, to identify this relationship, you would enter in the identifier in the **Protocol ID Container** field (column A)

### iii) Columns G and H:

- These are a date field (column G) and a free form field (column H) where you can enter in the indicated information.
- **Last edited** (column G) is where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

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

## **5) How to report metadata**

In this guide you will learn how to enter in the metadata of your wastewater data through a series of templates. Each entry in a template will usually represents what is found in the title of the template. For instance, in

## *How to use the ODM*

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.

### **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

*Images will be added*

## 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

*Images will be added*

## 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.

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## 2. Examples

*Images will be added*

### **Instrument (or instruments) Template**

#### 1. Mandatory fields

- **Instrument ID:** The unique identifier for the **Instrument** template. Each value represents an instrument.
- **Dataset ID:** The identifier of the dataset that stores information for measures, samples and other reporting tables.
- **Model:** Model number or version of the instrument.
- **Instrument type:** The type of instrument used to perform the measurement.

#### 2. Examples

*Images will be added*

### **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

*Images will be added*

## **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**

*Images will be added*

## **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.
- **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.
- **Report set 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**

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*Images will be added*

## **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**

*Images will be added*

## **Detailed Description**

### **Address template**

### **1. Columns A to E**

### *Detailed Description*

	A	B	C	D	E
1	<b>Address ID</b>	<b>Dataset ID</b>	<b>Address Line 1</b>	<b>Address Line 2</b>	<b>City</b>
2					
3					

i) Columns A and B:

- These are identifier fields.
- **Address ID** (column A) is the unique identifier for this template, and cannot be repeated between entries. You can think of each **Address ID** value as representing a unique address. This field can be any combination of letters or words up to 30 characters.
- For **Dataset ID** (column B), you can repeat the value between entries (if needed). For instance, if you are entering two different addresses from the same dataset, then this column will be the same.
- You may have already created the **Dataset ID** in the **Dataset** template.

ii) Columns C to E:

- These are free form fields in which you can enter various information about the address.

## 2. Columns F to J

	F	G	H	I	J
1	<b>State, Province, or Region</b>	<b>Postal or Zip Code</b>	<b>Country</b>	<b>Last Edited</b>	<b>Notes</b>
2					
3					

## *How to use the ODM*

### i) Columns F to J:

- Most of these are free form fields where you can enter the indicated information about the address.
- **Last edited** (column I) is a date field where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

This date will be in the format yyyy-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.

## **Contact template**

### 1. Columns A to E

	A	B	C	D	E
1	Contact ID	Dataset ID	Organization ID	First name of contact	Last Name of Contact
2					
3					

### i) Columns A to C:

- These are identifier fields.
- **Contact ID** (column A) is the unique identifier for this template, and cannot be repeated between entries. You can think of each **Contact ID** value as representing a unique contact person. This field can be any combination of letters or words up to 30 characters.

### *Detailed Description*

- For the rest of the fields, you can repeat the values between entries (if needed). For instance, if you are entering two different contacts that came from the same organization, then the **Organization ID** (column C) will be the same.
- You may have already created these Identifiers in another template. For instance you may have created **Organization ID** in the **Organization** template.

#### ii) Columns D and E:

- These are free form fields in which you can enter the name of the contact.

## 2. Columns F to J

	F	G	H	I	J
1	Contact email	Contact phone	Role of Contact	Last Edited	Notes
2					
3					

#### i) Columns F to J:

- Most of these fields are free form in which you can enter various information regarding the contact.
- **Last Edited** (column I) is a date field where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

## *How to use the ODM*

### **Dataset template**

#### **1. Columns A to G**

	A	B	C	D	E	F	G
	Parent	Dataset					Reference
1	Dataset ID	Dataset ID	Creation Date	Name	License	Description	link
2							
3							

##### i) Columns A and B:

- These are identifier fields.
- **Dataset ID** (column B) is the unique identifier for this template, and cannot be repeated between entries. You can think of each value of **Dataset ID** as representing a unique dataset. This field can be any combination of letters or words up to 30 characters.
- For **Parent dataset ID** (column A), you can repeat the value between entries (if needed). For instance, if you are entering two different datasets that came from the same parent dataset, then the **Parent dataset ID** will be the same.

##### ii) Column C

- **Dataset creation date** is a date field where you can enter the date that the dataset was created.

##### iii) Columns D to G:

- These are free form fields in which you can enter various information related to the dataset.

#### **2. Columns H to N**

*Detailed Description*

	H	I	J	K	L	M	N
1	Funder	Custody	Funding	Data			
2	Language ID	Contact ID	Contact ID	agency ID	custodian ID	Last edited	Notes
3							

i) Columns H to L:

- These are identifier fields.
- For information regarding funders, you can enter their **Funder Contact ID** (which is a **Contact ID** created in the **Contact template**) and **Funding Agency** (which is a **Organization ID** created in the **Organization template**) in columns I and K.
- For information regarding Data Custodians, you can enter their **Custody Contact ID** (which is a **Contact ID** created in the **Contact template**) and **Data Custodian ID** (which is a **Organization ID** created in the **Organization template**) in columns J and L.

ii) Columns M and N:

- These are a date field (column M) and a free form field (column N) where you can enter in the indicated information.
- **Last edited** (column M) is the date when the entry was updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

## Instrument template

### 1. Columns A to G

## How to use the ODM

	A	B	C	D	E	F	G
1	Instrument ID	Dataset ID	Name	Model	Manufacturer	Contact ID	Organization ID
2							
3							

### i) Columns A, B, F and G:

- These are identifier fields.
- **Instrument ID** (column A) is the unique identifier for this template, and cannot be repeated between entries. In essence, you can think of each **Instrument ID** value as representing a unique instrument. This field can be any combination of letters or words up to 30 characters.
- For the rest of the columns, you can repeat the value between entries (if needed). For instance, if you are entering two different instruments from the same dataset, then **Dataset ID** column will be the same.
- You may have already created some of the identifiers in other templates. For instance, you may have already created **Dataset ID** in the **Datasets** template.

### ii) Columns C to E

- These are free form fields where you can enter the **Name** (column C), **Model** (column D) and **Manufacturer** (column E) of the instrument.

## 2. Columns H to N

	H	I	J	K	L	M	N
1	Description	Reference link	Instrument Type	Describe other instrument type, if applicable	Index	Last Edited	Notes
2							
3							

### i) Columns H, I, L to N:

- Most of these fields are free form in which you can enter relevant information regarding your instrument

### *Detailed Description*

- You can use **Index** (column L) to differentiate two entries of data that are the same in the other fields.
- **Last Edited** (column M) is a date field where you can indicate the date when the entry was updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

#### ii) Columns J and K:

- For **Instrument type** (column J), you can select from the drop-down menu the type of instrument. If you do not see your instrument, you can enter **Other instrument**.
- If you entered **Other instrument** in the **Instrument type** field, you can use the **Describe other instrument type, if applicable** field (column K) to describe your instrument.

## **Organization template**

### 1. Columns A to E

	A	B	C	D	E
1	Organization ID	Name	Description	Dataset ID	Address ID
2					
3					

#### i) Columns A, D and E:

- These are identifier fields.
- **Organization ID** (column A) is the unique identifier for this template, and cannot be repeated between entries. You can think of each value of **Orgnization ID** as representing a unique organization. This field can be any combination of letters or words up to 30 characters.

## *How to use the ODM*

- For the rest of the columns, you can repeat the value between entries (if needed). For instance, if you are entering two different organizations with the same address, then the **Address ID** will be the same.
- You may have already created some of the identifiers in other templates. For instance, you may have already created the **Address ID** in the **Address** template.
  - ii) Columns B and C:
    - These columns are free form fields in which you can enter additional information regarding the organization.

### **2. Columns F to J**

F	G	H	I	J
Organization type	Organization level	Organization sector	Last edited	Notes

- i) Columns F to H:
  - These are fields with drop-down menus where you can select various characteristics of the organization that you are entering.
- ii) Columns I and J:
  - These are a date field (column I) and a free form field (column J) where you can enter in the indicated information.
  - **Last edited** (column I) is the date when the entry was updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

## **Polygon template**

### **1. Columns A to G**

### *Detailed Description*

	A	B	C	D	E	F	G
1	Polygon ID	Dataset ID	Name	Description	Polygon Population	Type of geography	European Petroleum Survey Group Coordinates
2							
3							

i) Columns A and B:

- These are identifier fields.
- **Polygon ID** (column A) is the unique identifier for this template, and cannot be repeated between entries. A polygon is something that describes the geometry of a geographic area. You can think of each value of **Polygon ID** as representing a unique polygon. This field can be any combination of letters or words up to 30 characters.
- For **Dataset ID** (column B), you can repeat the value between entries (if needed). For instance, if you are entering two different polygons from the same dataset, then this column will have the same value.
- You may have already created the **Dataset ID** in the **Dataset** template.

ii) Columns C to E, G:

- These are free form fields in which you can enter additional information regarding the Polygon.
- **Name** (column C) is the name of the polygon.
- **European Petroleum Survey Group Coordinates** (column G) is a coordinate system that can be used to identify where a polygon is.

iii) Columns F:

- For **Type of geography** (column F) of the polygon, you can select one of the values from the drop-down menu.

## 2. Columns H to N

## How to use the ODM

H	I	J	K	L	M	N
Well-known text	File Location	Reference link	Organization ID	Contact ID	Last Edited	Notes
1						
2						
3						

### i) Columns H to J, M and N:

- These are free form fields and a date field in which you can enter relevant information regarding the polygon.
- **Well-known text** (column H) refers to the text markup language that can be used to represent the polygon.
- **Last edited** (column M) is a date field where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

### ii) Columns K and L:

- These are identifier fields in which the **Organization ID** and the **Contact ID** associated with the polygon are entered.

## Quality reports template

### 1. Columns A to H

A	B	C	D	E	F	G	H
Quality Report ID	Report ID	Sample ID	Report Set ID	Quality Flag	Severity Indicator	Last Edited	Notes
1							
2							
3							

### 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 between entries. You

### *Detailed Description*

can think of each value of **Quality Report ID** as representing a unique quality issue that you want to report. This field can be any combination of letters or words up to 30 characters.

- For the rest of the columns, you can repeat the value between entries (if needed). For instance, if you are entering two different quality reports for the same sample, then the **Sample ID** column will be the same.
- You may have already created some of the identifiers in other templates. For instance, you may have already created the **Sample ID** in the **Sample report** template.

ii) Columns E and F:

- **Quality flag** (column E) is a drop-down menu field where you can select the type of quality issue that you would like to enter.
- **Severity indicator** (column F) is also a drop-down menu field where you can indicate the severity of the quality flag.

iii) Columns G and H:

- These are a free form field and a date field in which you can enter the indicated information.
- **Last edited** (column M) is a date field where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

## **Sites template**

### **1. Columns A to F**

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	A	B	C	D	E	F
1	Parent Site ID	Site ID	Dataset ID	Polygon ID	Site Type	Sample shed
2						
3						

### i) Columns A to D:

- These are identifier fields.
- **Site ID** (column B) is the unique identifier for this template, and cannot be repeated between entries. You can think of each value of **Site ID** as representing a unique site. This field can be any combination of letters or words up to 30 characters.
- For the rest of the columns, you can repeat the value between entries (if needed). For instance, if you are entering two different sites that are found in the same polygon, then the **Polygon ID** values will be the same.
- **Parent site ID** (column A) refers to the site that is parent to the site that is being entered. For example if the site that is being entered is a room in a facility, then the **Parent site ID** would refer to the facility.

### ii) Columns E and F:

- These are drop-down menu fields in which you can specify the **Site Type** (column E) and the type of **Sample shed** (column F).

## 2. Columns G to M

	G	H	I	J	K	L	M
1	Address ID	Organization ID	Contact ID	Name	Description	Primary reporting authority ID	Secondary reporting authority ID
2							
3							

### i) Columns G to I, L and M:

### *Detailed Description*

- These are identifier fields that you can use to record additional information about the site. Primary reporting authority ID (column L) and Secondary reporting authority ID (column M) are Organization IDs that you would have created using the Organization template.

#### ii) Columns J and K:

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

### 3. Columns N to S

	N	O	P	Q	R	S
1	Population Served	Latitude	Longitude	European Petroleum Survey Group Coordinates	Last Edited	Notes
2						
3						

#### i) Columns N to S:

- These are free form fields and a date field where you can enter in additional information about the Site.
- European Petroleum Survey Group Coordinates (column Q) is a coordinate system that can be used to identify where your site is.
- Last Edited (column S) is a date field where you can enter the date when the entry was last updated. This field is used when you modify an entry after your initial recording. Leave this field blank if the measure was entered with no updates.

You have now entered in your metadata, congratulations!

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## Notes regarding templates

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

#### Adding more conditional menus

- The code to determine the entries for the conditional menus are found to the right of the main template. Unlike the main template, the rows containing the code will not be alternating in colour.
- The code is only present for the first three rows. If you want to use conditional menus for additional rows, you will need to copy the code to these rows as well as create the menus in the desired cells. As an example, pretend that you wanted to add a **Measure** field conditional menu to row 5 in the **Measure report** template. The first thing you would do is copy the code from AF4 to AF5 (see below, all images in this example are from Excel Online).

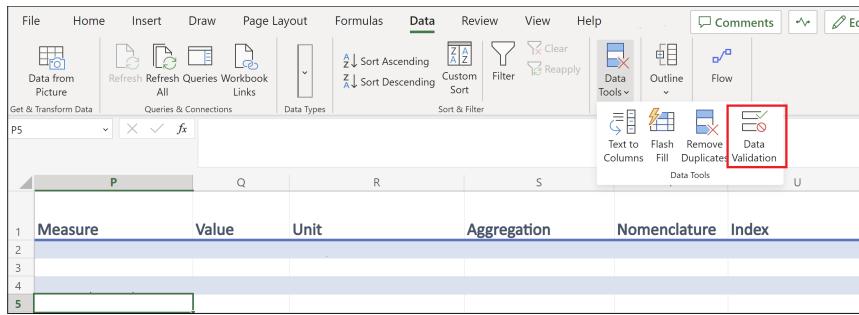
The screenshot shows a Microsoft Excel Online interface. The formula bar at the top contains the formula: =TRANSPOSE(IF(O4=" ",FILTER(label,(partType="measure")+(partType="missingness")),FILTER(FILTER(label,(parts!AE:AE="Input")\*(partType="measure")\*(parts!G:G<>"NA")),(FILTER(parts!K:K,(parts!AE:AE="Input")\*(partType="measure")\*(parts!G:G<>"NA"))=FILTER(parts!K:K,(label=O4)\*(parts!C:C="class")))))

The table below has columns AE, AF, AG, IF, IG, KF, KG, MF, MG. Row 1 contains the text "Conditional menus -> measureID menu unitID menu aggregationID menu". Rows 2, 3, and 4 are empty. Row 5 is also empty. The cell AF4 is selected.

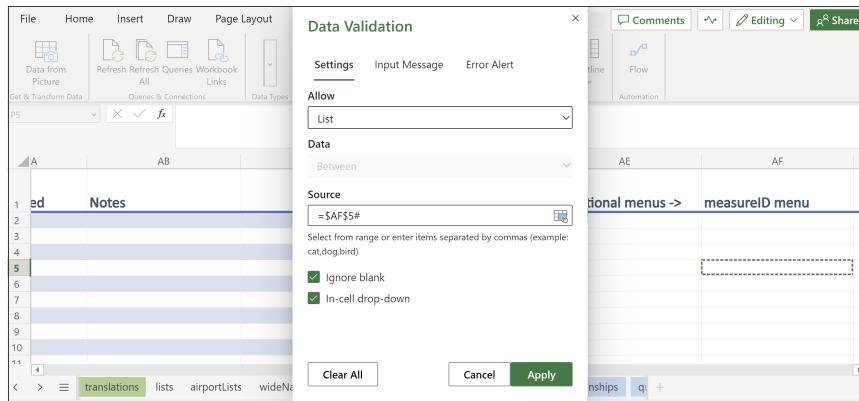
AE	AF	AG	IF	IG	KF	KG	MF	MG
1	Conditional menus ->	measureID menu	unitID menu	aggregationID menu				
2								
3								
4								
5								

- 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).

## Notes regarding templates



- 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

New names:

```
* `` -> `...108`  
* `` -> `...109`  
* `` -> `...110`  
* `` -> `...111`  
* `` -> `...112`  
* `` -> `...113`  
* `` -> `...114`  
* `` -> `...115`  
* `` -> `...116`  
* `` -> `...117`  
* `` -> `...118`  
* `` -> `...119`  
* `` -> `...120`  
* `` -> `...121`  
* `` -> `...122`  
* `` -> `...123`  
* `` -> `...124`  
* `` -> `...125`  
* `` -> `...126`  
* `` -> `...127`  
* `` -> `...128`  
* `` -> `...129`  
* `` -> `...130`  
* `` -> `...131`  
* `` -> `...132`
```

*Sample Relationships*

\* `` -> `...133`  
\* `` -> `...134`  
\* `` -> `...135`  
\* `` -> `...136`  
\* `` -> `...137`  
\* `` -> `...138`  
\* `` -> `...139`  
\* `` -> `...140`  
\* `` -> `...141`  
\* `` -> `...142`  
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\* `` -> `...163`  
\* `` -> `...164`  
\* `` -> `...165`  
\* `` -> `...166`

*Sample Relationships*

```
* `` -> `...167`  
* `` -> `...168`  
* `` -> `...169`  
* `` -> `...170`  
* `` -> `...171`  
* `` -> `...172`  
* `` -> `...173`  
* `` -> `...174`  
* `` -> `...175`  
* `` -> `...176`  
* `` -> `...177`  
* `` -> `...178`  
* `` -> `...179`  
* `` -> `...180`  
* `` -> `...181`  
* `` -> `...182`  
* `` -> `...183`  
* `` -> `...184`  
* `` -> `...185`  
* `` -> `...186`  
* `` -> `...187`  
* `` -> `...188`  
* `` -> `...189`  
* `` -> `...190`  
* `` -> `...191`  
* `` -> `...192`  
* `` -> `...193`  
* `` -> `...194`  
* `` -> `...195`  
* `` -> `...196`  
* `` -> `...197`  
* `` -> `...198`  
* `` -> `...199`  
* `` -> `...200`
```

### *Sample Relationships*

```
* `` -> `...201`  
* `` -> `...202`  
* `` -> `...203`  
* `` -> `...204`  
* `` -> `...205`  
* `` -> `...206`  
* `` -> `...207`  
* `` -> `...208`  
* `` -> `...209`  
* `` -> `...210`  
* `` -> `...211`  
* `` -> `...212`  
* `` -> `...213`  
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* `` -> `...223`  
* `` -> `...224`  
* `` -> `...225`  
* `` -> `...226`  
* `` -> `...227`  
* `` -> `...228`  
* `` -> `...229`  
* `` -> `...230`  
* `` -> `...231`  
* `` -> `...232`  
* `` -> `...233`  
* `` -> `...234`
```

*Sample Relationships*

```
* `` -> `...235`  
* `` -> `...236`  
* `` -> `...237`  
* `` -> `...238`  
* `` -> `...239`  
* `` -> `...240`  
* `` -> `...241`  
* `` -> `...242`  
* `` -> `...243`  
* `` -> `...244`  
* `` -> `...245`  
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* `` -> `...257`  
* `` -> `...258`  
* `` -> `...259`  
* `` -> `...260`  
* `` -> `...261`  
* `` -> `...262`  
* `` -> `...263`  
* `` -> `...264`  
* `` -> `...265`  
* `` -> `...266`  
* `` -> `...267`  
* `` -> `...268`
```

### *Sample Relationships*

\* `` -> `...269`  
\* `` -> `...270`  
\* `` -> `...271`  
\* `` -> `...272`  
\* `` -> `...273`  
\* `` -> `...274`  
\* `` -> `...275`  
\* `` -> `...276`  
\* `` -> `...277`  
\* `` -> `...278`  
\* `` -> `...279`  
\* `` -> `...280`  
\* `` -> `...281`  
\* `` -> `...282`  
\* `` -> `...283`  
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\* `` -> `...287`  
\* `` -> `...288`  
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\* `` -> `...290`  
\* `` -> `...291`  
\* `` -> `...292`  
\* `` -> `...293`  
\* `` -> `...294`  
\* `` -> `...295`  
\* `` -> `...296`  
\* `` -> `...297`  
\* `` -> `...298`  
\* `` -> `...299`  
\* `` -> `...300`  
\* `` -> `...301`  
\* `` -> `...302`

*Sample Relationships*

```
* `` -> `...303`  
* `` -> `...304`  
* `` -> `...305`  
* `` -> `...306`  
* `` -> `...307`  
* `` -> `...308`  
* `` -> `...309`  
* `` -> `...310`  
* `` -> `...311`  
* `` -> `...312`  
* `` -> `...313`  
* `` -> `...314`  
* `` -> `...315`  
* `` -> `...316`  
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* `` -> `...327`  
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* `` -> `...329`  
* `` -> `...330`  
* `` -> `...331`  
* `` -> `...332`  
* `` -> `...333`  
* `` -> `...334`  
* `` -> `...335`  
* `` -> `...336`
```

### *Sample Relationships*

```
* `` -> `...337`  
* `` -> `...338`  
* `` -> `...339`  
* `` -> `...340`  
* `` -> `...341`  
* `` -> `...342`  
* `` -> `...343`  
* `` -> `...344`  
* `` -> `...345`  
* `` -> `...346`  
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* `` -> `...360`  
* `` -> `...361`  
* `` -> `...362`  
* `` -> `...363`  
* `` -> `...364`  
* `` -> `...365`  
* `` -> `...366`  
* `` -> `...367`  
* `` -> `...368`  
* `` -> `...369`  
* `` -> `...370`
```

*Sample Relationships*

```
* `` -> `...371`  
* `` -> `...372`  
* `` -> `...373`  
* `` -> `...374`  
* `` -> `...375`  
* `` -> `...376`  
* `` -> `...377`  
* `` -> `...378`  
* `` -> `...379`  
* `` -> `...380`  
* `` -> `...381`  
* `` -> `...382`  
* `` -> `...383`  
* `` -> `...384`  
* `` -> `...385`  
* `` -> `...386`  
* `` -> `...387`  
* `` -> `...388`  
* `` -> `...389`  
* `` -> `...390`  
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* `` -> `...392`  
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* `` -> `...394`  
* `` -> `...395`  
* `` -> `...396`  
* `` -> `...397`  
* `` -> `...398`  
* `` -> `...399`  
* `` -> `...400`  
* `` -> `...401`  
* `` -> `...402`  
* `` -> `...403`  
* `` -> `...404`
```

## *Sample Relationships*

```
* `` -> `...405`  
* `` -> `...406`  
* `` -> `...407`  
* `` -> `...408`  
* `` -> `...409`  
* `` -> `...410`  
* `` -> `...411`  
* `` -> `...412`  
* `` -> `...413`  
* `` -> `...414`  
* `` -> `...415`  
* `` -> `...416`  
* `` -> `...417`  
* `` -> `...418`
```

Dictionary v3.0.0 Documentation v2.1.0

## **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 in the sampling strategy. When samples are composited from several subsamples, it is useful to know which subsamples were used and to what pooled samples they are related. 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
  1. A subsample is related to its parent sample
  2. A sample split at the sampling location yields field replicates who are related to each other.
  3. A field sample is related to a control sample processed alongside it.
  4. A field sample is related to a subsample that has been modified as part of a quality control procedure.
2. The combination of several samples
  1. Parent samples related to the final pooled sample

Example of sample relationship webs are found in Figure A.

## Sample Relationships

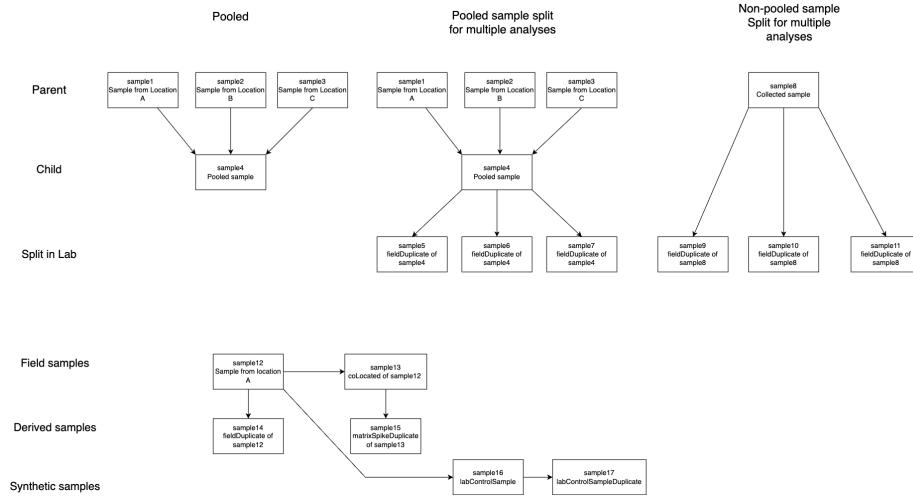


Figure 4.: Figure A: Various possible sample relationships.

Figure A: Various possible sample relationships.

Because a single sample can be related to many others, the sample information and the relationships to other samples can't be efficiently stored in a single database table.

## 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 three attributes:

1. sampleIDSubject
2. relationshipID
3. sampleIDObject

## *Implementation*

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:

- `child`
- `replicate`

To complete the picture presented by the `SampleRelationships` table, one can read the sample attributes 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)
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`.

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

*Sample Relationships*

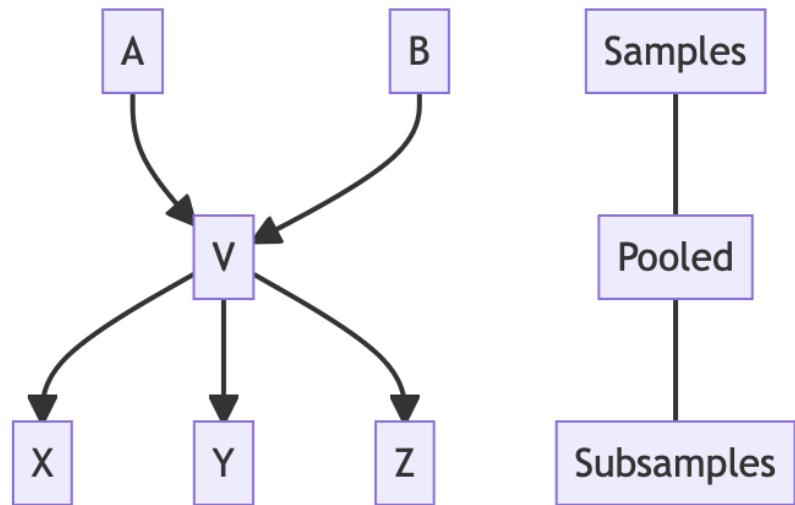


Figure 5.: Example A

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

*Implementation*

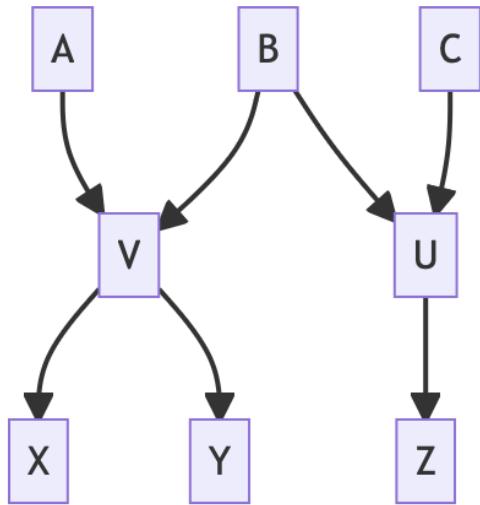


Figure 6.: Example B

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**

New names:

```
* `` -> `...108`  
* `` -> `...109`  
* `` -> `...110`  
* `` -> `...111`  
* `` -> `...112`  
* `` -> `...113`  
* `` -> `...114`  
* `` -> `...115`  
* `` -> `...116`  
* `` -> `...117`  
* `` -> `...118`  
* `` -> `...119`  
* `` -> `...120`  
* `` -> `...121`  
* `` -> `...122`  
* `` -> `...123`  
* `` -> `...124`  
* `` -> `...125`  
* `` -> `...126`  
* `` -> `...127`  
* `` -> `...128`  
* `` -> `...129`  
* `` -> `...130`
```

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

```
* `` -> `...131`  
* `` -> `...132`  
* `` -> `...133`  
* `` -> `...134`  
* `` -> `...135`  
* `` -> `...136`  
* `` -> `...137`  
* `` -> `...138`  
* `` -> `...139`  
* `` -> `...140`  
* `` -> `...141`  
* `` -> `...142`  
* `` -> `...143`  
* `` -> `...144`  
* `` -> `...145`  
* `` -> `...146`  
* `` -> `...147`  
* `` -> `...148`  
* `` -> `...149`  
* `` -> `...150`  
* `` -> `...151`  
* `` -> `...152`  
* `` -> `...153`  
* `` -> `...154`  
* `` -> `...155`  
* `` -> `...156`  
* `` -> `...157`  
* `` -> `...158`  
* `` -> `...159`  
* `` -> `...160`  
* `` -> `...161`  
* `` -> `...162`  
* `` -> `...163`  
* `` -> `...164`
```

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

```
* `` -> `...165`  
* `` -> `...166`  
* `` -> `...167`  
* `` -> `...168`  
* `` -> `...169`  
* `` -> `...170`  
* `` -> `...171`  
* `` -> `...172`  
* `` -> `...173`  
* `` -> `...174`  
* `` -> `...175`  
* `` -> `...176`  
* `` -> `...177`  
* `` -> `...178`  
* `` -> `...179`  
* `` -> `...180`  
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* `` -> `...183`  
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* `` -> `...187`  
* `` -> `...188`  
* `` -> `...189`  
* `` -> `...190`  
* `` -> `...191`  
* `` -> `...192`  
* `` -> `...193`  
* `` -> `...194`  
* `` -> `...195`  
* `` -> `...196`  
* `` -> `...197`  
* `` -> `...198`
```

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

```
* `` -> `...199`  
* `` -> `...200`  
* `` -> `...201`  
* `` -> `...202`  
* `` -> `...203`  
* `` -> `...204`  
* `` -> `...205`  
* `` -> `...206`  
* `` -> `...207`  
* `` -> `...208`  
* `` -> `...209`  
* `` -> `...210`  
* `` -> `...211`  
* `` -> `...212`  
* `` -> `...213`  
* `` -> `...214`  
* `` -> `...215`  
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* `` -> `...219`  
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* `` -> `...221`  
* `` -> `...222`  
* `` -> `...223`  
* `` -> `...224`  
* `` -> `...225`  
* `` -> `...226`  
* `` -> `...227`  
* `` -> `...228`  
* `` -> `...229`  
* `` -> `...230`  
* `` -> `...231`  
* `` -> `...232`
```

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

```
* `` -> `...233`  
* `` -> `...234`  
* `` -> `...235`  
* `` -> `...236`  
* `` -> `...237`  
* `` -> `...238`  
* `` -> `...239`  
* `` -> `...240`  
* `` -> `...241`  
* `` -> `...242`  
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* `` -> `...244`  
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* `` -> `...248`  
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* `` -> `...257`  
* `` -> `...258`  
* `` -> `...259`  
* `` -> `...260`  
* `` -> `...261`  
* `` -> `...262`  
* `` -> `...263`  
* `` -> `...264`  
* `` -> `...265`  
* `` -> `...266`
```

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

```
* `` -> `...267`  
* `` -> `...268`  
* `` -> `...269`  
* `` -> `...270`  
* `` -> `...271`  
* `` -> `...272`  
* `` -> `...273`  
* `` -> `...274`  
* `` -> `...275`  
* `` -> `...276`  
* `` -> `...277`  
* `` -> `...278`  
* `` -> `...279`  
* `` -> `...280`  
* `` -> `...281`  
* `` -> `...282`  
* `` -> `...283`  
* `` -> `...284`  
* `` -> `...285`  
* `` -> `...286`  
* `` -> `...287`  
* `` -> `...288`  
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* `` -> `...290`  
* `` -> `...291`  
* `` -> `...292`  
* `` -> `...293`  
* `` -> `...294`  
* `` -> `...295`  
* `` -> `...296`  
* `` -> `...297`  
* `` -> `...298`  
* `` -> `...299`  
* `` -> `...300`
```

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

```
* `` -> `...301`  
* `` -> `...302`  
* `` -> `...303`  
* `` -> `...304`  
* `` -> `...305`  
* `` -> `...306`  
* `` -> `...307`  
* `` -> `...308`  
* `` -> `...309`  
* `` -> `...310`  
* `` -> `...311`  
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* `` -> `...314`  
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* `` -> `...323`  
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* `` -> `...325`  
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* `` -> `...327`  
* `` -> `...328`  
* `` -> `...329`  
* `` -> `...330`  
* `` -> `...331`  
* `` -> `...332`  
* `` -> `...333`  
* `` -> `...334`
```

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

```
* `` -> `...335`  
* `` -> `...336`  
* `` -> `...337`  
* `` -> `...338`  
* `` -> `...339`  
* `` -> `...340`  
* `` -> `...341`  
* `` -> `...342`  
* `` -> `...343`  
* `` -> `...344`  
* `` -> `...345`  
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* `` -> `...362`  
* `` -> `...363`  
* `` -> `...364`  
* `` -> `...365`  
* `` -> `...366`  
* `` -> `...367`  
* `` -> `...368`
```

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

```
* `` -> `...369`  
* `` -> `...370`  
* `` -> `...371`  
* `` -> `...372`  
* `` -> `...373`  
* `` -> `...374`  
* `` -> `...375`  
* `` -> `...376`  
* `` -> `...377`  
* `` -> `...378`  
* `` -> `...379`  
* `` -> `...380`  
* `` -> `...381`  
* `` -> `...382`  
* `` -> `...383`  
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* `` -> `...391`  
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* `` -> `...393`  
* `` -> `...394`  
* `` -> `...395`  
* `` -> `...396`  
* `` -> `...397`  
* `` -> `...398`  
* `` -> `...399`  
* `` -> `...400`  
* `` -> `...401`  
* `` -> `...402`
```

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

```
* `` -> `...403`  
* `` -> `...404`  
* `` -> `...405`  
* `` -> `...406`  
* `` -> `...407`  
* `` -> `...408`  
* `` -> `...409`  
* `` -> `...410`  
* `` -> `...411`  
* `` -> `...412`  
* `` -> `...413`  
* `` -> `...414`  
* `` -> `...415`  
* `` -> `...416`  
* `` -> `...417`  
* `` -> `...418`
```

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## **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

### *Issues with moving between formats*

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

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

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

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

## **Issues with moving between formats**

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

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

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

## 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).

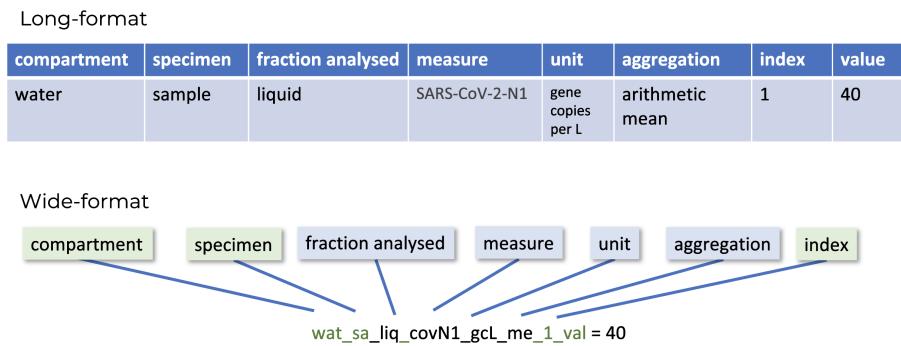


Figure 7.: **Figure 1 - Wide- and Long-names**

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	sitID	...
sas100x245	rawWW	ropec	...

Contacts Table

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

Wide-format

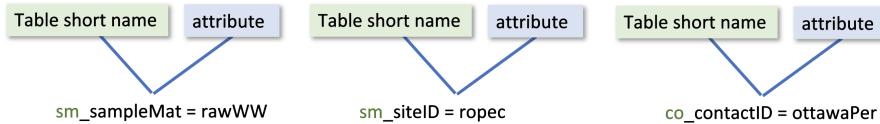


Figure 8.: **Figure 2 - Wide- to Long-format for Attributes**

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**

## Measures

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

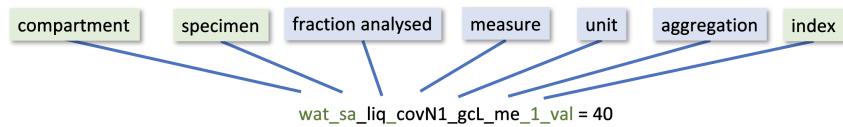


Figure 9.: **Figure 3 - Wide- to Long-format for Measures**

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`).

*Wide-names*

## 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`.

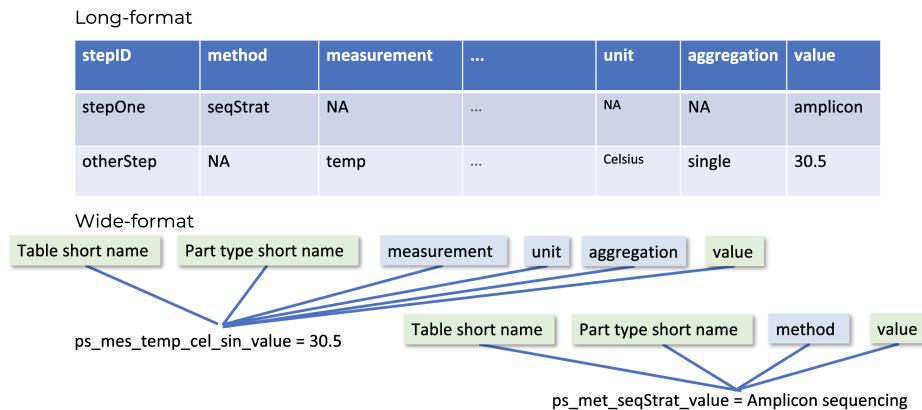


Figure 10.: **Figure 4 - Wide- to Long-format for protocol**

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- date	ment	spec- imen	frac- tion	mea- sure	value	unit	ag- gre- ga- tion	PM- MoV (unit- (gc/ML)ess)	pH
dec	wa-	sam-	liq-	covid	32.1	gc/mL	sin-	16.2	8.2	
17	ter	ple	uid	N1			gle			
dec	wa-	sam-	liq-	covid	34.6	gc/mL	sin-	19.6	7.9	
20	ter	ple	uid	N1			gle			

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

```
wat_sa_hFr_hMr_hUn_hAg_NR_value
```

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

mr_	mr_	mr_	mr_	mr_	hCo_hSp_	mr_	hCo_hSpFr_pH_
re-	com-	mr_	mr_	mr_	hFr_hMr_	ag-	hFr_pm-unit-
port	part-	speci-	frac-	mea-	hUn_hAg_mr_	gre-	mov less
Date	ment	men	tion	sure	NR_valuenit	ga-	_gcMl_sisin_NR_
dec	wa-	sam-	liq-	covid	32.1	NR_value	NR_value
17	ter	ple	uid	N1	gc/mIsin-	16.2	8.2
dec	wa-	sam-	liq-	covid	34.6	gle	
20	ter	ple	uid	N1	gc/mIsin-	19.6	7.9
					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)_mea` where all measures must share the same units and aggregation. For example, a column to measure the presence of “other” mutations, alleles, or variants uses the wide-name `wat_sa_liq_3_OR_otherM_otherA_otherV_gcM1_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.

*Tutorials*

measures		
PK	<b>measureRepID</b>	varchar
FK	protocolID	varchar
FK	<b>sampleID</b>	varchar
FK	purposeID	varchar
FK	polygonID	varchar
FK	<b>siteID</b>	varchar
FK	datasetID	varchar
FK	measureSetRepID	varchar
	aDateStart	datetime
	<b>aDateEnd</b>	datetime
	reportDate	datetime
FK	compartment	varchar
FK	<b>specimenID</b>	varchar
FK	fraction	varchar
FK	group	varchar
FK	class	varchar
FK	<b>measure</b>	varchar
	<b>value</b>	varchar
FK	<b>unit</b>	varchar
FK	<b>aggregation</b>	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	8.2	gc	single	NA
				omicron-variant				
				gene target				
dec 20	water	site	liquid	Flow rate	34.6	ML/dayarith.	NA	
dec 20	sur-face	sam-ple	NA	In-fluenza virus A1	19.6	gc/mL	single	NA

*Building a wide-format ODM table*

	com-						aggre-	
date	part-	speci-	frac-	measure	value	unit	ga-	index
	ment	men	tion				tion	
dec	water	sam-	liquid	pH	7.9	unit-	single	2
20		ple				less		

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:

	wat_sa_	wat_si_	liq_pH_			
mr_	wat_sa_	mix_pm_	air_sa_	liq_flo_	surf_sa_	unit-
report-	liq_mpox	mov	NA_s2083iRate	NA_fluA1less_		
Date	_gcml_sin_	_gcml_sin_gc_	_sin_NA	mld_me_	gcml_sin_	_sin_2_
	1_value	2_value	_value	NA_value	NA_value	value

dec 17	32.1	16.2	8.2	NA	NA	NA
dec 20	NA	NA	NA	34.6	19.6	7.9



# **How-To Guides**

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

## **Wide-name Templates**

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



# **Part I.**

# **Reference guide**



New names:

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## Dictionary v3.0.0 Documentation v2.1.0

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 900 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 21 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

New names:

```
* `` -> `...108`  
* `` -> `...109`  
* `` -> `...110`  
* `` -> `...111`  
* `` -> `...112`  
* `` -> `...113`  
* `` -> `...114`  
* `` -> `...115`  
* `` -> `...116`  
* `` -> `...117`  
* `` -> `...118`  
* `` -> `...119`  
* `` -> `...120`  
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* `` -> `...122`  
* `` -> `...123`  
* `` -> `...124`  
* `` -> `...125`  
* `` -> `...126`  
* `` -> `...127`  
* `` -> `...128`  
* `` -> `...129`  
* `` -> `...130`  
* `` -> `...131`  
* `` -> `...132`
```

*Parts*

\* `` -> `...133`  
\* `` -> `...134`  
\* `` -> `...135`  
\* `` -> `...136`  
\* `` -> `...137`  
\* `` -> `...138`  
\* `` -> `...139`  
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\* `` -> `...164`  
\* `` -> `...165`  
\* `` -> `...166`

*Parts*

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* `` -> `...167`  
* `` -> `...168`  
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* `` -> `...172`  
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* `` -> `...195`  
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* `` -> `...198`  
* `` -> `...199`  
* `` -> `...200`
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*Parts*

\* `` -> `...201`  
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*Parts*

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*Parts*

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*Parts*

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*Parts*

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\* `` -> `...376`  
\* `` -> `...377`  
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\* `` -> `...404`

## Parts

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* `` -> `...405`  
* `` -> `...406`  
* `` -> `...407`  
* `` -> `...408`  
* `` -> `...409`  
* `` -> `...410`  
* `` -> `...411`  
* `` -> `...412`  
* `` -> `...413`  
* `` -> `...414`  
* `` -> `...415`  
* `` -> `...416`  
* `` -> `...417`  
* `` -> `...418`
```

Dictionary v3.0.0 Documentation v2.1.0

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. The wide variable naming method will be added to the documentation.

## 16S Ribosomal Gene Sequencing

(16rgs). An amplicon sequencing assay in which the amplicon is derived from universal primers used to amplify the 16S ribosomal RNA gene from isolate bacterial genomic DNA or metagenomic DNA from a 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*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## a1306s delta-variant gene target

(a1306s). a1306s delta-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **a1918v delta-variant gene target**

(a1918v). a1918v delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **a2710t omicron-variant gene target**

(a2710t). a2710t omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **a63t omicron-variant gene target**

(a63t). a63t omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology*

## Parts

*Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### a67v omicron-variant gene target

(a67v). a67v omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Omicron Variant a67v del69 and del70 mutations

(a67vDel69Del70). Omicron Variant a67v mutation mutation, and del69 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.

## Parts

### **Atline Analyzer**

(aas). Atline analyzer with sampler. An atline analyzer with sampler.  
*Part Type*: categories *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.

### **ABRicate Software**

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

### **Absolute humidity**

(absHum). A measure of the total mass of water vapour present in the air per volume of air. *Part Type*: measurements *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: siteFeat *Class*: humid *Nomenclature*: humid *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: absHumidUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### Absolute humidity unit set

(absHumidUnitSet). Unit set for absolute 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:* 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.

### ABySS

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

### Accessions report table Shorthand

(ac). The abbreviated short name used to reference the report table for accessions and accessionIDs. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet

## 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: 2.2.2.

## Academic institution

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

## Accel-NGS 2S Plus DNA Library Kit

(accelNGS2Splus). Accel-NGS 2S Plus DNA Library Kit by Swift Bio-sciences. A library prep kit designed for efficient library prep from fragmented or damaged DNA. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* na-Group *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* 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.

## Accessions Index ID

(accessIndexID). Provisional ID to act as a primary key for each row of the accessions table. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: 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: 3.0.0.

## accessions Table

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

## Accessions table column order

(accessionsOrder). Specifies the order of the columns in the accessions table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## Parts

*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.

## Accessions table required headers

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

## Accession Number in Repository

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

## Acinetobacter

(acinetobacter). Acinetobacter *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

## Parts

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

## Acinetobacter Group

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

## Number of active cases

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

## *Parts*

### **Number of active cases by Onset date**

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

### **Number of active cases by episode date**

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

### **Public health action**

(action). The specific public health action or designation being taken or applied. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: allActionsSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness*

## Parts

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

### **Public health action datetime**

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

### **Public Health Action Group ID**

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

### **Public health action type**

(actionType). The type of public health action being taken. Sets out the category, with the detailed action being defined in ‘action’ field. *Part Type:* attributes *Domain: naDomain Speciment ID: naSpecimenSet Compartment*

## *Parts*

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

## **Public Health Action Type Value Set**

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

## **Number of active cases by Report date**

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

### **Number of active cases by test date**

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

### **Active**

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

### **Address table Shorthand**

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

## Parts

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

## AdapterRemoval

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

## Analysis date

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

## Analysis date end

(aDateEnd). Date the measurement or analysis was completed. *Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment*

## Parts

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

## Analysis date start

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

## Address Line 1

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

*Parts*

## **Address Line 2**

(addL2). Line 2 (the unit number) for a given address. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Address table**

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

## **Addresses table column order**

(addressesOrder). Specifies the order of the columns in the Addresses table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## Parts

*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.

## Address table required headers

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

## Address ID

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

## Adenovirus (F40/41)

(adenovirusF40). Adenovirus (F40/41) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* adenovirusGrp *Class:* organism *Nomenclature:* organism *Ontology*

## Parts

*Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Adenovirus Group

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

## Administrative regions

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

## **Adenovirus 40**

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

## **Adenovirus 41**

(adv41). Adenovirus serotype 41. *Part Type*: measurements *Domain*: bio Speciment ID: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: adenovirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **Adenovirus F41 Fibre Gene Target**

(advF41Fibre). Human Adenovirus Group F41 Fiber gene target *Part Type*: measurements *Domain*: bio Speciment ID: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: adenovirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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: 2.1.0.

## **Aeration tank**

(aerTank). A chamber in wastewater treatment where air is introduced to promote microbial breakdown of organic pollutants. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## **Academic Free License v3.0**

(afl30). The licensing for the measure or data set is managed under the Academic Free License v3.0. *Part Type:* categories *Domain:* naDomain *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/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.

## **Afternoon**

(aft). Sample was collected in the afternoon, sometime after lunch. *Part Type:* categories *Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* timeClass

## Parts

*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.

## AfterQC

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

## Air filter

(afu). Air filter as part of filtration or circulating unit. Typically the unit would have a fan or blower. *Part Type:* categories *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* airCompartmentSet *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

### Aggregation scale

(aggregationScale). A scale used for an aggregation. Only applicable for measures and units. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

### Aggregation

(aggregation). Statistical measures used to report a measure. Each aggregation has a corresponding value. The default aggregation is ‘single’, which corresponds to a single measurement. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

### Aggregation input (wide table)

(aggregationInput). The partID for the aggregation being used in a wide name. *Part Type*: attributes *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

## Parts

*Reference Link:* NA *Data Type:* varchar *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.

## Aggregation name (wide table)

(aggregationName). The aggregation referenced for the wide name. *Part Type:* attributes *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: 2.2.0.

## Aggregations

(aggregations). Statistical measures used to report a measure. Each measure reported as a number should be reported with an aggregation. The default aggregation is ‘sin’, which corresponds to a single measurement. *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

## Aggregation scales

(aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative. *Part Type:* partType *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*: 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.

## Aggregation set

(aggregationSet). The aggregation set for a unit. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

## Aggregation sets

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## GNU Afferro General Public License v3.0

(agpl30). The licensing for the measure or data set is managed under the GNU Afferro 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/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.

## Agricultural activity

(agri). Agricultural activity occurred upstream of the sampling site. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSpecimenSet *Compartment Set*: waterCompartmentSet *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.

## Antimicrobial gradient test

(agt). A gradient strip test is performed according to the manufacturer's instructions: a short plastic or paper strip impregnated with antibiotic is placed on inoculated agar. On the standardised 100 mm Petri dish, two strips may be placed, while on the larger 150 mm Petri dish, up to six antibiotics may be tested simultaneously. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet

## *Parts*

*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.

## **Air compartment**

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

## **Air compartment set**

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

## Airplane

(airpln). Airplane sample shed category type *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Airport

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

## Airport lists worksheet

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

## *Parts*

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

## **Airport Sheets Set**

(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.

## **Airport Surveillance Template**

(airportTemplate). The input template for airport and airplane surveillance in the EU. *Part Type:* dictionarySupport *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.0.

## **Air and surface compartment set**

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

*Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* air-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.

## **Environmental temperature**

(airTemp). Environmental temperature. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnit-Set *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.

## **Air and water compartment set**

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

## Parts

### **Alias depreciated**

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

### **Alias ID depreciated**

(aliasIDDep). Alias id ID of an assay that is the same or similar. a comma separated list. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **AliView**

(aliView). Sequencing software that is a user-friendly alignment editor with consensus sequence options. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggrega-*

*tion 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.

## Alkalinity

(alkaline). Measure of alkalinity *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: 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.

## Alkalinity unit set

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

## All Public Health Actions Set

(allActionsSet). A set of all valid categories for public health action, regardless of action type. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:*

## *Parts*

*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.

## **All domains**

(allDo). Domain that specifies that it could apply to all 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.

## **Alleles class**

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

### Allele unit set

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

### Access to all org

(allOrgs). If this is ‘no’, this data will not be available to any partner organization. If missing, data will be available to the all organizations. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: boolean *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: depreciated. First released: depreciated. Last updated: 2.0.0.

### AllPaths-LG

(allpathsLG). A sequencing software that was designed for high-quality assemblies using large, paired-end Illumina data. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## *Parts*

*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.

## **Data Adjustment Standard Value Set**

(allStandardSet). Set of valid input values for the standard field. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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: 3.0.0.

## **Assay Limit of Detection (LOD)**

(alod). The minimum level of a target consistently detectable (e.g., with 95% probability) using the assay considering only the amplification and quantification steps of RT-qPCR. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### Aloh3 precipitation

(aloh3). Aloh3 precipitation *Part Type*: categories *Domain*: che *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### The number of ambiguous bases (Ns) normalized

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

### Assay method id default deprecated

(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*:

## *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:* 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.

## **Amicon ultrafiltration**

(amiconUf). Amicon ultrafiltration *Part Type:* categories *Domain:* che *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## **Amicon filter, extract with MP96**

(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:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## Amplicon sequencing

(amp). Specifies the amplicon strategy for genetic sequencing *Part Type*: categories *Domain*: bio *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.

## Sequence Amplification Artifacts

(ampliArtifact). Sequence amplification artifacts detected. *Part Type*: qualityIndicators *Domain*: bio *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: 2.3.0.

## Amplicon Size

(ampSize). The length of the amplicon generated by PCR amplification. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: basePairSet *Aggregation Scale*: quantAggScale *Quality Set*: 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: 3.0.0.

## **Antimicrobial resistance (AMR) classification**

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

## **Antimicrobial Resistance (AMR) Classification Value Set**

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

## **AMRFinderPlus Software**

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

## **Anti-microbial resistance Group**

(amrGrp). The group for measures and methods pertaining to anti-microbial resistant microbes (general). *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *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.

## **AMR Analysis Software**

(amrSoft). Software use to analyse bacterial genomes and genes for anti-microbial 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:*

## *Parts*

*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.*

## **AMR Software Set**

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

## **Anaplasma Group**

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

## **AND Boolean aggregation**

(andBoo). “AND” aggregation. If all values in the aggregation is “TRUE” then the AND aggregation is also “TRUE”. If all values in the aggregation

## Parts

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.

## annealing/extension

(anneal). Describes the annealing and/or extension cycle in a PCR process. *Part Type*: categories *Domain*: bio *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: 2.2.0.

## Any compartment set

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

## Parts

### Any specimen set

(anySpecimenSet). A specimen set that includes 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.

### Apache license 2.0

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

### Anaplasma phagocytophilum

(aPhagocytophilum). Anaplasma phagocytophilum *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: anaplasmaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Apollo PrepX Library Preparation Kits**

(apolloPrepX). Apollo PrepX Library Preparation Kit by Takara Bio. An automated library preparation kit for Illumina sequencing on Apollo systems. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **ARACHNE**

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

### **Antibiotic Resistance Genes Database (ARDB)**

(ardb). An archive for antibiotic resistance genes and associated information. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database

## *Parts*

*Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA  
*Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA  
*Reference Link:* ardb.cbcn.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.

## **Area proportional sample**

(areaPr). An area proportional sample. Used for surface testing. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* surfaceCompartmentSet *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.

## **A-Tier Region-level Aggregation at Site**

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

## **ARG-ANNOT Annotation Tool**

(argAnnotSoft). Software annotation tool for antimicrobial resistance genes. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: [https://pmc.ncbi.nlm.nih.gov/articles/PMC3910750/](https://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.

## **ARIBA**

(ariba). ARIBA. Focus: Genotyping, MLST, and serotyping from raw sequencing reads. Applications: *Salmonella*, *Escherichia coli*, *Klebsiella pneumoniae*, and more. Features: Works with custom databases for serotyping and resistance gene identification. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *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*: 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.

## **Arrival temperature**

(arTemp). The temperature of a sample upon arrival at the laboratory for analysis. *Part Type*: measurements *Domain*: phy *Speciment ID*: siSaS-

## *Parts*

pecimenSet *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*: seeU-  
nitData *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.

## **Artic V1 Primer Set**

(articV1). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 1.0.0. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **Artic V2 Primer Set**

(articV2). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 2.0.0. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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*

## Parts

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

### Use of the articV3 primer

(articV3). Initial implementation of an ARTIC bioinformatics platform for nanopore sequencing of nCoV2019 novel coronavirus; Artic Foundation v3 primer. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### Use of the articV4 primer

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

### Artic V4.1 Primer Set

(articV41). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 4.1.0. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:*

## Parts

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.

## Artic V5 Primer Set

(articV500). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.0.0 which produces amplicons approximately 400bp in length. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Artic V5.1 Primer Set

(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*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## *Parts*

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

### **Artic V5.2 Primer Set, 1200bp**

(articV520bp1200). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### **Artic V5.2 Primer Set, 400bp**

(articV520bp400). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 400bp in length. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

*Parts*

### **Artic V5.3.2 Primer Set**

(articV532). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.3.2 which produces amplicons approximately 400bp in length. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Artistic license 2.0**

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

### **Assay ID**

(asID). Links with the AssayMethod used to perform the analysis. Use instrument.ID for measures that are not viral measures. Deprecated as of version 2, please avoid use. Refer to methodID instead. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment*

## Parts

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

## Astrovirus

(astrovirus). Astrovirus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* astrovirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Astrovirus Group

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

## Parts

### **Amies Transport Medium**

(atm). A buffer solution/medium that maintains viability of bacteria in wastewater and environmental samples during transport. *Part Type*: categories *Domain*: naDomain *Speciment ID*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Atropos**

(atropos). A QC pipeline tool for sequencing data that performs adapter trimming and quality filtering with built-in QC reporting. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://atropos.readthedocs.io/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Attribute input (wide table)**

(attributeInput). The partID for the attribute being used in a wide name. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: 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*

## 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: 2.2.0.

### Attribute name (wide table)

(attributeName). The attribute referenced for the wide name. *Part Type:* attributes *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: 2.2.0.

### Attributes

(attributes). Attributes describe the who, where, when, and why of environmental surveillance. There are attributes for domain, specimen, compartment, or table. Attributes are one of the three main components or ways to report environment surviellence data. The other two components are measures and methods. *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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

### Automatic composite sampling

(autoComp). A composite sampler which is automated to collect and store multiple wastewater samples across multiple time points. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Autosamplers

(autoInst). Autosampler instruments, used to automatically collect flow- or time-proportional samples over a period (e.g., ISCO autosamplers). *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Automatic sequential sampling

(autoSeq). A composite sampler which is automated to collect and combine multiple samples of equal volume taken at a set time interval. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*

## 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: 3.0.0.

### Babesia

(babesia). Babesia *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* babesiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Babesia or Nuttallia Group

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

### Bacterial culture

(bacCul). Growing a bacterial culture to test for bacterial presence. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bactMisc *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **BacMet Database**

(bacMet). Database of antibacterial biocide and metal resistance genes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* bacmet.biomedicine.gu.se *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Bacteroides 16S forward primer (HF183) (ABI)**

(bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bacteroidesGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* 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.

### **Bacteroides 16S probe (BacP234) (ABI)**

(bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bacteroidesGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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.

### **Bacteroides 16S reverse primer (BacR287) (ABI)**

(bact16sABIRev). Bacteroides 16S reverse primer (BacR287) (ABI) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bacteroidesGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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.

### **Bacteria unit set**

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

## Parts

### **Bacteroides Group**

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

### **Bacteria and Fungus Class**

(bactFung). Measures and methods relating to bacteria. *Part Type:* classes *Domain:* bio *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* bactFung *Nomenclature:* bactFung *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteri-aUnitSet *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.

### **Bacterial testing method**

(bactMeth). Description of the bacterial testing/detection method. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bactMisc *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* bactMethSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## **Bacterial testing method set**

(bactMethSet). The set capturing containing all of the valid methods for the bacterial testing method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bactMisc *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* bactMethSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Miscellaneous bacteria group**

(bactMisc). A group of measures/methods related to miscellaneous bacteria. The miscellaneous 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:* naSpecimenSet *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.

## *Parts*

### **Bag Mediated Filtration**

(bagFilt). Sample was collected using bag-mediated filtration. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **BamQC (from Qualimap)**

(bamQC). A QC pipeline tool for sequencing data that focuses on quality control for mapped data in BAM format, reporting alignment quality. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://qualimap.bioinfo.cipf.es/> (QC for BAM files) *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **bamUtil Dedup**

(bamUtil). A deduplication method that removes duplicate reads directly from BAM files. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale

## Parts

*Quality Set:* NA *Reference Link:* [https://genome.sph.umich.edu/wiki/BamUtil%3A\\_dedup](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.

## Bar screen

(barScreen). A bar screen is a mechanical device used to remove large solid debris from wastewater or sewage as it enters a treatment plant. It consists of a series of parallel bars or rods, spaced at specific intervals, that allow water to pass through while capturing larger objects. This process prevents damage to downstream equipment and ensures efficient treatment. Bar screens are typically installed at the inlet of wastewater treatment facilities and can be cleaned manually or mechanically, depending on the design and operational requirements. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## Base-pair unit set

(basePairSet). Unit set for base-pair measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum*

## Parts

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

### **BayesHammer (from SPAdes)**

(bayesHammer). A sequencing data processing application that does error correction tool specifically for Illumina reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://bioinf.spbau.ru/en/spades/bayeshammer> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Bayesian Smoothing applied**

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

### **BBDuk (from BBTools)**

(bbduk). A QC pipeline tool for sequencing data that is a part of the BBMap suite, performs filtering and trimming, and generates QC statistics.

*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://jgi.doe.gov/data-and-tools/bbtools/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## BBMap

(bbmap). BBMap. A general-purpose read mapper. High-sensitivity aligner for DNA and RNA reads. Best for: Error-prone reads from platforms like Nanopore or PacBio. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## BBMap Reformat

(bbmapReformat). 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*

## *Parts*

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

## **BBMap Suite**

(bbmapSuite). A sequencing data processing application library that includes tools like BBduk for quality trimming, adapter removal, and quality filtering. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://sourceforge.net/projects/bbmap/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Bead beating, extract with MP96**

(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:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## **Borrelia burgdorferi**

(bBurgdorferi). Borrelia burgdorferi *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

*Group:* borreliaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Bcftools

(bcfTools). Sequencing software that works with SAMtools to call variants and produce consensus sequences from alignments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/samtools/bcftools> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## bcov

(bcov). Measure of the amount of bovine coronavirus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* betaCoronaGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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

### **bcov culture spike target**

(bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **bcov spike target (unspecified)**

(bcovGen). The bovine coronavirus (unspecified) is used as the recovery efficiency control target. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **bcov vaccine spike target**

(bcovVac). The bovine coronavirus vaccine is used as the recovery efficiency control target. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **Bayesian Evolutionary Analysis by Sampling Trees (BEAST) Software**

(beast). A lineage or clade analysis software tool for estimating evolutionary relationships and divergence times in a Bayesian framework. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <http://www.beast2.org/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Beef extract flocculation**

(beeExtractFloc). Beef extract flocculation. *Part Type:* categories *Domain:* che *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## **Is Before**

(before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Use only for

## *Parts*

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.

## **Below LOD**

(beLOD). Measure is below the limit of detection (LOD) for a specific analyte. *Part Type*: qualityIndicators *Domain*: bio *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.

## **Measured levels below LOQ**

(belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.3.

## Beta

(beta). B.1.351 *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Beta Coronavirus Group

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

## BIGSdb (Bacterial Isolate Genome Sequence Database)

(bigsdb). BIGSdb (Bacterial Isolate Genome Sequence Database). A flexible platform that supports serotyping alongside sequence typing and other typing schemes. Can be customized for various bacterial species, including Neisseria meningitidis. *Part Type*: categories *Domain*: bio *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

## *Parts*

*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.

## **Biologic**

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

## **Fragment analyzers or bioanalyzers**

(bioanalys). Fragment analyzer or bioanalyzer instruments, used to assess fragment size distribution in libraries. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## BioEdit

(bioEdit). Sequencing software that offers sequence alignment and visualization, used to manually generate consensus sequences. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <http://www.mbio.ncsu.edu/bioedit/bioedit.html> (site may vary) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Bioo Scientific NEXTflex Rapid DNA-Seq Kit

(biooSci). Bioo Scientific NEXTflex Rapid DNA-Seq Kit by PerkinElmer. A rapid and flexible library prep kit for DNA sequencing on Illumina platforms. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Digital droplet emulsification PCR

(bioRadDdpcr). Describes a PCR analysis done using BioRad's digital droplet emulsification PCR technology. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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: 2.0.0.

## **Biological replicate**

(bioRep). A biological replicate not otherwise specified - these are parallel measurements of biologically distinct samples that capture random biological variation, which can be a subject of study or a source of noise itself. Biological replicates are important because they address how widely your experimental results can be generalized. They indicate if an experimental effect is sustainable under a different set of biological variables. Further examples of biological replicates are the more specific co-located samples and field sample replicate types for the repType field. *Part Type*: categories *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Beta-Lactamase Anti-microbial resistance Group**

(bLacAMRGrp). The group for measures and methods pertaining to beta-lactamase-related anti-microbial resistance. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bLacAMRGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*:

## Parts

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.

### Cephamycin Beta-Lactamase-Resistance gene target

(blaCMY). Cephamycin Beta-Lactamase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bLacAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### CTX-M Beta-Lactamase-Resistance gene target

(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.

*Parts*

### **Impenemase (IMP) Beta-Lactamase-Resistance gene target**

(blaIMP). Impenemase (IMP) Beta-Lactamase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bLacAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase-Resistance gene target**

(blaKPC). Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bLacAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **New-Delhi Metallo- (NDM) Beta-Lactamase-Resistance gene target**

(blaNDM). New-Delhi Metallo- (NDM) Beta-Lactamase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bLacAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **OXA-type Beta-Lactamase-Resistance gene target**

(blaOXA48). OXA-type Beta-Lactamase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: bLacAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **SHV Beta-Lactamase-Resistance gene target**

(blaSHV). SHV-type Beta-Lactamase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet

## Parts

*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.mediterrane-infection.com/accesressources/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.

## **BLASR (Basic Local Alignment with Successive Refinement)**

(blasr). BLASR (Basic Local Alignment with Successive Refinement). A long-read specific mapper. Optimized for PacBio data. Best for: High-quality long-read alignment. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **TEM Beta-Lactamase-Resistance gene target**

(blaTEM). TEM-type Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* <https://www.mediterrane-infection.com/accesressources/base-de-donnees/arg-annot-2/> *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: 2.2.0.

### **Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase-Resistance-resistance gene target**

(blaVIM). Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* bLacAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

### **Binary Large Object (BLOB) data type**

(blob). The data type for Binary Large Object (BLOB) data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

*Parts*

### **BMTagger**

(bmtagger). A dehosting software developed by NCBI for identifying and removing host sequences based on local alignment. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: ftp://ftp.ncbi.nlm.nih.gov/pub/agarwala/bmtagger/ *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Breadth of coverage (>=5x depth)**

(boc). The percentage of the reference genome covered by the sequenced data, to a prescribed read depth greater or equal to 5. Report as percentage of positions. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: 100 *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **5-Day carbonaceous biochemical oxygen demand**

(bod5c). The quantity of oxygen utilized for the biochemical degradation of organic matter under standard laboratory procedures in five (5) days in the presence of a nitrification inhibitor, expressed in milligrams per litre (mg/l). *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.

## 5-day total biochemical oxygen demand

(bod5t). 5 day total biochemical oxygen demand. *Part Type*: measurements *Domain*: bio *Speciment ID*: siSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: miscMeas *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

## Boolean data type

(boolean). The data type for boolean/binary data. Encoded as ‘TRUE’ or ‘FALSE’ *Part Type*: dataTypes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Parts

### Boolean aggregation set

(booleanAggrSet). Aggregation 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.

### Boolean value set

(booleanSet). Set that contains the valid possible values for a boolean measure (TRUE or FALSE). *Part Type*: mmaSets *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: booleanSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Border closure

(borderClos). A measure shutting entry points to limit cross-border movement and disease spread. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*:

## Parts

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

### **Borrelia burgdorferi or Lyme Disease Group**

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

### **Body of water**

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

### **Bowtie2**

(bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that

## *Parts*

maps reads against a host reference genome to remove aligned reads. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **Host Subtraction with Bowtie2 & SAMtools**

(bowtie2XSam). A combined workflow for dehosting where reads mapped to the host are removed from downstream analysis. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: Bowtie2: <https://bowtie-bio.sourceforge.net/bowtie2/> and Samtools: <https://www.htslib.org/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Base-pairs**

(bps). A base pair (bp) is a unit of measurement in molecular biology that represents a pair of complementary nucleotides in DNA or RNA. The length of DNA sequences is often measured in base pairs. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet

## Parts

*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.

## Buffered Peptone Water

(bpw). A buffer solution/medium used for bacterial enrichment, can also serve as a temporary preservative. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Bracken

(bracken). A QC pipeline tool for sequencing data and taxonomic profiling that can also be used to identify contamination and assess data quality in metagenomics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://ccb.jhu.edu/software/bracken/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Parts

### **B-Tier Region-level Aggregation at Site**

(bRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an “B-Tier” region, and thus a region within a greater metropolitan area and larger than a single municipality, but smaller than the entire metropolitan area. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Bovine respiratory syncytial virus group**

(brsv). Bovine respiratory syncytial virus. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: rsvGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **brsv culture spike target**

(brsvCul). Cultured bovine respiratory syncytial virus (BRSV) is used as the recovery efficiency control target. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *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: 2.0.0.

## BRSV-N

(brsvN). bovine respiratory syncytial virus capsid protein gene region *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: rsvGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## brsv vaccine spike target

(brsvVac). The bovine respiratory syncytial virus (BRSV) vaccine is used as the recovery efficiency control target. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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

### **Brucella**

(brucella). Brucella *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: brucellaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Brucella Group**

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

### **BSD Zero-Clause license**

(bsd0). The licensing for the measure or data set is managed under the BSD Zero-Clause license. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/0bsd/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum*

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

## **BSD 2-clause “Simplified” license**

(bsd2Clause). The licensing for the measure or data set is managed under the BSD 2-clause “Simplified” license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/bsd-2-clause/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## **BSD 3-clause “New” or “Revised” license**

(bsd3Clause). The licensing for the measure or data set is managed under the BSD 3-clause “New” or “Revised” license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/bsd-3-clause/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

*Parts*

### **BSD 3-clause Clear license**

(bsd3ClauseClear). The licensing for the measure or data set is managed under the BSD 3-clause Clear license. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://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.

### **BSD 4-clause “Original” or “Old” license**

(bsd4Clause). The licensing for the measure or data set is managed under the BSD 4-clause “Original” or “Old” license. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://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.

### **Boost Software License 1.0**

(bsl10). The licensing for the measure or data set is managed under the Boost Software License 1.0. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA

## Parts

*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.

## Branch sewer pipeline

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

## Building cleanout

(buildCO). Specifies a site type that is a capped pipe that connects to a building's main sewer line. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Parts

### **Building-level Surveillance**

(builLev). Surveillance is done only at the level of a single building.  
*Part Type*: categories *Domain*: naDomain *Speciment ID*: anySpecimenSet  
*Compartment Set*: anyCompartmentSet *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.

### **Bus**

(bus). A large motor vehicle carrying passengers by road, typically one serving the public on a fixed route and for a fare. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Bus Station**

(busStat). A terminal where buses arrive and depart. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **BWA (Burrows-Wheeler Aligner)**

(bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **BWA for Host Filtering**

(bwaHost). A dehosting software that maps reads to a host genome, filtering mapped reads from analysis. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/lh3/bwa> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

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### **BWA-MEM with Duplicate Marking**

(bwaMEM). A deduplication method that is used with SAMtools or Picard to mark duplicates during read mapping. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.htslib.org/algorithms/duplicate.html> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **C28311T Omicron N1 Point Mutation**

(c28311t). A measure of the C to T point mutation at position 28311 (C28311T) of the N1 probe, present in all Omicron sub-lineages. *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.

### **Caffeine**

(caff). Caffeine (usually measured as a human fecal chemical indicator) *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category*

*Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Calculation Type

(calcType). A field to explain the purpose/nature of a single calculation/data treatment. Possible inputs are: normalization, standardization, smoothing, and predictiveModelling. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* calcTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Calculation type set

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

## Parts

### Calculation ID

(calculationID). A unique identifier and primary key for every row of the calculations table. Typically generated as a composite key of container ID and step ID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Calculations Table

(calculations). Table for recording data on data treatments and calculations applied to measurements and reported values. cl *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: programDescr *Nomenclature*: programDescr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.3.0.

### Calculations table column order

(calculationsOrder). Specifies the order of the columns in the calculations table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA

*Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Calculations table required headers**

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

## **Calprotectin**

(Calprotectin). Calprotectin is a calcium- and zinc-binding protein of the S-100 protein family which is mainly found within neutrophils and throughout the human body. The presence of calprotectin in faeces is a consequence of neutrophil migration into the gastrointestinal tissue due to an inflammatory process. *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.

## Parts

### **Campylobacter**

(camp). Campylobacter. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: campGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: bacteriaUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Campylobacter Group**

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

### **Canal**

(canal). Artificial watercourse with no flow or a controlled flow used for navigation, drainage or irrigation. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*

## *Parts*

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

### **Canu**

(canu). A sequencing software that is a de novo assembler specifically optimized for long-read data from PacBio and Oxford Nanopore. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/marbl/canu> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Capacity class**

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

### **Capacity unit set**

(capacityUnitSet). Unit set for capacity measurements. *Part Type:* unitSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:*

## *Parts*

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.

## **CapsuleFinder**

(capFin). CapsuleFinder Used for typing capsular polysaccharides in a variety of bacteria, especially Escherichia coli and Klebsiella species. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Capital city endonym**

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

### **Capital city exonym**

(capitalExonym). The English name foreigners use for the country's capital. Preprogrammed into dictionary tables, not editable by users. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 75 *Part Status*: active. First released: active. Last updated: 2.1.0.

### **Comprehensive Antibiotic Resistance Database (CARD)**

(cardDbase). Database that provides high-quality reference sequences for resistance genes. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: database *Nomenclature*: database *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://card.mcmaster.ca> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **CARD Resistance Gene Identifier (RGI)**

(cardRGI). Software tool that is a part of the Comprehensive Antibiotic Resistance Database (CARD) used for annotation and prediction of AMR. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## *Parts*

*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.

## **Case report date**

(caRepDate). Date that the numbers were reported publicly. Typically, reported data and this measure is most commonly reported and used. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

## **Episode date of confirmed cases**

(caseEpDate). Episode date is the earliest of onset, test or reported date for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Onset date of confirmed cases**

(caseOnDate). Earliest that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: datetime *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Report date of confirmed cases**

(caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and this measure is most commonly reported and used. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: datetime *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Test date of confirmed cases**

(caseTestDate). Date that the covid-19 test was performed for a confirmed case. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: datetime *Missingness Set*: NA *Minimum Value*:

## *Parts*

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

## **Central average smoothing applied**

(caSmooth). This data treatment smooths the measurement value using central average smoothing. *Part Type*: categories *Domain*: naDomain *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.

## **Categorical data type**

(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.

## **Categories**

(categories). A discrete list of values that can be reported for a measure, method or attribute. A use-case example of categories would be how they are used to record the site where a measure is taken (partID =

geoType). For the geoType attribute there are different type of sites where samples can be taken: a 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*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## Candida auris

(cAuris). The yeast species Candida auris, or C. auris. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: cAurisGrp *Class*: bactFung *Nomenclature*: bactFung *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: bacteri-aUnitSet *Aggregation Scale*: seeUnitAggScale *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: 2.1.0.

## Candida auris Group

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

## 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: 2.2.0.

## Carbonaceous Biochemical Oxygen Demand

(cbod). A measure of the amount of oxygen required by microorganisms to break down organic carbon-based compounds in water over a specified period, typically five days at 20°C (CBOD). Unlike BOD (Biochemical Oxygen Demand), CBOD excludes oxygen demand from the oxidation of nitrogenous compounds (such as ammonia). It is used to assess organic pollution in wastewater and natural waters. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

## Carbapenemase-encoding genes

(cbp). Carbapenemase-encoding genes. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Cary-Blair Transport Medium**

(cbtm). A buffer solution/medium commonly used for bacterial preservation in stool and wastewater samples. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Creative Commons Zero v1.0 Universal**

(cc010). The licensing for the measure or data set is managed under the Creative Commons Zero v1.0 Universal. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://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.

### **Creative Commons Attribution 4.0**

(ccby40). The licensing for the measure or data set is managed under the Creative Commons Attribution 4.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation*

## *Parts*

*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.

## **CC BY-NC 4.0 license**

(ccbync40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial international license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://creativecommons.org/licenses/by-nc/4.0/deed.en> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.3.

## **CC BY-NC-SA 4.0 license**

(ccbyncsa40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial, and sharealike international license. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://creativecommons.org/licenses/by-nc-sa/4.0/deed.en> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.3.

## Creative Commons Attribution ShareAlike 4.0

(ccbysa40). The licensing for the measure or data set is managed under the Creative Commons Attribution ShareAlike 4.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentsSet *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.

## Long-term acute care hospital

(ccc). Acute care hospitals, or complex continuing 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:* anyCompartmentsSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Child day care

(cdc). Child day care facility. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentsSet *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

## 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.*

### **Sarboco\_E forward primer (IDT)**

(cdcCovEIDTFor). Sarboco\_E forward primer (IDT) *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet Aggregation Scale: 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.*

### **Sarboco\_E probe (IDT)**

(cdcCovEIDTProbe). Sarboco\_E probe (IDT) *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet Aggregation Scale: 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.*

### **Sarboco\_E reverse primer (IDT)**

(cdcCovEIDTRev). Sarboco\_E reverse primer (IDT) *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet*

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

### **2019-nCoV\_N1 forward primer (IDT)**

(cdcCovN1IDTFor). 2019-nCoV\_N1 forward primer (IDT) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* 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.

### **2019-nCoV\_N1 probe (IDT)**

(cdcCovN1IDTProbe). 2019-nCoV\_N1 probe (IDT) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* 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.

### **2019-nCoV\_N1 reverse primer (IDT)**

(cdcCovN1IDTRev). 2019-nCoV\_N1 reverse primer (IDT) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr

## Parts

*Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet  
*Aggregation Scale:* 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.

### **2019-nCoV\_N2 forward primer (IDT)**

(cdcCovN2IDTFor). 2019-nCoV\_N2 forward primer (IDT) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* 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.

### **2019-nCoV\_N2 probe (IDT)**

(cdcCovN2IDTProbe). 2019-nCoV\_N2 probe (IDT) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* 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.

### **2019-nCoV\_N2 reverse primer (IDT)**

(cdcCovN2IDTRev). 2019-nCoV\_N2 reverse primer (IDT) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

## Parts

anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr  
*Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet  
*Aggregation Scale*: 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.

### **2019-nCoV\_N3 forward primer (IDT)**

(cdcCovN3IDTFor). 2019-nCoV\_N3 forward primer (IDT) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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.

### **2019-nCoV\_N3 probe (IDT)**

(cdcCovN3IDTProbe). 2019-nCoV\_N3 probe (IDT) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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*

### **2019-nCoV\_N3 reverse primer (IDT)**

(cdcCovN3IDTRev). 2019-nCoV\_N3 reverse primer (IDT) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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.

### **CD-HIT**

(cdHIT). A sequencing data processing application that clusters and removes duplicate sequences, useful for dereplication. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://sites.google.com/view/cd-hit/home> (main page) *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Clostridium difficile**

(cDiff). Clostridium difficile *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: clostridiumGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Corynebacterium diphtheriae**

(cDip). *Corynebacterium diphtheriae Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* diphteriaGrp *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.

### **CeCILL Free Software License Agreement v2.1**

(cecill21). The licensing for the measure or data set is managed under the CeCILL Free Software License Agreement v2.1. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/cecill-2.1/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

### **Degrees Celcius**

(cel). Degrees Celsius. *Part Type:* units *Domain:* phy *Speciment ID:* siSaS-pecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:*

## *Parts*

*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.

## **Celera Assembler**

(celera). A sequencing software that was initially developed for the Human Genome Project, still used in some workflows for large genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://sourceforge.net/projects/wgs-assembler/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Population census**

(census). Government or other agency census for determining site/polygon population. *Part Type:* categories *Domain:* naDomain *Speciment ID:* poSiSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **Centrifugation**

(cent). Describes solid separation from a wastewater sample via centrifugation. Likely connected to other method steps prior to analysis. *Part Type*: categories *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: waterCompartmentSet *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.

## **Centricon ultrafiltration**

(centriconUf). Centricon ultrafiltration. *Part Type*: categories *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

## **Centrifuges**

(centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Ultracentrifuge are a separate instrument type option. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## *Parts*

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

## **Centrifugation speed**

(centSpeed). Centrifugation speed *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* speed *Nomenclature:* speed *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* speedUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## **Ceres nanotrap**

(ceres). Ceres nanotrap. *Part Type:* categories *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## **Cesspit**

(cesspit). Cesspit, cesspool and soak pit in some contexts are terms with various meanings: they are used to describe either an underground holding tank (sealed at the bottom) or a soak pit (not sealed at the bottom). A cesspit can be used for the temporary collection and storage of feces, excreta, or fecal sludge as part of an on-site sanitation system and has

## Parts

some similarities with septic tanks or with soak pits. *Part Type*: categories *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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.3.

## Colony Forming Units

(cfu). Colony forming units *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## CFU per 100 ml

(cfu100). Colony forming units per 100 ml of filtered sample. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## *Parts*

### **Colony forming units per grams total solids**

(cfugTS). colony forming units per grams total solids (CFU/gTS) *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Colony forming units per milliliter**

(cfumL). colony forming units per milliliter (CFU/mL) *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Changes column**

(changes). A column for recording the changes from a previous version. Use this column as a short-hand change log for dictionary development. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## Parts

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

### character length

(charLength). The number of characters used for the wide names. *Part Type:* attributes *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: 2.2.0.

## Chemical

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

### Chemical contaminant surveillance

(chemSurv). Purpose of sampling/measure is to test for the presence of certain chemicals or chemical contaminants. *Part Type:* categories *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## **Chemagic viral dna/rna 300 kit**

(chemVir). Nucleic acid extraction performed using the chemagic viral dna/rna 300 kit. *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet 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.*

## **ChewBBACA**

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

## Chikungunya Group

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

## Chikungunya virus (CHIKV)

(chikv). Chikungunya virus (CHIKV) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: chikungunyaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Child relationship

(child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar

## *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.

## **Chlamydia**

(chlamydia). Chlamydia *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* chlamydiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **Chlamydia Group**

(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.

## **City**

(city). The city where a site or organization is located; part of the address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

## 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: 2.0.0.

## Campylobacter jejuni bacteria

(cJejuni). Campylobacter jejuni gene target/measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* campGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## Composite Key

(cK). Composite key for a table. All report tables have a primary key - the composite key acts as a primary key, but it is produced 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*

## *Parts*

*Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.2.2.*

## **Calculations Table Short Name**

(cl). The abbreviated short name used to reference the table for recording data on data treatments and calculations applied to measurements and reported values. *table Part Type: shortName Domain: naDomain 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.*

## **Lineage- or Clade-analysis Software**

(cladeAn). Software tool or pipeline for determining the clade or lineage of an organism. *Part Type: methods Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: sequence Nomenclature: sequence Ontology Reference: NA Category Set ID: cladeAnSet Unit Set: naUnitSet Aggregation Scale: qualAggScale Quality Set: 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.*

## **Lineage- or Clade-analysis Software Set**

(cladeAnSet). Valid category set for lineage or clade analysis software types. *Part Type: mmaSets Domain: bio Speciment ID: naSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: sequence Nomenclature: sequence Ontology Reference: NA Category Set ID: cladeAnSet Unit Set: naUnitSet Aggregation Scale: 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.*

*ment 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.

### Clarified sample

(clari). Clarified sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

### CLARK

(clark). A dehosting software that classifies reads taxonomically, which helps filter out host reads in metagenomic data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://clark.cs.ucr.edu/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## *Parts*

### **Class**

(class). A unique identifier for a class, which is akin to a sub-group; it's a way of grouping parts within a given group. A group can have one or more classes to describe different parts of the class. Currently, class is only used for biologics. For example, SARS-CoV-2 is a group of measures with the following classes of allele, variant, mutation, sequence, and protein.  
*Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

### **Classes**

(classes). A class is a collection of one or more related measures or methods within a group. A group can have one or more classes to describe different parts of the class. *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

## **CleanPlex DNA Library Prep Kit**

(cleanPlex). CleanPlex DNA Library Prep Kit by Paragon Genomics. A library target enrichment kit optimized for high sensitivity and low input. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **ClermonTyping**

(clermonTyp). ClermonTyping. Focus: MLST and phylogenetic typing for Escherichia coli. Applications: Ideal for epidemiological studies. Features: Combines MLST and phylogroup-specific information. *Part Type*: categories *Domain*: bio *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*: 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.

## **Clinic**

(clinic). A medical clinic, may be used to provide treatment, remedial work, and/or instruction. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## ClonalFrameML Software

(clonalFrameML). A lineage or clade analysis software tool for reconstructing phylogenetic relationships considering recombination, used in bacterial lineage analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *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.

## Clostridium Group

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

## **Cloudy**

(cloudy). Qualitative category for the weather measure, specifying an overcast day with no rain. *Part Type*: categories *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **BBMap's Clumpify**

(clumpify). A deduplication method that groups identical sequences, often used to deduplicate reads efficiently. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/BioInfoTools/BBMap/blob/master/sh/clumpify.sh> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Clustal Omega**

(clustalO). Sequencing software that is widely used for multiple sequence alignment and producing consensus sequences. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*:

## *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*: <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.

## **Centimetres**

(cm). Unit part for the SI unit of centimetres. *Part Type*: units *Domain*: phy Speciment ID: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Contact table Shorthand**

(co). The abbreviated short name used to reference the The table that contains information about a contact; a person who is the contact of a site or laboratory. table *Part Type*: shortName *Domain*: naDomain Speciment ID: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.2.

## Carbon Dioxide

(co2). A measure of an amount or concentration 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.

## Chemical Oxygen Demand

(cod). Chemical oxygen demand. *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: waterQualityGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Time from collection to storage

(col2Frdg). The amount of time between sample collection and the samples placement in stable storage/refrigeration. *Part Type*: measurements *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: timeClass *Nomenclature*: timeClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: timeUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA

## Parts

*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.

## Colistin Anti-microbial resistance group

(colAMRGrp). The group for measures and methods pertaining to colistin-related anti-microbial resistance. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* colAMRGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* quantAggScale *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.

## Collection group

(colGrp). A group of measurement-like attributes related to sample collection. *Part Type:* groups *Domain:* allDo *Speciment ID:* saSpecimenSet *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.

## Colistin resistance

(colis). Colistin-resistant bacteria. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* amrGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA

## Parts

*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.

## Collection Approximate Time Period Set

(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:* 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.

## Collection Approximate Time Period

(collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection. used when exact time in unknown. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* collAppxSet *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.

## *Parts*

### **Collection Date (time not included)**

(collDate). Sample collection date, where time is reported in a separate field. Only for use in combination with the collection approximate time period field. Otherwise report date and time together. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* date *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Collection date time**

(collDT). For grab samples this is the date, time and timezone the sample was taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Collection date time end**

(collDTEnd). For integrated time average samples this is the date, time and timezone the sample was finished being taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass

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

### **Collection date time start**

(collDTStart). For integrated time averaged samples this is the date, time and timezone the sample was started being taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Sample collection set**

(collectSet). Methods for collection samples. Sample collection methods include water, air, and surface. See the attribute ‘Compartment set’ of the sample collection method. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* collectSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Parts

### Collection number

(collNum). The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling.  
*Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* 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:* 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.

### Collection period and number

(collNumPer). Composite collection number.period. This a composite measure that combines ‘collection period’ (collPer) and ‘collection number’ (collNum). Collection number and period can be used to reduce the number of table headings during data collection. In data storage, ‘collNum’ and ‘collPeriod’ should be transformed to ‘collPer’ and ‘collNum’. For Grab sample, Surface swab, or Area proportional sample just enter 1

In case of Composite, Flow-proportional collection, the number of subsamples followed by a dot, followed by the period of the sampling, in hours. For example, for 4 composite subsamples covering a 8 hours period, the entry would be 4.2 For time-proportional 24 subsamples collected every hour, the entry would be 24.1 For volume-proportional, the entry for 24 subsamples collected over 24 hours should be 24.24, in this case the period part of the entry should be understood as the total collection time instead of the periodicity of the collection.

For a COSCA ball or Moore swab collecting for 24 hours, the entry would be 1.24 *Part Type:* attributes *Domain:* naDomain *Speciment ID:* saSpecimenSet *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*: 6 *Part Status*: **deprecated**. First released: depreciated.  
Last updated: 3.0.0.

## Collection period

(collPer). Collection period. The time period over which the sample was collected, in hours. Alternatively, use collectionStart and collectionEnd. Examples: 1 hour, 6 hours, 24 hours *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: 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*: 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.

## Sample collection type

(collType). The type of collection. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: colGrp *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.

## Parts

### **Co-located relationship**

(colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Column name depreciiated**

(columnNameDep). Name for the column Deprecated in ODM version 2. Look-up tables are now incoprated into parts and sets. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Commercial facility - not specified**

(commFacOth). Specifies a site type which is a commercial facility/worksit that is not otherwise captured or described in the geotype set. *Part Type:*

## Parts

categories *Domain*: naDomain *Speciment ID*: siSpecimenSet *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: 2.2.0.

## Community-level Surveillance

(communitLev). Surveillance is done at the level of an entire community. *Part Type*: categories *Domain*: naDomain *Speciment ID*: anySpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Communitor

(communitor). A mechanical device that grinds large solid waste in wastewater into smaller particles to prevent clogging. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: wa-terCompartmentSet *Group*: colGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: ENVO:03501472 *Category Set ID*: NA *Unit Set*: naU-nitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maxi-mum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Parts

### Composite sample - archival

(comp). A composite sample, usually generated by an autosampler. This is intended for use in updating and mapping archival data into the newest version of the ODM. Generally, autosamplers do time or flow-proportional sampling, and so those collection methods should be used instead. This is only for composite/autosampler samples where these additional details have not yet been specified. Use collectionPeriod to describe how many hours the sample was taken, and collectionNum to record the number of samples.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* saSpecimenSet  
*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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Composite grab sample of 3

(comp3). A grab-composite sample composed of 3 separate grab samples.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* 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:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

### Composite grab sample of 3 deprecate

(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:* 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:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Composite 3hr grab sample**

(comp3h). A 3-hour composite with 3 grab samples each taken once per hour, generally manually performed. *Part Type:* categories *Domain:* 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:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Composite 3hr grab sample deprecate**

(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:* 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:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

## *Parts*

### **Composite 8hr grab sample deprecated**

(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*: 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*: NA *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Composite 8hr grab sample deprecated**

(comp8hDep). A 8-hour composite with 8 grab samples each taken once per hour, generally manually performed. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: NA *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

## **Compartment**

(compartment). The attribute identifying the substance from which where a sample was taken. For more information, see partID = compartment. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## Parts

*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.*

### Compartment input (wide table)

(compartmentInput). The partID for the compartment being used in a wide name. *Part Type: attributes 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: 2.2.0.*

### Compartment name (wide table)

(compartmentName). The compartment referenced for the wide name. *Part Type: attributes 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: 2.2.0.*

## Parts

### Compartments

(compartments). The substance from which a sample was taken. For example, wastewater has component of “water”. Compartments are attributes of measures, methods, units, and aggregations. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

### Compartment Set Header

(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*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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: 2.2.2.

### Compartment sets

(compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured in people (humans), water, surface, or air. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup

*Class:* 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.

## **Composting toilet**

(compToi). A self-contained toilet system wherein human waste is designed to be composted. Usually with the addition of secondary materials, like sawdust. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.3.

## **Concentration measure**

(conc). Measurement of concentration (generalized) - designed for describing protocols. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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

### Is concurrent to

(concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Use only for protocolRelationships table relationshipID. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Sample volume after concentration

(concVol). The total volume of a sample after the concentration step. *Part Type*: measurements *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: volumeUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### Water conductivity

(cond). Measurement of conductivity of sample or site. *Part Type*: measurements *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: siteFeat *Class*: conductivity *Nomenclature*: conductivity *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: conductivityUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*:

## Parts

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

## Conductivity class

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

## Conductivity unit set

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

## Cone-shaped sampling

(cone). Instrument 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

## *Parts*

sample out. *Part Type*: categories *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*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Number of confirmed cases**

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

## **Number of confirmed cases by episode date**

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

### **Number of confirmed Cases Onset date**

(confOn). Number of confirmed cases of a given disease, totaled by onset date. Onset date is the earliest date that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

### **Number of confirmed cases by report date**

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

### **Number of confirmed cases test date**

(confTest). Number of confirmed cases of a given disease, totaled by test date. Test date is the date that the covid-19 test was performed for a confirmed case. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

## Parts

*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.

## consensus genome length

(conGenLen). The length of the genome defined by the most common nucleotides at each position. Provide a numerical value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## Consensus Sequence Software

(conSeqSoft). Software use to run consensus sequence on sequencing analyses. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* conSeqSoftSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## **Consensus Sequence Software Set**

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

## **Contact ID**

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

## **Contact name**

(contactName). Contact person or group, for the lab. Deprecated 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*

## *Parts*

*Length: 0 Maximum Length: 100 Part Status: depreciated.* First released: depreciated. Last updated: 2.0.0.

## **Contact table**

(contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. *co Part Type: tables Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: programDescr Nomenclature: programDescr Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active.* First released: active. Last updated: 2.0.0.

## **Contacts table column order**

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

## **Contact table required headers**

(contactsRequired). Specifies the columns required in a Contacts table. *Part Type: tableSupport Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass*

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

## Contact table set

(contactTableSet). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Contamination

(contam). The presence of a constituent, impurity, or some other undesirable element that spoils, corrupts, infects, makes unfit, or makes inferior a material, physical body, natural environment, place of human occupancy, or other material entity. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSaSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **Control measure implementation**

(contMeasImp). A public health action type wherein authorities have begun implementing infection control measures. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Control Measure Implementation Value Set**

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

### **Control sample**

(control). Denotes a relationship to a primary sample where the object sample serves as a control to the subject sample. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*

## 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: 3.0.0.

### Contact phone

(coPhone). Contact phone number, for the lab. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 10 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Core sampling

(core). Instrument 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:* 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:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### Correctional facility

(corFcil). Correctional facility *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet

## 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:* active. First released: active. Last updated: 2.0.0.

## COSCa ball

(cosca). COSCa passive sampling device. Use collectionPeriod to describe how many hours the ball was used to collect the sample *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* <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.

## Population count

(count). A count of residents for determining site/polygon population. *Part Type:* categories *Domain:* naDomain *Speciment ID:* poSiSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Country-level Aggregation at Site

(countLevel). Specifies that a sewershed/site represents an entire nation or country. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Countries look-up tables

(countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. cu *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: lookup *Nomenclature*: lookup *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.1.0.

## Countries table column order

(countriesOrder). Specifies the order of the columns in the countries table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 1

## Parts

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

### Countries table required headers

(countriesRequired). Required headers in the countries table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *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.

### Country

(country). The country where a site or organization is located; part of the address. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Country endonym

(countryEndonym). The name locals use for their country. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology*

## Parts

*Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: active. Last updated: 2.1.0.

## Country exonym

(countryExonym). The English name foreigners use for the country. 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:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: active. Last updated: 2.1.0.

## Countries or sovereign states

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

## *Parts*

### **Districts, counties, regions**

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

### **Covid-19**

(cov). Covid-19 infection. Any form of Covid-19 human infetion - including testing for Covid-19, symptomatic Covid-19, asymptomatic Covid-19, hospitalized Covid-19, long-Covid-19, etc. If needed, define the specific form Covid-19 with units. See populationUnits. *Part Type*: measurements *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: human-CompartmentSet *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 *Data Type*: seeUnitData *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.

### **SARS-CoV-2 measure**

(cov2Me). Measure the amount of SARS-CoV-2 virus. This measure should only be used if there is no other SARS-CoV-2 measure. See groupID = sarsCov2. Use a note to describe the specific measure used. *Part Type*: measurements *Domain*: bio *Speciment ID*: anySpecimenSet *Compartment*

## Parts

*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.

## Covaris truXTRAC FFPE DNA Library Kit

(covarisTruXTRAC). Covaris truXTRAC FFPE DNA Library Kit. A specialized library prep kit for extracting and preparing DNA from FFPE tissue. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## SARS-CoV-2-B.1.1.7

(covB117). Variant B.1.1.7 of the SARS-CoV-2 virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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*

### **SARS-CoV-2-B.1.351**

(covB135). Variant B.1.351 of the SARS-CoV-2 virus. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **SARS-CoV-2-E**

(covE). SARS-CoV-2 E gene. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: allele *Nomenclature*: allele *Ontology Reference*: GENEPIO:0100151 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **SARS-CoV-2 M Gene target**

(covM). SARS-CoV-2 M gene (orf5) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENEPIO:0100152 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*:

*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.

## **SARS-CoV-2-N1**

(covN1). SARS-CoV-2 nucleocapsid gene, allele 1. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **SARS-CoV-2-N2**

(covN2). SARS-CoV-2 nucleocapsid gene, allele 2. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **SARS-CoV-2-N200**

(covN200). SARS-CoV-2 nucleocapsid gene, amino acids 199-202. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

## Parts

*ment 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.

## SARS-CoV-2-N3

(covN3). SARS-CoV-2 nucleocapsid gene, allele 3. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## SARS-CoV-2-P.1

(covP1). Variant P.1 of the SARS-CoV-2 virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### SARS-CoV-2-RdRp

(covRdrp). SARS-CoV-2 RdRp gene. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: allele *Nomenclature*: allele *Ontology Reference*: GENEPIO:0100168 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### SARS-CoV-2 S Gene Target

(covS). S sars-cov-2 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### SARS-COV-2 5' UTR Gene target

(covUTR5). SARS-COV-2 5' UTR Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENEPIO:0100183 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Clostridium perfringens**

(cPerfrigens). Clostridium perfringens *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* clostridiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Covid-19 population measurement date**

(cphDate). date of reporting for covid-19 measure. Deprecated in ODM version 2. The measure identification is now measureReportID with report dates as for any measure report. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* depreciated. First released: depreciated. Last updated: 2.0.0.

### **Cphd ID**

(cphid). Unique identifier for the table. Deprecated in ODM version 2. The measure identification is now measureReportID. *Part Type:* at-

tributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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: depreciated. Last updated: 2.0.0.

## Critical priority pathogen

(cpp). A microorganism with resistance to multiple drugs and a high threat to human health. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Gene copies per well

(cpWell). Gene or variant copies per well. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

*Parts*

### **crAssphage-N**

(cra). crAssphage virus capsid protein gene region *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: any-CompartmentSet *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.

### **Crassphage Standardized**

(crassStand). This data treatment standardizes the measurement value to concentration levels of crassphage. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Creatinine**

(crea). Creatinine (usually measured as a human fecal chemical indicator) *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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: 2.2.0.

### Crosswalk table set

(crosswalkTableSet). Tables used to translate to and from other environmental dictionaries and models. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Cryptosporidium

(cryptosporidium). Cryptosporidium *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* cryptosporidiumGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Cryptosporidium Group

(cryptosporidiumGrp). A group of measures/methods related to cryptosporidium parasites. Used to describe the organism information for

## *Parts*

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.

## **Cycle threshold or quantification cycle (Ct or Cq)**

(ct). Cycle thresholds in a PCR assay. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Cycle threshold per quantification cycle**

(ctcq). cycle threshold (Ct) / quantification cycle (Cq) *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## CTFinder

(ctFinder). CTFinder. Designed for Clostridioides difficile serotyping and subtyping. Identifies capsular polysaccharide synthesis gene clusters to assign serogroups. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Countries look-up tables Shorthand

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

## Cumulative count

(cuCo). The cumulative count of cases of a given disease. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: poSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA

## Parts

*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.

## Cufflinks (with TopHat integration)

(cufflinks). Cufflinks (with TopHat integration). A specialized read mapper. Combines mapping with transcriptome assembly and quantification. Best for: RNA-seq studies with integrated analysis. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Custody Contact ID

(custodyCont). A unique identifier for data custodians. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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.

## Data custodian ID

(custodyID). The data custodian of a database. Use Organization ID to populate this field, and the organizations table to describe contact information and other details for the data custodian. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Cutadapt

(cutadapt). A sequencing data processing application that does adapter removal and trimming tool for high-throughput sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://cutadapt.readthedocs.io/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Circulating vaccine-derived poliovirus type 2

(cVDPV2). Circulating vaccine-derived poliovirus type 2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* polioGrp *Class:* organism *Nomenclature:*

## Parts

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.

## Number of cycles

(cyNum). The number of cycles of a PCR machine, or any other cycling process. *Part Type*: measurements *Domain*: phy *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.

## D339H Mutation

(d339h). The FLiT/SLip variant mutation D339H. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flirtSLipGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **d377y delta-variant gene target**

(d377y). d377y 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.

### **d3g omicron-variant gene target**

(d3g). d3g 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.

### **d63g delta-variant gene target**

(d63g). d63g delta-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **d796y omicron-variant gene target**

(d796y). d796y omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **d950n delta-variant gene target**

(d950n). d950n delta-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **DADA2**

(dada2). A sequencing data processing application that is primarily used in amplicon sequencing for error correction and generating amplicon sequence

## Parts

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.

## Daily count

(daiCo). The daily count of cases of a given disease. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: poSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Database and Data Repository Class

(database). Measures and methods related to databases and data repositories. *Part Type*: classes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: database *Nomenclature*: database *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

*Parts*

### **Data collection sector or organization**

(dataColl). Describes organization who collect compile, analyze, and or manage data as their central focus. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### **Host Data Repository or Bank**

(dataHost). The external repository or database/bank in which a sequence (or other external data) is stored. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: dataRepoSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Data Repository Set**

(dataRepoSet). The mma set for all valid input categories for the dataRepo field. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: dataRepoSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA

## Parts

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

### **Dataset creation date**

(datasetDate). Specifies the date a given dataset was created. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Dataset ID**

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

## Parts

### Dataset table

(datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. *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.

### Datasets table column order

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

### Dataset table required headers

(datasetsRequired). Specifies the columns required in a Datasets table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

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

## Data types

(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. *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

## Date data type

(date). The data type for date data (does not include time). Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Parts

### Date

(dateDep). Date date on which the assayMethod was created or updated (for version update). *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: datetime *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 3.0.0.

### Datetime data type

(datetime). The data type for date and time data. Only used for the dictionary entries of parts. *Part Type*: dataTypes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### 7-day smoothing of values

(day7Smooth). This data treatment smooths the measurement value across 7-days. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum*

## Parts

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

## Days

(days). A unit for indicating a length of time in days. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

## DNA Data Bank of Japan (DDBJ)

(ddbj). DNA Data Bank of Japan (DDBJ) archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://www.ddbj.nig.ac.jp/index-e.html> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## ddcov\_e sars-cov-2 gene target

(ddcovE). ddcoev\_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.

## **ddcov\_n sars-cov-2 gene target**

(ddcovN). ddcov\_n sars-cov-2 mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **Digital Droplet PCR (ddPCR)**

(ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). *Part Type:* categories *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:* 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.

## Deaths

(death). Units for describing a population measure of patients who have died from a given cause. Unit for a population or disease measure to explain population-level clinical effects. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: na-Group *Class*: 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.

## DeconSeq

(deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <http://deconseq.sourceforge.net/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## DecontaMiner

(decontaMiner). A QC pipeline tool for sequencing data for contamination detection and removal in NGS datasets, especially useful in clinical samples. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## 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.

## Decreased surveillance

(decSurv). Scaling back of monitoring activities, often due to reduced risk. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Deduplication Method

(dedup). Sequencing and PCR deduplication method. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* dedupSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## Deduplication Method Set

(dedupSet). The valid set of deduplication method categorical inputs. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment*

## Parts

*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.

## DeepARG Software

(deepARG). Software tool that predicts AMR genes using deep learning on metagenomic data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/gaarangoa/deeparg> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Dehosting Method

(dehost). Sequencing and PCR dehosting method. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* dehostSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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

### Dehosting Method Set

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

### Omicron Variant 142-144 Deletion

(del142144). Omicron Variant 142-144 Deletion mutation *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### del143/145

(del143). 143 or 145 deletion omicron-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Delta Variant 156-157 Deletion**

(del156157). Delta Variant 156-157 Deletion mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **del 157/158**

(del157). 157 or 158 deletion delta-variant gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **del2084/2084**

(del2084). 2084 or 2084 deletion omicron-variant mutation gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:*

## 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.

## del212/212

(del212). 212 or 212 deletion omicron-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet  
*Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA  
*Data Type*: seeUnitData *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.

## Omicron Variant 142-14431-33 Deletion

(del3133). Omicron Variant 142-14431-33 Deletion mutation. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet  
*Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA  
*Data Type*: seeUnitData *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.

### **del3674/3676**

(del3674). 3674 or 3676 deletion omicron-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **del69/70**

(del6970). 69 or 70 deletion omicron-variant mutation gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Delayed Arrival or Prolonged Transit**

(delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*

## 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.

## Delta

(delta). B.1.617.2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## SARS-CoV-2 Delta Variant Group

(deltaGrp). A group of measures/methods related to the SARS-CoV-2 Delta Variant. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* [http://purl.obolibrary.org/obo/NCIT\\_C169076](http://purl.obolibrary.org/obo/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.

## Dengue Virus Type 1

(den1). Dengue virus, Type 1, general measurement *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:*

anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

## Dengue Virus Type 2

(den2). Dengue virus, Type 2, general measurement *Part Type*: measurements *Domain*: bio *Speciment ID*: poSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

## Dengue Virus Type 3

(den3). Dengue virus, Type 3, general measurement *Part Type*: measurements *Domain*: bio *Speciment ID*: poSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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

### Dengue Virus Type 4

(den4). Dengue virus, Type 4, general measurement *Part Type*: measurements *Domain*: bio *Speciment ID*: poSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### denaturation

(denat). Describes the denaturation cycle in a PCR process. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: na-Class *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *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.

### Dengue

(dengue). Dengue virus, general measurement *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### depth of coverage threshold

(depCovThresh). The threshold used as a cut-off for the depth of coverage. Provide the threshold fold coverage. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

### Deprecated

(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.

### Derived data

(derived). Derived data, data that has undergone aggregation, standardization, adjustment, or any cleaning prior to reporting. *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: 3.0.0.

## **Derived sample**

(derivedSamp). A sample that is derived or made from another sample or material. A derived sample is a type of sample created by mixing material obtained from a field sample (e.g., wastewater, soil, or air) with additional additives in a laboratory setting. This process can involve diluting the original field sample with clean water or other solutions, as needed. Derived samples are typically used to adjust the concentration of the target substance or organism, making it more suitable for analysis or to test the efficiency and sensitivity of detection methods. In the example given, a derived sample might be a sub-sample of wastewater that is diluted with clean water to achieve a specific concentration, allowing for more accurate and reliable analysis. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Description

(descr). A detailed description of a measure, method, or attribute. A description of the part that serves a clear presentation of the part to a wide audience including technical and non 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* 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.

## Description of change

(descrChange). A description of change in a part from the previous version. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Desk or counter

(desk). Desk, table, countertop or other flat working surface. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: surfaceCompartmentSet *Group*: colGrp *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.*

## **Dewatered solids**

(deso). Dewatered solids. *Part Type: categories Domain: naDomain Specimen ID: naSpecimenSet Compartment Set: waterCompartmentSet 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.*

## **Detected**

(det). Substance detected or not detected. TRUE = detected, FALSE = not detected *Part Type: units Domain: bio Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: qualAggScale Quality Set: NA Reference Link: NA Data Type: boolean Missingness Set: NA Minimum Value: 0 Maximum Value: 1 Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.*

## **Access to details deprecated**

(detailsDep). More details on the existing confidentiality requirements of this measurement. *Part Type: attributes Domain: naDomain Speciment ID:*

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

### **Detected Lineage or Clade Name**

(detLinClade). The measurement for reporting detected lineage or clade information - used as an “other” for measurements not already captured in the ODM structure. Most useful if bundled into a measurement set with other relevant measures. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: miscMeas *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: othAgg *Quality Set*: 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.

### **De-escalated variant**

(dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup  
*Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum*

## *Parts*

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

## **Development**

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

## **Dictionary reference table set**

(dictionaryRefTableSet). Reference or look-up tables. For example, the parts table describe all elements of the ODM, including tables, table headers, measures, methods, categories, and units. sets are collections of parts. For example, units can be grouped together in a unitSet. languages and translations support translations. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Additional dictionary sheets**

(dictionarySupport). Additional sheets for the Excel version of the ODM dictionary. Sheets or tabs for the ODM Excel dictionary include: all ERD tables (look-up tables and data entry tables) and additional supportig tables.  
*Part Type*: partType  
*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.

### **Dictionary set type**

(dictSets). Sets used to describe and group dictionary tables.  
*Part Type*: partType  
*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.

### **Dilution factor**

(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*: allDo  
*Speciment ID*: saSpecimenSet  
*Compartment Set*: anyCompartmentSet  
*Group*: procGrp  
*Class*: dilution  
*Nomenclature*: dilution  
*Ontology Reference*: NA  
*Category Set ID*: NA  
*Unit Set*: unitlessUnitSet  
*Aggregation Scale*:

## *Parts*

*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.*

## **Point dillutions**

(dillute). Exact concentration or dillutions for generating a standard curve. *Part Type: measurements Domain: bio 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.*

## **Dilution Class**

(dilution). Measures and methods relating to dilutions. *Part Type: classes Domain: phy 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.*

## **Diphtheria Group**

(diphtheriaGrp). A group of measures/methods related to the diphtheria bacteria. Used to describe the organism information for general measures.

## Parts

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

## DISCOVAR de novo

(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.

## Diseases (human) class

(disease). Measure and methods related to disease or infection in humans. *Part Type:* classes *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* disease *Nomenclature:* disease *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* 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*

### **Dissolved gas concentration unit set**

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

### **Dissolved oxygen**

(dissOxy). Measure of dissolved oxygen in liquid medium *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: miscMeas *Class*: physical *Nomenclature*: physical *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **DNA Template**

(dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## DNA Fragment Length

(*dnaFragLen*). The length of the DNA fragment generated by mechanical shearing or enzymatic digestion for the purposes of library preparation. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* basePairSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## Nextera DNA Flex/DNA Prep Library Prep Kit

(*dnaPrep*). Nextera DNA Flex Library Prep Kit, now called DNA Prep, by Illumina. A flexible, transposase-based library prep kit for a wide range of DNA input amounts, suitable for microbial and human DNA. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **DNA/RNA Shield**

(dnRNAshield). A stabilizing solution for nucleic acids in samples, including wastewater, protecting against degradation at room temperature. *Part Type*: categories *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Data Not Collected**

(dnc). A missingness value for 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.

### **Dengue Virus E Gene**

(dnvE). Dengue Type 2-specific gene taget. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *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: 3.0.0.

### Dengue Virus NS5 Gene

(dnvNS5). Dengue Type 1-specific gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### Dengue Virus prM Gene

(dnvprM). Dengue Type 3 and 4-specific gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### Depth of coverage

(doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Used to interpret the confidence in a presence or amount of a variant. *Part*

## Parts

*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.

## Domain

(domain). Domain is the highest level of describing of a measure. The domain ID that corresponds to a given part. Mostly applicable for measures, methods, units, and aggregations. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

## Domains

(domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature). *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

### **Domestic travel hub surveillance**

(domSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to domestic travel.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet  
*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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Higher education dormitory or residential building**

(dorm). Higher education dormitory or residential building *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### **Digital PCR (dPCR)**

(dpcr). Describes a PCR analysis done using digital PCR technology (general). *Part Type:* categories *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:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

## *Parts*

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

## **Digital PCR (dPCR) instruments**

(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.

## **DDBJ sequence Read Archive (DRA)**

(dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://www.ddbj.nig.ac.jp/dra/index-e.html> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Sewer (drain)**

(drain). A pipe that carries water or sewage away from a place, or an opening in a surface that leads to said pipe. *Part Type:* categories *Domain:*

naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.3.

## Drug surveillance

(drugSurv). Purpose of sampling/measure is to surveil drug use in a population. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSpecimenSet *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Dataset table Shorthand

(ds). The abbreviated short name used to reference the report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. table *Part Type*: shortName *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.2.

## Parts

### Duration time of a method

(duration). The duration of time for a given method as described in protocols. *Part Type*: measurements *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: timeClass *Nomenclature*: timeClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: timeUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### e156g delta-variant gene target

(e156g). e156g delta-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### e484a omicron-variant gene target

(e484a). e484a omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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: 2.0.0.

## Enteropathogenic Escherichia coli (EAEC)

(eaec). Enteropathogenic 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.

## EAGER

(eager). A QC pipeline tool for sequencing data for ancient DNA, providing quality filtering, contamination estimates, and other QC metrics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/ComputationalGenomicsBeijing/EAGER> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **EasySeq NGS Targeted Capture Kit**

(easySeqNGS). EasySeq NGS Targeted Capture Kit by Nimagen. A library preparation kit and targeted capture in one, ideal for small panels. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Epstein–Barr virus (EBV)**

(ebv). Epstein–Barr virus (EBV), formerly known as Human gammaherpesvirus 4 *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: herpesGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Educational Community License v2.0**

(ecl20). The licensing for the measure or data set is managed under the Educational Community License v2.0. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation*

## Parts

*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.

## **Escherichia coli**

(ecoli). Concentration of bacteria that are passed through the faecal excrement of humans, livestock and wildlife *Part Type:* measurements *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* surfaceWaterCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* bacteriaUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **Escherichia coli group**

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

## Parts

### **Eden V1 Primer Set**

(edenV1). An amplicon strategy which was developed by John-Sebastian Eden with primers for SARS-CoV-2 and attributes of version 1.0.0 which produces amplicons approximately 2500bp in length. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: any-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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Educational facility**

(edFac). A school or other educational facility not otherwise specified. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Education**

(education). A measure or sample taken for education or training. Use this purpose, for example, when teaching how to use the PHES-ODM. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## 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.

## Efficiency

(efficient). The efficiency reported for a standard curve. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Wastewater Effluent - non-specified

(effluNS). Sample material is wastewater effluent - whether primary, secondary or other is unspecified. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Enterohemorrhagic Escherichia coli (EHEC)

(ehec). Enterohemorrhagic Escherichia coli (EHEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

## Parts

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.

## Enteroinvasive Escherichia coli (EIEC)

(eiec). Enteroinvasive Escherichia coli (EIEC) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: ecoliGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Electrical potential unit set

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

### **Eluate/Resuspended filter material retained**

(eluate). The eluate fraction, or material resuspended from filtration, is retained after solid separation/centrifugation. *Part Type*: categories *Domain*: phy Speciment ID: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Elution buffer**

(elutionBuff). Elution buffer is used to resuspend material. *Part Type*: categories *Domain*: phy Speciment ID: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Contact email**

(email). Contact e-mail address, for the lab. *Part Type*: attributes *Domain*: naDomain Speciment ID: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*:

## *Parts*

NA *Minimum Length*: 0 *Maximum Length*: 100 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Emboss Cons**

(embossCons). Sequencing software that is part of the EMBOSS suite, generates consensus sequences from multiple alignments. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.bioinformatics.nl/cgi-bin/emboss/help/cons> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Emergency targetted surveillance program**

(emergSurv). A targeted surveillance strategy which is considered important and/or urgent. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSpecimenSet *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **European Nucleotide Archive (ENA)**

(ena). European Nucleotide Archive (ENA). *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: na-

## Parts

CompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: na-Class *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnit-Set *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.

## ENA Format

(enaForm). Dataset was originally recorded and/or stored in ENA 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://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.

## European Nucleotide Association Mapping Column

(enaMap). ENA 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*: 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*

### **European Nucleotide Association (ENA) - notes**

(enaNotes). ENA notes *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Enterobase archives**

(enterobase). Enterobase archives. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://enterobase.warwick.ac.uk> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Enterovirus**

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

## Enterovirus Group

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

## Enumeration for set values

(enumeration). The numeric value that corresponds to a given value in a set, defined in the sets table. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: genMissingnessSet *Minimum Value*: 0 *Maximum Value*: 100 *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

## Temperature and pH probes

(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*

## 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.

## Rainfall

(envRnF). Rainfall, i.e. amount of precipitation in the form of rain. *Part Type:* measurements *Domain:* phy Speciment ID: siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* precipitation *Nomenclature:* precipitation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## Ground snow depth

(envSnwD). Total depth of snow on the ground. *Part Type:* measurements *Domain:* phy Speciment ID: siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* precipitation *Nomenclature:* precipitation *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## Snowfall

(envSnwF). Snowfall, i.e. amount of precipitation in the form of snow. *Part Type:* measurements *Domain:* phy Speciment ID: siSpecimenSet *Com-*

## Parts

*partment 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.

## Enteropathogenic Escherichia coli (EPEC)

(epec). Enteropathogenic Escherichia coli (EPEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Episode date

(epiDate). Episode date is the earliest of onset, test or reported date. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* NA *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.

*Parts*

### **EpiWeek Mean**

(epiMean). The mean of all measures taken in one epiweek. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **EpiWeek Number**

(epiWeek). The number of the epi week in which a sample was 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*: NA *Minimum Value*: 1 *Maximum Value*: 52 *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **EpiWeek Start Date**

(epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start date resolves the possible ambiguity. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: date

## Parts

*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.

## Year of the EpiWeek

(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:* NA *Minimum Value:* 1900 *Maximum Value:* 3000 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## Eclipse Public License 1.0

(epl10). The licensing for the measure or data set is managed under the Eclipse Public License 1.0. *Part Type:* categories *Domain:* naDomain *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.

## Eclipse Public License 2.0

(epl20). The licensing for the measure or data set is managed under the Eclipse Public License 2.0. *Part Type:* categories *Domain:* naDomain *Spec-*

## Parts

*iment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/epl-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.

## Equation

(equation). The equation used in the calculation/data treatment. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 300 *Part Status:* active. First released: active. Last updated: 3.0.0.

## ERD table set

(erdTableSet). All tables listed in the Entity Relationship Diagram. The full ODM model is commonly referred to as “long” tables as it stores data with one measurement per row. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Sarbecovirus-specific E sars-cov-2 gene target**

(eSarbec). Sarbecovirus-specific E sars-cov-2 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **ESBL-encoding genes**

(esbl). Extended-spectrum beta-lactamase-encoding genes. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: amrGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: bacteriaUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **exclusions based sample preparation (ESP)**

(esp). exclusions based sample preparation (ESP) *Part Type*: categories *Domain*: naDomain *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeUnitAggScale *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.

## **Estimated frequency of reads**

(estFreqReads). Estimated frequency of reads in a sequencing assay *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: gen-MissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Estimated data**

(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.

## **Estuary, natural water body**

(estuary). Estuary, natural water body *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: colGrp *Class*: naClass *Nomenclature*: naClass *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:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Enterotoxicigenic Escherichia coli (ETEC)

(etec). Enterotoxicigenic 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.

## European Union Public License 1.1

(eupl11). The licensing for the measure or data set is managed under the European Union Public License 1.1. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/eupl-1.1/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## *Parts*

### **European Union Public License 1.2**

(eupl12). The licensing for the measure or data set is managed under the European Union Public License 1.2. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/eupl-1.2/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### **Evening**

(eve). Sample was collected in the evening, late in the day. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: timeClass *Nomenclature*: timeClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Exceptions Part Type**

(exceptions). An exception part type for use in creating wide names that do not follow the general structure. *Part Type*: partType *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

## 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.

### SARS-CoV-2 exoN gene (nsp14)

(exoNnsp14). SARS-CoV-2 exoN gene (nsp14) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100170 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### Extraintestinal pathogenic Escherichia coli (ExPEC)

(expec). Extraintestinal pathogenic Escherichia coli (ExPEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Experiment Failed

(expFail). PCR experiment failed. No value reported. Value should be blank for a measure with this qualityFlag value. *Part Type:* qual-

## Parts

ityIndicators *Domain*: bio *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.

## Extraction Blank - Control

(extBlank). Binary Y/N indicator for if extraction blank was used as a control for the nucleic acid extraction process. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: booleanSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: boolean *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.

## 4s method

(extract4s). Nucleic acid extraction performed using the 4s method. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### Nucleic acid extraction method

(extraction). Description of the nucleic acid extraction method. Description of the method used to extract the sample *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: extractSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

### Extraction Recovery Percent

(extractRecov). The percentage of spiked in or endogenous compound used to assess extraction recovery of nucleic acids. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: percentUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

### Nucleic Acid Extraction set

(extractSet). set used for storing all the valid category values for the nucleic acid extraction method. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: extractSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical

## 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.*

## Extraction volume of sample

(exvol). Extraction volume of sample. Size of the sample that is analyzed. *Part Type: measurements Domain: phy Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: physical Nomenclature: physical Ontology Reference: NA Category Set ID: NA Unit Set: volumeUnitSet Aggregation Scale: seeUnitAggScale Quality Set: 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.*

## F456L Mutation

(f456l). The FLiRT/SLip variant mutation F456L. *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: flirtSLipGrp Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: seeUnitData 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.*

## Fecal matter

(faeces). Fecal matter. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: waterCompartmentSet Group:*

## Parts

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.

## Fast-flowing

(faFlow). A quality of a body of water wherein there is a fast flow. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSaSpecimenSet *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Degree Fahrenheit

(fah). Unit for temperature, degrees Fahrenheit. *Part Type*: units *Domain*: phy *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## Parts

### **FALSE**

(FALSE). Boolean data type = FALSE Use these values and their set for any boolean measure or attribute. Use only “FALSE” (case sensitive) *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: boolean *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 5 *Maximum Length*: 5 *Part Status*: active. First released: active. Last updated: 2.3.0.

### **Farm**

(farm). An agricultural area, builing, or tract of land. Used for the cultivation of crops or grazing of livestock, including any buildings. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **FastMLST**

(fastMLST). FastMLST. Focus: Lightweight MLST and serotyping from assembled genomes or raw reads. Applications: Broad bacterial species. Features: Quick and simple, designed for routine use. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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:* 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.

## FASTP

(fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/OpenGene/fastp> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## FastQC

(fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

## **FASTQ Screen**

(fastqScreen). A dehosting software that checks reads against multiple reference genomes, including host genomes, to remove contamination. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: [https://www.bioinformatics.babraham.ac.uk/projects/fastq\\_screen/](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.

## **FastUniq**

(fastUniq). A deduplication method that is specifically designed to remove duplicates in paired-end sequencing data. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://sourceforge.net/projects/fastuniq/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **FASTX Toolkit**

(fastXTools). A sequencing data processing application that provides various functions for FASTQ processing, including quality filtering. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*:

## Parts

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/](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.

### **Male-specific (F+) coliphage - general**

(fColiphage). Male-specific (F+) coliphage - general *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: phageGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **F+ DNA coliphage**

(fDNA). F+ DNA coliphage *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: phageGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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*

### **Fecal coliform count**

(fecalCol). Measure of prevalence of fecal coliform bacteria *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: miscMeas *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: bacteriaUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

### **Fecal-contamination**

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

### **Field sample**

(field). Specifies a sample taken from the field; directly collected from an area for testing. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum*

## *Parts*

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

### **Field sample replicate**

(fieldReplicate). A sample divided into two or more homogeneous parts. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **File location of polygon**

(fileLocation). The location of the file containing the geometry of the polygon. File path specified, or a URL *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 65535 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Filtration**

(filt). Describes solid separation from a wastewater sample via filtration. Proceeds further concentration or analysis of the liquid filtrate. *Part Type:* categories *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *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.*

## **Filtration units**

(filtInst). Filtration instruments; remove large particulates or concentrate targets (e.g., tangential flow filtration). *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## **First Nation**

(fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Likely for internal use only, Indigenous data can and should not be shared without explicit consent of the nation in question. *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.*

### **Final volume**

(finVol). The final volume of a testing solution or sample. *Part Type*: measurements *Domain*: che *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

### **First name of contact**

(firstName). Specifies the first name of a given contact. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **First released version**

(firstReleased). The version in which a part was first released *Part Type*: partSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## *Parts*

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

## **Foreign key**

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

## **AI - Inhibition present but addressed**

(flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. *Part Type:* qualityIndicators *Domain:* bio *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.

## **B - Trace levels of contamination**

(flagB). Analytical result may be subject to “trace” levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. *Part Type:* qualityIndicators *Domain:* bio *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.

## **FI - Inhibition present and unaddressed**

(flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. *Part Type*: qualityIndicators *Domain*: bio *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.

## **J - Weak signal extrapolation**

(flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. *Part Type*: qualityIndicators *Domain*: bio *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*

## *Parts*

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

### **ND - Non-detect**

(flagND). No amplification occurred in the reaction; non-detect. For the value of a non-detected measure, report the actual value even if it is below the limit of detection. The flag here ensures that it's recorded as a non-detect regardless. In instances where the original data doesn't record a value, but only has the flag, please populate the value field with either a 0 if dealing with variant percentages, and a 1 for all other purposes to further indicate a null result. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **UJ - Trace signal extrapolation**

(flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., “trace” signal observed); the reported value is based on the extrapolation of the standard curve in the non-linear region. *Part Type:* qualityIndicators *Domain:* bio *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:*

## Parts

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

### **UQ - Unquantifiable**

(flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. *Part Type*: qualityIndicators *Domain*: bio *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.

### **Flavivirus (West Nile, Dengue, Zika) Group**

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

### **FLiRT/SLip Variant Group**

(flirtSLipGrp). The group for measures and methods pertaining to the FLiRT and SLip variants of SARS-CoV-2. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet

## Parts

*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.

## FLiRT Variants

(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.

## Float data type

(float). The data type for float data. Only used for the dictionary entries of parts. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Flocculation

(floc). The process of aggregating suspended particles into larger clusters (flocs) using coagulants to aid in sedimentation or filtration. *Part Type:* categories *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* na-Class *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* 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.

## Flow-normalized mean

(floMean). Mean measure normalized to wastewater flow. Mostly used for reporting specific alleles (N1, N2, E, etc.) *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## Floor

(floor). Floor of a building or room. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* surfaceCompartmentSet *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*

## *Parts*

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

## **Flow rate**

(floRate). Wastewater volumetric flow rate at the sample collection location over the 24-hr period during which the sample was collected. If only an instantaneous flow measurement is available, it may be reported in units of million gallons per day. *Part Type:* measurements *Domain:* phy Speciment ID: siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* flowClass *Nomenclature:* flowClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* flowUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **Flow proportional 24hr sample depreciated**

(flow24hDep). A flow proportional 24-hour composite sample generally collected by an autosampler. *Part Type:* categories *Domain:* naDomain Speciment ID: naSpecimenSet *Compartment Set:* 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:* NA *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.

## Flow class

(flowClass). Measures and methods related to flow. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* naGroup *Class:* flowClass *Nomenclature:* flowClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* flowUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

## Flow meters

(flowInst). Flow meter instruments; 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.

## Flow proportional sample

(flowPr). A flow proportional composite sample generally collected by an autosampler. Use collectionPeriod to describe how many hours the sample was taken. The volume of wastewater taken is proportional to the flow rate flowing at each instant of sampling. This is also called constant time, variable volume (CTVV). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

## Parts

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

## Flow Standardized

(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.

## Volume flow rate unit set

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

### **Flow volume**

(flowVol). Volume of influent. *Part Type*: measurements *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: siteFeat *Class*: flowClass *Nomenclature*: flowClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: flowUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Influenza virus measure**

(flu). General influenza virus measure This measure should only be used if there is no other influenza virus measure. See groupID = virusMisc. Use a note to describe the specific measure used. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: fluGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: [http://purl.obolibrary.org/obo/MONDO\\_0005812](http://purl.obolibrary.org/obo/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.

### **Influenza A virus**

(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*

## *Parts*

*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.

### **Influenza virus A1**

(fluA1). Influenza virus A1 type *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Influenza virus A1 and A2 combined**

(fluA1A2c). Measure of influenza virus A1 and A2 combined, usually due to single fluorescence channel. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **influenza virus A2**

(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.

## Influenza A Virus Group

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

## Influenza virus B

(fluB). Influenza virus B type *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluBGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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

### **Influenza B Virus Group**

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

### **Influenza Virus General Group**

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

### **Influenza A H5 hemagglutinin gene**

(fluH5hema). Measure of the H5 hemagglutinin gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: fluAGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale

## 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.

### Influenza A M gene

(fluIAVm). A measure of the M gene found in Influenza A viruses (IAV). The virus has segmented RNA genome and 7th segment, M gene, encodes 2 proteins. M1 is a matrix protein and M2 is a membrane protein. The M gene may be involved in determining host tropism. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* fluAGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* <https://virologyj.biomedcentral.com/articles/10.1186/1743-422X-6-67#:~:text=The%20M%20gene%20of%20all%20known%20human%20influenza%20A%20viruses,of%20the%2019> *Data Type:* seeUnitData *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.

### Fluidigm digital PCR

(fluIDpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. *Part Type:* categories *Domain:* bio *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.

*Parts*

### **Influenza A N1 neuraminidase gene**

(fluN1neur). Measure of the N1 neuraminidase gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: fluAGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Flye**

(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.

### **First Nation Territory/Métis Settlement-level Aggregation at Site**

(fnmiLevel). Specifies that a sewershed/site represents the entirety of a First Nations territory or reservation, or a Métis settlement. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment*

## Parts

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

## Formazin nephelometric unit

(fnu). formazin nephelometric unit (FNU) *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## Foggy

(foggy). Qualitative category for the weather measure, specifying a foggy or hazy day. *Part Type:* categories *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *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*

## **Feet**

(foot). foot (ft) *Part Type*: units *Domain*: phy *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Fqtrim**

(fqtrim). A sequencing data processing fast tool for adapter removal, quality trimming, and quality control. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://ccb.jhu.edu/software/fqtrim/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Fraction analyzed**

(fraction). Fraction of the sample that is analyzed. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: fractionSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: genMissingnessSet *Minimum Value*:

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

### Fraction input (wide table)

(fractionInput). The partID for the fraction being used in a wide name. *Part Type: attributes Domain: naDomain Specimen 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: 2.2.0.*

### Fraction name (wide table)

(fractionName). The fraction analyzed referenced for the wide name. *Part Type: attributes Domain: naDomain Specimen 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: 2.2.0.*

### Sample fraction set

(fractionSet). set for the fraction of the sample (solid, liquid, etc.). *Part Type: mmaSets Domain: naDomain Specimen ID: naSpecimenSet Compartment Set: anyCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: fractionSet Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA*

## 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: 2.0.0.

## FRCbam

(frcBam). A QC pipeline tool for sequencing data that assesses read quality and genome assembly quality metrics for high-throughput data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* [https://github.com/vezzi/FRC\\_align](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.

## Freyja Script

(freyja). Freyja Script for sequencing. *Part Type:* categories *Domain:* bio *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:* <https://github.com/andersen-lab/Freyja> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### F-Specific RNA bacteriophages

(fRNABact). A measure for amount of F-Specific RNA bacteriophages.  
*Part Type*: measurements *Domain*: bio *Specimen 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.

### F+ RNA coliphage

(fRNAColi). F+ RNA coliphage *Part Type*: measurements *Domain*: bio *Specimen 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.

### F-Specific RNA bacteriophages, G2

(frnaG2). A measure for amount of G2 F-Specific RNA bacteriophages.  
*Part Type*: measurements *Domain*: bio *Specimen 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

## *Parts*

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

## **Sample frozen**

(frozen). Sample was frozen before analysis or processing *Part Type:* qualityIndicators *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.

## **Field sample temperature**

(fst). Temperature that the sample is stored at while it is being sampled. This field is mainly relevant for composite samples which are either kept at ambient temperature or refrigerated while being sampled. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## **Francisella tularensis**

(fTularensis). Francisella tularensis *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

*Group:* tularemiaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Full dictionary sheets set

(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.

## Funder contact ID

(funderCont). A unique identifier for a funder. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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*

### **Funding agency ID**

(funderID). The funding agency of the dataset. Use Organization ID to populate this field, and the organizations table to describe contact information and other details for the funding agency. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **g215c delta-variant gene target**

(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.

### **g339d omicron-variant gene target**

(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

## 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.

### **g496s omicron-variant gene target**

(g496s). g496s omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **g662s delta-variant gene target**

(g662s). g662s delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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

### Gamma

(gam). P.1 *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### Gas class

(gas). Measures and methods relating to gas and gases. *Part Type*: classes *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: gas *Nomenclature*: gas *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: dissGasUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Gaussian distribution stanrdized/Normalized

(gauss). Standardize the data to a gaussian/normal distribution, such that the data have a mean of zero and a standard deviation of one. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*:

## *Parts*

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

### **Gene copies**

(gc). Gene or variant copies *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Gene copies per copy of crAssphage**

(gcCrA). Gene or variant copies per copy of crAssphage. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Gene copies per day**

(gcDay). Unit of measurement of the number of gene copies per day. *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA

## Parts

*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.

### **gene copies per day per 100,000 people**

(gcDay100k). The unit for measures reflecting the gene copies per day per 100,000 people in the population. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Gene copies per gram solids**

(gCGS). Gene or variant copies per gram solids. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Gene copies per L**

(gcL). Gene or variant copies per litre. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

## *Parts*

*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.

### **Gene copies per mL**

(gcMl). Gene or variant copies per millilitre of solution. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Gene copies per millilitre per 100,000 people**

(gcMl100k). Unit of measurement of the number of gene copies per millilitre per 100,000 people. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **Gene copies per PMMoV copy**

(gcPpmov). Gene or variant copies per copy of PMMoV. *Part Type*: units  
*Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet  
*Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Gene copies per Reaction**

(gcRx). Gene or variant copies per reaction in PCR *Part Type*: units  
*Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet  
*Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **GEM Mapper**

(gemMapper). GEM Mapper. A specialized read mapper. High-speed and accurate alignment tool for short reads. Best for: Genomic applications with short reads. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality*

## Parts

*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.

## **GenBank Archives**

(genBank). GenBank Archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://www.ncbi.nlm.nih.gov/genbank/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **genome completeness**

(genComplete). The percentage of expected genes identified in the genome being sequenced. Missing genes indicate missing genomic regions (incompleteness) in the data. Provide the genome completeness as a percent (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## Parts

### **Geneious**

(geneious). Sequencing software that is popular for sequence assembly, alignment, and consensus sequence generation. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.geneious.com/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Genetics unit set**

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

### **General missingness set**

(genMissingnessSet). The general set for missingness values. *Part Type*: missingnessSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## Parts

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

## GenoTyphi

(genoTyphi). GenoTyphi. Focus: Specific MLST and serotyping for Salmonella Typhi. Applications: Outbreak investigations and epidemiology. Features: Highly specialized for typhoidal Salmonella. *Part Type:* categories *Domain:* bio *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:* GitHub: <https://github.com/typhoidgenomics/genotyphi> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Generic quality flag set

(genQualitySet). A quality set to specify any generic quality concerns about a measure or sample. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* 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

### **European Petroleum Survey Group Coordinates**

(geoEPSG). The unique EPSG code specifying a given geospatial area.  
*Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet  
*Compartment Set*: naCompartmentSet *Group*: miscAttr *Class*: 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.

### **Latitude**

(geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721) *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: miscAttr *Class*: 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.

### **Longitude**

(geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000) *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: miscAttr *Class*: 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*:

## *Parts*

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

### **Type of geography**

(geoType). Type of geography that is represented by the polygon. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: geoTypeSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Geographic set**

(geoTypeSet). set for different type of geographic components. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: geoTypeSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Well-known text**

(geoWKT). Well-known text of the polygon *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*:

## *Parts*

*naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: genMissingnessSet Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 63 Part Status: active. First released: active. Last updated: 2.0.0.*

## **GNU Free Documentation License v1.3**

(gfdl13). The licensing for the measure or data set is managed under the GNU Free Documentation License v1.3. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *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.

## **Global Initiative on Sharing All Influenza Data (GISAID) archives**

(gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://gisaid.org> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## GitHub

(github). GitHub external data storage. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Gram per kilogram

(gkg). gram per kilogram (g/kg) *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## Gram per liter

(gL). gram per liter (g/L) *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## Parts

### **10% Glycerol Solution**

(glycerol10). 10% Glycerol Solution - Common cryoprotectant for bacterial and viral storage in environmental samples. *Part Type:* categories *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Gram per cubic metre**

(gm3). Density unit. Used for absolute humidity and other measures. *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### **GMAP**

(gmap). GMAP. A specialized read mapper. A long-read aligner for genomic mapping. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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

## Parts

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

### Geometric mean

(gmn). Geometric mean. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### Nitrogen per total solids

(gNgTS). nitrogen per total solids (gN/gTS) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

### Gonococcus Group

(gonococcusGrp). A group of measures/methods related to gonococcus bacteria. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* gonococcusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA

## *Parts*

*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.

## **Government agency**

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

## **Grams per total solids**

(gPergTS). Grams per total solids (g/gTS) *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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.

## **GNU General Public License v2.0**

(gpl20). The licensing for the measure or data set is managed under the GNU General Public License v2.0. *Part Type:* categories *Domain:*

naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/gpl-2.0/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### GNU General Public License v3.0

(gpl30). The licensing for the measure or data set is managed under the GNU General Public License v3.0. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/gpl-3.0/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### Orthophosphate per total solids

(gPO43gTS). orthophosphate per total solids (gPO43-/gTS) *Part Type*: units *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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.

## Parts

### Orthophosphate as phosphorus per total solids

(gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS)  
*Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

### Grab samplers

(grabInst). Grab sampler instruments; manually collect a single sample at a point in time. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### Grams

(grams). A unit of mass or weight. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA

## Parts

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

### Gram stain

(gramSt). After the sample is taken, the Gram stain is colored purple. Then, a solvent is added to the stain. When the solvent combines with bacteria in a sample, the bacteria will either stay purple or turn pink or red. If the bacteria remain purple, they are Gram-positive. If the bacteria turn pink or red, they are Gram-negative. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### GraphMap

(graphmap). GraphMap. A long-read specific mapper. Long-read aligner optimized for highly error-prone reads. Best for: De novo assemblies using long-read data. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Parts

### Gravity settling

(graSet). Describes solid separation from a wastewater sample where the sample material is allowed to settle by gravity, and then separated.  
*Part Type:* categories *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *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.

### Grab sample

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

### Grit chamber

(gritCham). A sedimentation basin in wastewater treatment that removes heavy, inorganic particles (e.g., sand, gravel) before biological treatment.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* ENVO:03501467 *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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## Gromstole 1.0 Script

(gromstole). Gromstole 1.0 Script for sequencing. *Part Type: categories Domain: bio 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: https://github.com/Poon-Lab/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.*

## Group

(group). Unique identifier for a group of measures. Mostly applicable for measures, methods, units, and aggregations. A collection of related measures. For example, SARS-CoV-2 is a group. Within the SARS-CoV-2 group, there are measure classes 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 Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: 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*

## **Groups**

(groups). A collection of related measures. Used primary to group measurements and methods, this helps pare down the drop down list for a given measurement or methods. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## **Growth in enrichment broth**

(growBroth). The selective cultivation of microorganisms in a nutrient-rich liquid medium to increase their concentration before analysis. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **Ground water**

(grWa). Underground water which is located in pore spaces found in rock or unconsolidated deposits such as soil, clay, or gravel. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Genome Sequence Archive (GSA)

(gsa). Genome Sequence Archive (GSA). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://ngdc.cncb.ac.cn/gsa/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## GSNAP

(gsnap). GSNAP. A specialized read mapper. A splice-aware aligner for RNA-seq reads. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Guanidine Thiocyanate

(gt). A buffer solution/medium that serves as a strong preservative for viral RNA, commonly used in molecular biology for RNA preservation.

## Parts

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

## Genomic Target Enrichment

(gte). The molecular technique used to selectively capture and amplify specific regions of interest from a genome. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* gteSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## Genomic Target Enrichment Methods Set

(gteSet). The set for valid inputs for the Genomic Target Enrichment method. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* gteSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **H5N1 avian influenza A virus (IAV)**

(h5n1). General measurement for the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: fluAGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Haemophilus Group**

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

### **See Header for Aggregation**

(hAg). An indicator to show in a wide-name that aggregation information is located in a different column. Not a valid value for aggregation in the standard long-format. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA

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

## Hand hygiene advisory

(handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. *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.

## Hank's Balanced Salt Solution (HBSS)

(hbss). Hank's Balanced Salt Solution (HBSS) - Nutrient-rich buffer that maintains cell and microbial integrity in samples. *Part Type:* categories *Domain:* naDomain *Specimen ID:* saSpecimenSet *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:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Healthcare activity**

(hcAct). Healthcare activity occurred upstream of the sampling site. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSpecimenSet *Compartment Set*: waterCompartmentSet *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.

## **Healthcare facility**

(hcf). A building for the provision of healthcare, not otherwise specified. *Part Type*: categories *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **See Header for Compartment**

(hCo). A indicator for wide-names that the compartment information is stored in a separate column. Not a valid value for compartment in the standard long-format. *Part Type*: compartments *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: wideCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*:

## *Parts*

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

## **Haemophilus ducreyi**

(hDucreyi). *Haemophilus ducreyi Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: haemophilusGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **Header**

(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.

## **Health administration or planning agency**

(healthAdm). Health administrative or planning organization. *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.

## Health Region for a Site

(healthRegion). A free-text variable for listing the health region for a given site. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.1.0.

## Heat inactivated sars-cov-2 virus spike target

(heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control target. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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*

### **SARS-CoV-2 hel gene (nsp13)**

(hel). SARS-CoV-2 hel gene (nsp13) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENE-PIO: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.

### **Hepatitis A**

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

### **Hepatitis B**

(hepB). Hepatitis B *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: hepGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Hepatitis C

(hepC). Hepatitis C *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: hepGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Hepatitis E

(hepE). Hepatitis E *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: hepGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## hep g armored rna

(hepGRna). Measure of the amount Hepatitis G Armored RNA. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: hepGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **hep g armored rna spike target**

(hepGRnaMat). Hepatitis G armored RNA is used as the recovery efficiency control target. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### **Hepatitis Group**

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

### **Herpes Virus Group**

(herpesGrp). A group of measures/methods related to herpes viruses. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

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

## HF183 Bacteriodes 16S

(hf183). Human-Specific HF183 Bacteriodes 16S rRNA *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: 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.

## See Header for Fraction Analyzed

(hFr). An indicator in wide-names to show that information on the fraction analyzed in found under a separate header. Not a valid value for fraction analyzed in the standard long-format. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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: 2.2.0.

## *Parts*

### **5-hydroxyindoleacetic acid (5-HIAA)**

(hiaa5). 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 *Speciment ID:* siSaSpecimenSet *Compartment Set:* water-CompartmentSet *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:* gen-MissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

### **High severity**

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

## **Haemophilus influenzae**

(hInfluenzae). *Haemophilus influenzae Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* haemophilusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **HISAT2**

(hisat2). HISAT2. A general-purpose read mapper. Successor to TopHat, optimized for RNA-seq data with splicing awareness. Best for: Large-scale RNA-seq experiments. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **Human Immunodeficiency Virus (HIV)**

(hiv). Human Immunodeficiency Virus (HIV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hivGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## **HIV Group**

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

## **Sewer Network Health Region**

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

## **Hand Measurement**

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

menSet *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.

## See Header for Measure

(hMe). An indicator to show in a wide-name that measure information is located in a different column. Not a valid value for measure in the standard long-format. *Part Type*: measurements *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: othAgg *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *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.

## Human Metapneumovirus (HMPV)

(hmpv). Human Metapneumovirus (HMPV) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpvGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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

### **Hollow fiber dead end ultrafiltration**

(hollowFiberUF). Hollow fiber dead end ultrafiltration *Part Type*: categories *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Stay-at-home order**

(homeOrder). A directive requiring people to remain at home except for essential activities. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Horizontal grab sampling**

(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. *Part Type*: categories *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

## Parts

*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.*

### **General Hospital Admissions**

(hosa). Hospital admissions or patients newly admitted to hospital. *Part Type: units Domain: bio Speciment ID: poSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.*

### **Hospital Census**

(hosc). Hospital census or the number of people admitted with an ailment. *Part Type: units Domain: bio Speciment ID: poSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.0.0.*

### **Hospital**

(hosptl). Hospital *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: anyCompartmentSet 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.*

## **Version of Data Hosting Platform/Repository**

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

## **Holding tank wastewater depreciated**

(hoTaWa). Wastewater from a holding tank, such as from an airplane or ship Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: 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: NA 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.*

## Hours

(hours). A unit for indicating a length of time in hours. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Human Parainfluenza Virus (HPIV)

(hpiv). Human Parainfluenza Virus (HPIV) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: parafluGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## High priority pathogen

(hpp). A resistant organism of serious concern, requiring urgent attention. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## *Parts*

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

### **Human Papiloma Virus (HPV)**

(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.

### **Human Rhinovirus (HRV)**

(hrv). Human Rhinovirus (HRV) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Human Rhinovirus (HRV) A**

(hrvA). Human Rhinovirus (HRV) A *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:*

## 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.*

### **Human Rhinovirus (HRV) B**

(hrvB). Human Rhinovirus (HRV) B *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Human Rhinovirus (HRV) C**

(hrvC). Human Rhinovirus (HRV) C *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* hrvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Rhinovirus Group**

(hrvGrp). A group of measures/methods related to rhinoviruses. Used to describe the organism information for general measures. *Part Type:*

## *Parts*

groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: any-  
*CompartmentSet 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.

## **See Header for Specimen**

(hSp). An indicator to show in a wide-name that specimen information is located in a different column. Not a valid value for specimen in the standard long-format. *Part Type*: specimens *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

## **Herpes Simplex Virus**

(hsv). Herpes Simplex Virus *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: herpesGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeU-  
*nitData 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.

### **Holding tank wastewater**

(htSam). Wastewater sampled from a holding tank, such as from an airplane or ship *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Holding tank**

(htSite). Holding tank *Part Type*: categories *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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Human compartment**

(hum). A measure or observation made about a human. *Part Type*: compartments *Domain*: bio *Speciment ID*: anySpecimenSet *Compartment Set*: humanCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*:

## *Parts*

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

## **Human compartment set**

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

## **Humidity class**

(humid). Measures and methods related to humidity. *Part Type*: classes *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: airCompartmentSet *Group*: naGroup *Class*: humid *Nomenclature*: humid *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: 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.

## **See Header for Unit**

(hUn). An indicator to show in a wide-name that unit information is located in a different column. Not a valid value for unit in the standard long-format. *Part Type*: units *Domain*: 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:* 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: 2.2.0.

## Animal husbandry

(husb). Animal husbandry occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *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.

## Hybrid Selection Method

(hySel). Selection by hybridization in array or solution for genomic target enrichment. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## i1566v omicron-variant gene target

(i1566v). i1566v 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.*

## **i3758v omicron-variant gene target**

(i3758v). i3758v omicron-variant mutation gene target *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: seeUnitData 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.*

## **i82t delta-variant gene target**

(i82t). i82t delta-variant mutation gene target *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: sarsCov2 Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: seeUnitData 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.*

## Ibuprofen

(ibu). Ibuprofen (usually measured as a human fecal chemical indicator)  
*Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet  
*Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc  
*Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA  
*Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale  
*Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData  
*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.

## International Classification of Diseases

(icd). Classification system for diseases in humans. *Part Type:* nomenclatures *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* humanCompartmentSet *Group:* naGroup *Class:* disease *Nomenclature:* disease *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Intensive care unit patients

(icu). Units for describing a population measure of patients who are in intensive care due to a given cause. Unit for a population or disease measure to explain population-level clinical effects. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer

## Parts

*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.

## IDBA-UD

(idbaUD). A sequencing software that is an iIterative assembler optimized for metagenomics and complex genomic datasets. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/loneknightpy/idba> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Illumina DNA Prep with Enrichment

(illuminaDNAprep). Illumina DNA Prep with Enrichment by Illumina. A library prep kit that integrates DNA library prep with enrichment for target regions, ideal for targeted sequencing. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### Instrument table Shorthand

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

### Inch

(inch). inch (in) *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### Increased surveillance

(incSurv). Intensified efforts to monitor disease trends or case counts. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## *Parts*

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

## **Index**

(index). Index number in case the measurement was taken multiple times. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Industrial plant**

(indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occasionally services, and making them into products. *Part Type:* categories *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Industrial activity**

(indus). Industrial activity occurred upstream of the sampling site. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet *Com-*

## Parts

*partment Set:* waterCompartmentSet *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.

## Industrial input

(indusIn). Percentage of total wastewater input coming from industrial sources. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartiment 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.

## Influent equilibration

(influEqui). Binary indicator for whether a site stores influent wastewater prior to treatment to equilibrate flow rates. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartiment 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.

## Parts

### Influent pump station

(infPump). A facility that lifts and transports raw wastewater from collection systems to treatment plants. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: colGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: ENVO:03501465 *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Inhibition set

(inhibitionSet). Category set for inhibition methods. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: inhibitionSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Inhibition measure

(inhibMe). Parameter to report whether or not inhibition was detected in the sample. Detected = TRUE, not detected = FALSE. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: miscMeas *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *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.

### **Inhibition method**

(inhibMeth). Description of the method used to evaluate molecular inhibition. Description of the inhibition parameters. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* inhibitionSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

### **Innovaprep ultrafiltration**

(innovaprepUF). Innovaprep ultrafiltration *Part Type:* categories *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *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.

### **Input**

(input). Input for a table. Indicates if a part can be used in a table. “Input” is used to indicate if a part can be used as an entry in a table (something

## *Parts*

with partType = table). For example, covN1 is a specific measure that can be entered in the measureID field of the measures table. Therefore, covN1 is has a value “input” in the measures column in the parts list. ODM users can generate their own custom template by modifying using the value “input” for only the parts that are applicable for their program.

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

## **Omicron Variant ins214epe Insertion**

(ins214epe). Omicron Variant ins214epe Insertion mutation. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **International Nucleotide Sequence Database Collaboration (INSDC) Archives**

(insdc). International Nucleotide Sequence Database Collaboration (INSDC) Archives - often includes ENA, NCBI, or DDBJ inputs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

## Parts

*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.

## Institution-level Surveillance

(instituLev). Surveillance is done at the level of an entire institution.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* anySpecimenSet  
*Compartment Set:* anyCompartmentSet *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.

## Instrument ID

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

## Parts

### Instrument table

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

### Instruments table column order

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

### Instrument table required headers

(instrumentsRequired). Specifies the columns required in the Instruments table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum*

## Parts

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

## Other instrument

(instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. An other type of measurement instrument. Add description to notes. See documentation for how to request new instruments added to the dictionary. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Instrument Type

(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:* 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*

### **Describe other instrument type, if applicable**

(insTypeOth). Description of the instrument in case it is not listed in instrumentType. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Instrument set**

(insTypeSet). List of instruments that are used for measures and methods *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

### **Integrase Anti-microbial resistance Group**

(intAMRGrp). The group for measures and methods pertaining to integrase-related anti-microbial resistance. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: intAMRGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *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.

### **Integer data type**

(integer). The data type for integers. Only used for the dictionary entries of parts. *Part Type*: dataTypes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Integrase Class I gene target**

(integraseCl1). Integrase anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: intAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Intercept**

(inter). Intercept value of the calibration curve. Used for storing calibration curve information, potentially also applicable for other curve types. *Part Type*: units *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*:

## *Parts*

*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.

## **Internal reference**

(internalRef). Reference an internal (i.e. private) database within the user's own organization. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **International travel hub surveillance**

(internatSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to international travel. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### Combined ip2 and ip4 sars-cov-2 gene target

(ip2ip4). Combined ip2 and ip4 sars-cov-2 gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### IQ-TREE Software

(iqTree). A lineage or clade analysis software tool for constructing phylogenetic trees with clade support. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://iqtree.org/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### ISC

(isc). The licensing for the measure or data set is managed under the ISC license. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/isc/> *Data*

## 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: 2.2.0.

### ISO639-1

(iso6391). The first part of the ISO 639 series of international standards for language codes. Part 1 covers the registration of two-letter codes. There are 183 two-letter codes registered as of June 2021. The registered codes cover the world's major languages. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### ISO639-2B

(iso6392B). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'B' specifies the bibliographic code (B code). Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:*

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

## ISO639-2T

(iso6392T). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'T' specifies the terminological code (T code). Part of the metedata for a languageID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

## ISO639-3

(iso6393). A set of international standards that lists short codes for language names. ISO 639-3 extends the ISO 639-2 alpha-3 codes with an aim to cover all known natural languages. Part of the metedata for a languageID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 3.0.0.

*Parts*

## **ISO639-6**

(iso6396). A set of international standards that lists short codes for language names. ISO 639-6 builds off ISO639-3 with the use of four-letter codes, and allowing users to 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:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 3.0.0.

## **ISO 3166-1 alpha-2 country code**

(isoCode). The ISO 3166-1 alpha-2 code, a two-letter country code which is also used to create the ISO 3166-2 country subdivision code and the Internet country code top-level domain. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 2 *Maximum Length:* 2 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **ISO 3166-1 alpha-3 country code**

(isoCodeX). The ISO 3166-1 alpha-3 code, a three-letter country code which may allow a better visual association between the code and the country names than the 3166-1 alpha-2 code. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 3 *Maximum Length:* 3 *Part Status:* active. First released: active. Last updated: 2.1.0.

### **ISO 3166-2 code for country sub-domain**

(isoZone). The ISO 3166-2 codes for the names of the principal subdivisions (e.g., provinces, states, departments, regions) of all countries coded in ISO 3166-1. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 4 *Maximum Length:* 6 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **iVar**

(iVar). A sequencing data processing application that is designed for viral amplicon data, removes primers and can trim low-quality bases. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet

## Parts

*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.

## JN.1.7 Variant

(jn17V). The JN.1.7 variant of SARS-CoV-2, one of the FLiRT variants.  
*Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet  
*Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant  
*Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA  
*Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA  
*Reference Link:* NA *Data Type:* seeUnitData *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.

## JN.1 Variant

(jn1V). The JN.1 variant is a subvariant of Omicron variant BA.2.86, and contains several mutations that are associated with escape from vaccine-mediated immune protection. The source of the FLiRT variants of SARS-CoV-2. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:*

## Parts

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

### k856r omicron-variant gene target

(k856r). k856r omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### KAPA HyperPrep Kit

(kapaHyperPrep). KAPA HyperPrep Kit by Roche. An optimized library prep kit for high-quality libraries from low-input or degraded DNA, commonly used for Illumina platforms. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## *Parts*

### **Kaptive**

(kaptive). Kaptive. Identifies capsular (K) serotypes in Klebsiella pneumoniae and related species using whole-genome sequence data. Useful for studying capsule diversity and epidemiology. *Part Type*: categories *Domain*: bio *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*: CLI: <https://github.com/klebgenomics/Kaptive> Web: <https://kaptive-web.erc.monash.edu/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Kilogram per cubic meter**

(kgm3). Kilogram per cubic meter ( $\text{kg}/\text{m}^3$ ) *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.

### **Kilogram per second**

(kgS). Kilograms per second. *Part Type*: units *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA

## Parts

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

### Kilolitres

(kl). Kilolitres of volume *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Klebsiella Group

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

### Klebsiella pneumoniae

(klebsiellaPneu). Klebsiella pneumoniae *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* klebsiellaGrp *Class:* organism *Nomenclature:* organism *Ontology*

## Parts

*Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## KneadData

(kneadData). A sequencing data processing pipeline for quality control, including trimming and host decontamination (uses Trimmomatic and Bowtie2). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://huttenhower.sph.harvard.edu/kneaddata/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### KP.1.1 Variant

(kp11V). The KP.1.1 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## KP.1 Variant

(kp1V). The KP.1 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flirtSLipGrp *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: gen-MissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## KP.2 Variant

(kp2V). The KP.2 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flirtSLipGrp *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: gen-MissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### KP.3.1.1 Variant

(kp311V). The KP.3.1.1 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flirtSLipGrp *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*:

## *Parts*

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

## **KP.3 Variant**

(kp3V). The KP.3 variant of SARS-CoV-2, one of the FLiRT variants. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *Missingness Set:* gen-MissingnessSet *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Kraken2**

(kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://ccb.jhu.edu/software/kraken2/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Litres

(l). Litres of volume *Part Type*: units *Domain*: phy *Speciment ID*: siSaS-pecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## Omicron Variant l24s mutation

(l24s). Omicron Variant l24s mutation *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## I452r delta-variant gene target

(l452r). I452r 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

### L455S Mutation

(l455s). 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.

### I981f omicron-variant gene target

(l981f). l981f 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.

### Language Look-up table Shorthand

(la). The abbreviated short name used to reference the Look up table for all languages, used to give structure to the translation table. table *Part Type*: shortName *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## 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: 2.2.2.

## Laboratory

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

## Lab ID default deprecated

(labDefDep). Used as default when a new sample is created by this reporter. See ID in Lab table. Deprecated as of version 2, no defaults please specify. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* depreciated. First released: depreciated. Last updated: 2.0.0.

## Laboratory duplicate

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

## 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.

## Label

(label). A human readable label of a part. Typically, a part label has no acrynomns (every word is spelled out). Equivalent to a LOINC common name. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Lab ID

(labID). Unique identifier for a laboratory. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: deprecated. Last updated: 2.1.0.

### **Lachnospiraceae (Lachno3)**

(lachno3). Human-associated bacteria in the family Lachnospiraceae (Lachno3), often used as microbial source tracking markers for human fecal pollution tracking in environmental waters. *Part Type*: measurements *Domain*: bio *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: miscMeas *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: booleanSet *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.

### **Low Average Genome Coverage**

(LAGC). Average coverage of the genome is low/poor. *Part Type*: qualityIndicators *Domain*: bio *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: 2.3.0.

### **Lagoon system**

(lagoon). Lagoon system for extensive wastewater treatment *Part Type*: categories *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*

## 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.

## Lake, natural water body

(lake). Lake, natural water body *Part Type:* categories *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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Lambda

(lamba). C.37 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Land-based Transit Hub

(landTH). A transport hub is a place where passengers and cargo are exchanged between land-based vehicles and/or between land-based transport modes. Used when not greater detail can be provided *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

## Parts

*Set:* anyCompartmentSet *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.

## Language ID

(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.

## Language family

(langFam). Specifies the language family of a given language for translation and language tracking purposes. Part of the metedata for a languageID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Parts

### Language name

(langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes. Part of the metedata for a languageID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### National language script

(langScript). The language(s) and script(s) used for the country's capital endonyms. The scripts are listed in parenthesis, in the order of their appearance. Preprogrammed into dictionary tables, not editable by users. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 75 *Part Status*: active. First released: active. Last updated: 2.1.0.

### Language Look-up table

(languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. *la* *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup

## Parts

*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.

## Language table column order

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

## Language table required headers

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

## Parts

### **LAST (Large-Scale Alignment and Search Tool)**

(last). LAST (Large-Scale Alignment and Search Tool). A long-read specific mapper. Flexible tool for aligning long and error-prone reads. Best for: Comparative genomics with long reads. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Last edited**

(lastEdited). The date the entry was last updated. Use lastEdited if an entry is updated. Leave lastEdited blank or ‘NA’ for the first entry. Updates can include additions or revisions of the entry for any reason. For example, a wastewater measure was repeated later with an improved method. You can revise the entry by updating the value and then adding the date the new measure was performed to ‘lastEdited’. To ensure data provenance, the best practice in this example is to generate a new entry with the same measureID as the original measureID. The original and new measures are kept in the database with a date in the ‘lastEdited’ field for the new entry but not the original one. Some databases may choose a delete-and-replace approach where the original entry is deleted and replaced by a new entry. In this approach, the ‘lastEdited’ field indicates the delete and replace occurred. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: datetime *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum*

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

### **Last name of contact**

(lastName). Specifies the last name of a given contact. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Last updated version**

(lastUpdated). The version in which the part was last updated. Any change to the part of list will result in a change in the lastUpdated field to the dictionary version where the update occurred. *Part Type:* 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.

### **LaTeX expression**

(latExp). LaTeX expression used to generate formulas, symbols, etc. Mainly relevant for units. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:*

## *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.*

## **Latrine**

(latrine). A toilet or outhouse, especially a communal one in a camp or barracks. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: 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: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.2.3.*

## **LB.1 Variant**

(lb1V). The LB.1 variant of SARS-CoV-2, similar to other FLiRT variants but with an additional mutation. *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: flirtSLipGrp Class: variant Nomenclature: variant Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: 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.*

### **Low breadth of coverage**

(lBC). The percentage of the genome covered by reads (the breadth) is low. *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Laboratory control sample duplicate**

(lcSD). Known amounts of an analyte or representative compounds are added to a second “clean” matrix (lab water or clean sand) in laboratory. Duplicate of LCS *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Litres per day**

(lday). Unit of litres per day, usually for measuring flow. *Part Type*: units *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data*

## *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.

## **Low depth of coverage**

(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.

## **Leaked sample**

(leaked). Sample leaked, some volume and material was lost. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Legionella**

(legionella). Legionella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* legionellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:*

## Parts

NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Legionella Group

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

## Lentivirus Group

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

## *Parts*

### **<10 people**

(less10). Fewer than 10 people. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **10 - 100 people**

(less100). Between 10 and 100 people. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **10,000 - 100,000 people**

(less100k). Between 10,000 and 100,000 people. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **1,000 - 10,000 people**

(less10k). Between 1,000 and 10,000 people. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **100 - 1,000 people**

(less1k). Between 100 and 1,000 people. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **100,000 - 1,000,000 people**

(less1mil). Between 100,000 and 1,000,000 people. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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*

### **GNU Lesser General Public License v2.1**

(lgpl21). The licensing for the measure or data set is managed under the GNU Lesser General Public License v2.1. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/lgpl-2.1/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### **GNU Lesser General Public License v3.0**

(lgpl30). The licensing for the measure or data set is managed under the GNU Lesser General Public License v3.0. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://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.

### **Liter per hour**

(lhour). liter per hour (L/h) *Part Type*: units *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality*

## Parts

*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.*

## Link

(li). Link to an external reference that describes the geometry of the polygon. Deprecated as of version 2, please avoid use. Use referenceLink instead.  
*Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: genMissingnessSet Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 100 Part Status: depreciated. First released: depreciated. Last updated: 2.0.0.*

## Library preparation instruments

(libPrepInst). Instruments for the preparation of sequencing libraries, e.g., automation platforms like the Illumina NeoPrep. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## Parts

### **Library Preparation Kit**

(libraryKit). The name of the DNA/RNA library preparation kit used to generate the library being sequenced. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: libraryKitSet *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

### **Library Preparation Kit Set**

(libraryKitSet). The valid set of categorical values for sequencing library preparation kits. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: libraryKitSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **License**

(license). The license of a dataset. Specify the dataset's license name or provide a description of the license. Individual measures may possess their own licenses, which take precedence over the overall database license. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: licSet

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

## **Data license set**

(licSet). The set to describe valid categorical values for the licensing fields for measures or datasets. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* licSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## **Ligase-Dependent Library Prep Kits**

(ligaseDep). Ligase-Dependent Library Prep Kits by Lucigen/Epicentre. A library prep kit suitable for long-read applications and used with Illumina platforms. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Parts

### **LINEAGE Software**

(lineage). LINEAGE - Tool for bacterial lineage analysis, often applied to genome sequences in epidemiology. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Linear scale aggregation set**

(linearAggrSet). The aggregation set that contains all aggregations that exist on the linear scale. *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Liquid fraction**

(liq). Liquid fraction of a sample. *Part Type:* categories *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*

## *Parts*

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

### **Liquid/Supernatant retained**

(liquid). The liquid or supernatant is retained after solid separation/centrifugation. *Part Type: categories Domain: phy Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet 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.*

### **Liquid**

(liquidMat). Material is liquid, ie. is a state of matter with a definite volume but no fixed shape, adapting to the shape of their container. *Part Type: categories Domain: naDomain Speciment ID: siSaSpecimenSet 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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

### **Listeria**

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

## 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.

## Listeria Group

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

## List worksheet

(lists). Parts lists for template dropdowns and other documentation. Sheets or tabs for the ODM Excel dictionary include: all ERD tables (look-up tables and data entry tables) and additional supportig tables. *Part Type:* dictionarySupport *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### List set

(listSet). PartTypes that contain categories, sets, or lists. Used to generate documentation. *Part Type*: dictSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: airCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Liter per minute

(lmin). liter per minute (L/min) *Part Type*: units *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### Limit of Blank (LOB)

(lob). The highest concentration of a target analyte (DNA or RNA) that can be expected in a blank sample (a sample with no target DNA/RNA) while still considering the sample as negative. Defines the upper limit of “noise” or background signal that should not be confused with a true positive. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA

## 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.

## Access to local ha

(localHA). If this is ‘no’, the, data will not be available to local health authorities. If missing, data will be available to local health authorities. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

## Lockdown

(lockdown). Broad restrictions on movement and activities within a region to control disease spread. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Limit of detection (LOD)**

(lod). Limit of detection, ie. the minimum level of a genetic target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **Limit of detection (LOD) - sewage**

(lodSewa). Limit of detection, ie. the minimum level of a genetic target, for sewage samples. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **log10 gene copies per g**

(log10cpG). Unit for log10 copies per gram *Part Type*: units *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum*

## Parts

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

### **log10 gene copies per L**

(log10cpL). Unit for log10 copies per litre *Part Type: units Domain: bio Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.2.0.*

### **log10 gene copies per mL**

(log10cpml). Unit for log10 copies per mililitre *Part Type: units Domain: bio Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 2.2.0.*

### **Log10 gene copies per 100 milliliter**

(log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) *Part Type: units Domain: bio Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA*

## Parts

*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.

### **Log10 gene copies per nanogram total DNA**

(log10gcngDNA). log10 gene copies per nanogram total DNA *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

### **log10 micrograms per g**

(log10ugG). Unit for log10 micrograms per gram *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

### **log10 micrograms per L**

(log10ugL). Unit for log10 micrograms per litre *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation*

## Parts

*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.

## Logarithmic scale aggregation set

(logAggrSet). The aggregation set that contains all aggregations that exist on the logarithmic scale (rather than linear or qualitative). *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Longitudinal, repeat sampling surveillance program

(longSurv). A surveillance strategy in which an individual or site is selected to undergo repeat sampling over a defined period of time. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Dictionary tables

(lookup). Tables to describe and support the ODM dictionary. These tables hold information on sets, all parts, and support multiple languages and translations. The tables are updated by the ODM development team when a new ODM version is created. *Part Type*: classes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: lookup *Nomenclature*: lookup *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Limit of quantification (LOQ)

(loq). Sample limit of quantification (LOQ) is defined as “the concentration of a target that can be quantified with an acceptable level of precision when present in a sample” (Ahmed et al., 2021). Limit of quantification (LOQ) for this method if one exists. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

## Low severity

(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.

## Low Coverage of Characteristic Mutations

(lowCovMut). Low coverage of characteristic mutations. *Part Type:* qualityIndicators *Domain:* bio *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: 2.3.0.

## Lower limit of a 95% confidence interval

(lowerCI95). Specifies the the lower limit of a 95% confidence interval. Should typically be linked to an upper limit, and some indication of data spread (ie. standard deviation), and a mean/median measure. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Low-quality Sequence**

(lowQualSeq). Low-quality sequence. *Part Type*: qualityIndicators *Domain*: bio *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: 2.3.0.

### **Low Signal-to-Noise Ratio**

(lowSNRatio). Low signal-to-noise ratio. *Part Type*: qualityIndicators *Domain*: bio *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: 2.3.0.

### **Low-volume sample**

(lowVol). Sample is low-volume, but was run regardless. *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

*Parts*

### **LP.8.1 Variant**

(lp81V). The LP.8.1 variant of SARS-CoV-2, a Omicron subvariant of JN.1, and FLiRT variant. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **Low Percent of Genome Captured**

(lPGC). Only captured a small/low percentage of the genome. *Part Type*: qualityIndicators *Domain*: bio *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: 2.3.0.

### **Omicron Variant LPPA24S mutation**

(lppa24s). Omicron Variant LPPA24S mutation *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*:

*seeUnitData 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.*

### **LaTeX Project Public License v1.3c**

(lppl13c). The licensing for the measure or data set is managed under the LaTeX Project Public License v1.3c. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: https://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.*

### **Lactated Ringer's Solution**

(lrs). A buffer solution/medium sometimes used in combination with other preservatives to stabilize microbial samples. *Part Type: categories Domain: naDomain Speciment ID: 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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## Parts

### **Liter per second**

(lsec). liter per second (L/s) *Part Type*: units *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Long-term care facility**

(ltcf). A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Long-term care - assisted living or retirement home**

(ltcfAl). A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*:

## *Parts*

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

### **Other long-term care**

(ltcfO). Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or assisted living facilities. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Life technologies digital PCR**

(ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **luminultra wastewater extraction kit**

(luminWWExtract). luminultra wastewater extraction kit *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*:

## *Parts*

*anyCompartmentSet Group: procGrp Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet 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: 2.2.0.*

## **Lysis buffer**

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

## **Cubic metres per day**

(m3D). Cubic metres per day. *Part Type: units 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: 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.*

### **Cubic metres per hour**

(m3H). Cubic metres per hour. *Part Type*: units *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*: 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.

### **Cubic meter per minute**

(m3min). cubic meter per minute ( $m^3/min$ ) *Part Type*: units *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Cubic metres per second**

(m3S). Cubic metre per second. *Part Type*: units *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*: 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

### MAFFT

(mafft). Sequencing software that performs multiple sequence alignment, commonly used in consensus sequence generation. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://mafft.cbrc.jp/alignment/software/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Magnetic nanobead binding

(magBead). The use of tiny, magnetized beads to selectively capture and isolate biological molecules (e.g., DNA, proteins) in a magnetic field. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### Magnetic separation racks

(magInst). Magnetic separation rack instrument; may be used with magnetic beads for nucleic acid extraction. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*:

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

## Plasmodium or Malaria Group

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

## Shopping mall

(mall). A large commercial complex with multiple retail stores, services, and restaurants. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## *Parts*

### **Manual Composite Sample**

(manComp). Specifies a composite sample where the sub-samples were collected manually. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### **Manufacturer**

(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.

### **MapSplice**

(mapSplice). MapSplice. A specialized read mapper. Designed specifically for spliced alignment of RNA-seq reads. Best for: Transcriptomics with a focus on detecting splice junctions. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.net-lab.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.

## **mash Software**

(mash). A lineage or clade analysis software tool for the clustering-based method of lineage and clade analysis, comparing large genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/marbl/Mash> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Mask mandate**

(maskMand). A legal requirement for individuals to wear masks in specified settings. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Parts

### **Mask recommendation**

(maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Maryland Super Read Celera Assembler (MaSuRCA)**

(masurca). A sequencing software that is a hybrid assembler that can integrate both short and long reads for high-quality assemblies, and large, complex genomes. *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.

### **Sample Material Characteristics**

(matChar). A site measurement for describing the qualitative characteristics of the sample material in situ (ie. The material from which the sample is collected. *Part Type*: measurements *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: physical *Nomenclature*: physical *Ontology Reference*: NA *Category*

## Parts

*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.

## Sample Material Characteristics Set

(matCharSet). The set for recording the possible valid values for describing the sample material characteristics. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* matCharSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Mate pair layout

(mateLay). Specifies the mate pair layout for a sequencing method. *Part Type:* categories *Domain:* bio *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.

## Parts

### Maximum length

(maxLength). The maximum length of the value of a part or measure.  
*Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA  
*Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA  
*Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* NA  
*Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Maximum value

(maxVal). Highest value in a range of values for a measure. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### Maximum value part support

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

## Concentration Factor

(mCF). Concentration Factor (CF) is the degree to which the concentration observed in the final qPCR assay volume has been magnified compared to concentration of the analyte in the original sample (see Box 2.1 Protocol). *Part Type*: measurements *Domain*: allDo *Specimen 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.

## MCR-1.1 Colistin-resistence gene target

(mcr11). The MCR-1.1 colistin anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Specimen 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*: gen-MissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

## Arithmetic mean

(me). Arithmetic mean. *Part Type*: aggregations *Domain*: naDomain *Specimen 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:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

## Measurement group

(measGrp). A group of measures that cannot be otherwise categorized.  
*Part Type:* groups *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Measles

(measles). Measles *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measlesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Measles Group

(measlesGrp). A group of measures/methods related to the measles virus. Used to describe the organism information for general measures. *Part*

*Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measlesGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## Other Measure

(measOth). Other measure, not otherwise specified in measures. Add description to categoryOther. *Part Type:* measurements *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* othAgg *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

## Measures quality set

(measQualitySet). A quality set for any measure, includes all the quality flag options for any measure. Used as an “any quality set” for measures, but excludes the sample quality flags to avoid confusion and data entry errors. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *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.

## **Measure**

(measure). A measurement or observation of any substance including a biological, physical or chemical substance. An measurement is recorded from a specimen (i.e. a site, sample, person or population). Measures are organized into groups and classes (sub-groups). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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:* 100 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Measure input (wide table)**

(measureInput). The partID for the measure being used in a wide name. *Part Type:* attributes *Domain:* 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:* 100 *Part Status:* active. First released: active. Last updated: 2.2.0.

## **Measure license**

(measureLic). Specifies the access and use licensing for a given single measurement. Populated by partID = licenseID *Part Type:* attributes

## Parts

*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.

## Measures

(measurements). The attribute to describe a part type of measures. All measures have ‘partType’ = “measure”. mes *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

### Measure name (wide table)

(measureName). The measure referenced for the wide name. *Part Type:* attributes *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:* 60 *Part Status:* active. First released: active. Last updated: 2.2.0.

*Parts*

## **Report ID**

(measureRepID). Unique identifier for a measurement. Report IDs cannot be repeated. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Measure report table**

(measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. mr *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: results *Nomenclature*: results *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Measure set report set ID**

(measureSetRepID). Unique identifier that links together a group of related measures. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category*

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

### Measure set report table

(measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or varients that are identified in a single sample. The short name for the table (partID) can be found in the instructions field. ms *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Measure sets table column order

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

## Parts

### **Measure Set table required headers**

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

### **Measures table column order**

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

### **Measures table required headers**

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

## Meat processing plant

(meatPl). A processing plant for slaughtering, processing, packaging, labelling, handling, and storing of food animal carcasses, parts of carcasses, and meat products. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: na-Group *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: 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.

## Median

(med). Median. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: na-Group *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *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.

## Molecular Evolutionary Genetics Analysis (MEGA)

(mega). Sequencing software that provides tools for sequence alignment and consensus sequence extraction. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*:

## *Parts*

*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.*

## **Mega-bases or Mega-base-pairs**

(megaB). A mega-base (Mb) or mega-base-pair (Mbp) is equal to one million base pairs (1,000,000 bp). It is commonly used to describe the size of genomes or large DNA sequences. *Part Type: units Domain: bio Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 3.0.0.*

## **MEGAHIT**

(megahit). A sequencing software that is a fast and memory-efficient assembler for large metagenomic datasets. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: procGrp Class: software Nomenclature: software Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: https://github.com/voutcn/megahit Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## MEGARes database

(megares). A comprehensive database of antimicrobial resistance genes.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database  
*Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA  
*Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA  
*Reference Link:* megares.meglab.org *Data Type:* varchar *Missingness Set:*  
NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0  
*Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## membrane filtration with addition of mgcl3

(memMgCl3). membrane filtration with addition of mgcl3 *Part Type:* categories *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Normalized arithmetic mean

(menr). Arithmetic mean, normalized. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

## Parts

*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.

## Other Measure Description

(meOthDe). Description of other measure (measOtherDesc). *Part Type:* measurements *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* othAgg *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 60 *Part Status:* depreciated. First released: depreciated. Last updated: 2.0.0.

## Milliequivalent per liter

(meqL). Unit for alkalinity, miliequivalents per litre. *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## Measures Part-type Shorthand

(mes). The abbreviated short name used to reference the The attribute to describe a part type of measures. All measures have ‘partType’ = “measurements”. part type *Part Type:* shortName *Domain:* naDomain *Speciment*

## Parts

*ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* na-  
*Group Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA  
*Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale  
*Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *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.

## Effective Sample Size/Volume

(mESV). Effective Sample Size/Volume (ESV) is the amount of the original sample size/volume that was actually analyzed in a qPCR reaction (see Box 2.1 Protocol) *Part Type:* measurements *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## Methods part-type Shorthand

(met). The abbreviated short name used to reference the Procedures or steps for collecting samples or performing measures. part type *Part Type:* 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.

*Parts*

### **Metabolite Group**

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

### **MetAMOS**

(metAMOS). A sequencing software that is an automated pipeline for metagenomic assembly and annotation. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/marbl/metAMOS> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **MetaPhiAn Software**

(metaPhiAn). Software tool that profiles microbial communities and can provide resistance gene insights. Also used for deduplication. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## *Parts*

*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.

## **Meter**

(meter). meter (m) *Part Type:* units *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Method**

(method). A procedure for collecting a sample or performing a measure. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

## **Concentration method**

(methodConc). Description of the method to concentrate a wastewater sample. Description of the method used to concentrate the sample *Part*

## Parts

*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.

## Concentration method set

(methodConcSet). A set a concentration methods. *Part Type:* mmaSets *Domain:* phy *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standard-Conc *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.

## Method input (wide table)

(methodInput). The partID for the method being used in a wide name. *Part Type:* attributes *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: 2.2.0.

### **Method name (wide table)**

(methodName). The method referenced for the wide name. *Part Type*: attributes *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: 2.2.0.

### **Methods**

(methods). Procedures or steps for collecting samples or performing measures. For example, ‘methodExtract’ is a method that describes the how a sample was extracted. met *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

### **Membrane filtration with acidification and mgcl2**

(mfAcidmgcl2). Membrane filtration with acidification and mgcl2 *Part Type*: categories *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*:

## *Parts*

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

### **Membrane filtration with acidification and mgcl2, membrane recombined with separated solids**

(mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids *Part Type: categories Domain: 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: 2.0.0.*

### **Membrane filtration with addition of mgcl2**

(mfMgcl2). Membrane filtration with addition of mgcl2 *Part Type: categories 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: 2.0.0.*

### **Membrane filtration with mgcl2 and separated solids**

(mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated solids *Part Type: categories Domain: allDo 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.

### **Membrane filtration with no amendment**

(mfNoAmend). Membrane filtration with no amendment *Part Type*: categories *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: 2.0.0.

### **Membrane filtration with no amendment, membrane recombined with separated solids**

(mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids *Part Type*: categories *Domain*: 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: 2.0.0.

*Parts*

### **Membrane filtration with sample acidification**

(mfSampleAcid). Membrane filtration with sample acidification *Part Type*: categories *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: 2.0.0.

### **Membrane filtration with sample acidification, membrane recombined with separated solids**

(mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids *Part Type*: categories *Domain*: 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: 2.0.0.

### **Millions of gallons per day (MG/D)**

(mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of gallons per day. Also can be used to measure flow. *Part Type*: units *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggrScale *Quality Set*:

## Parts

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.

### **Mycoplasma genitalus**

(mGenitalus). Mycoplasma genitalus *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mycoplasmaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **MGIEasy DNA Library Prep Kit**

(mgiEasy). MGIEasy DNA Library Prep Kit by MGI/BGI. A library prep kit designed for MGI sequencing platforms, offering flexibility in sample input. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Milligrams per litre**

(mgL). Milligrams per litre. *Part Type*: units *Domain*: allDo *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:* 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.

## Milligram per liter of calcium carbonate

(mgLCaCO<sub>3</sub>). Unit for alkalinity, milligram 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.

## Milligrams orthophosphate per liter

(mgPO<sub>4</sub>3L). milligrams orthophosphate per liter (mg PO<sub>4</sub>3-/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.

### **Milligrams orthophosphate as phosphorus per liter**

(mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) *Part Type*: units *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Murine Hepatitis Virus**

(mhv). A measure for amount of murine hepatitis viurs. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: hepGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **murine hepatitis virus (MHV) spike target**

(mhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. *Part Type*: categories *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

## *Parts*

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

## **Multiple issues**

(mi). Multiple issues have arisen in the sequencing process. When using the ‘multiple issues’ quality flag, please specify the issues and details in the notes section. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Mid-level severity**

(mid). A marker for med-level severity, where there are some concerns. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Midnight and BC-CDC V1 Primer Set**

(midnightBCCDCv1). An amplicon strategy which is for SARS-CoV-2 and based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the

attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Midnight and BC-CDC V2 Primer Set**

(midnightBCCDCv2). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Midnight and BC-CDC V3 Primer Set**

(midnightBCCDCv3). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 3.0.0 which produces amplicons approximately 1200bp in length. *Part Type*: categories *Domain*: bio *Speciment ID*:

## *Parts*

*saSpecimenSet Compartment Set:* anyCompartmentSet *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.

## **Midnight and BC-CDC V4 Primer Set**

(midnightBCCDCv4). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 4.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **Midnight scheme V1 Primer Set**

(midnightV1). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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*

## *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: 3.0.0.

### **Midnight scheme V2 Primer Set**

(midnightV2). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### **Midnight scheme V3 Primer Set**

(midnightV3). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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*

## **Miniasm**

(miniasm). A sequencing software that is a lightweight assembler for long reads, typically followed by polishing steps. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/lh3/miniasm> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Minimap2**

(minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/lh3/minimap2> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Minimum length**

(minLength). The maximum value of measure. *Part Type*: partSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: na-

## Parts

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

### **minimum post-trimming read length**

(minPTLength). The threshold used as a cut-off for the minimum length of a read after trimming. Provide a numerical value (no need to include units). *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: basePairSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

### **Minutes**

(minutes). A unit for indicating a length of time in minutes. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Parts

### Minimum value

(minVal). Lowest value in a range of values for a measure. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### Minimum value part support

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

### Miscellaneous attribute group

(miscAttr). A group of miscellaneous measurement-like attributes. Examples of these would be longitude and latitude, or EPSG coordinates. *Part Type*: groups *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category 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.

### Miscellaneous measure group

(miscMeas). A group of measures that cannot be otherwise categorized. *Part Type:* groups *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Missing data

(miss). A general missingness value for missing data, used when data is not included for an unknown reason. Missing value indicator when the value is unavailable for an unknown reason. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

### Missingness

(missingness). The part type for missingness values. Only used for the dictionary entries of parts. *Part Type:* partType *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*: 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.

## Missingness Set

(missingnessSet). Missingness sets for measures, methods or attributes. Inputted data into an ODM field may have missing data. The missingness set lists valid missing categories for the measure, method, or attribute. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

## Missingness sets

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## MIT

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

## MIT No Attribution

(mit0). The licensing for the measure or data set is managed under the MIT no attribution license. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/mit-0/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

## MitoZ Deduplication

(mitoZ). A deduplication method that is used primarily for mitochondrial genomes but can handle deduplication by read clustering. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*:

## *Parts*

<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.

## **Mixed/homogenized sample**

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

## **Millilitres**

(ml). Millilitres of volume *Part Type:* units *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:* quantAggrScale *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.

## **Megalitres per day (ML/d)**

(mld). Megalitres per day. *Part Type:* units *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category*

## Parts

*Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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.

### **Method Limit of Detection (LOD)**

(mlod). The minimum level of a target necessary for its consistent detection considering all sample processing steps as in the definition of SLOD), but considering biases attributable to method losses. The MLOD is experimentally determined using a rigorous and iterative testing approach and it is sensitive to the recovery surrogate used and the sample matrix encountered. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### **MLST (Center for Genomic Epidemiology)**

(mlst). MLST (Center for Genomic Epidemiology). Focus: Classical MLST and optional serotype determination. Applications: Compatible with curated schemes for various pathogens. Features: Web-based and command-line versions available. *Part Type:* categories *Domain:* bio *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:* <https://www.genomicepidemiology.org/services/>

## *Parts*

(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.

## **Millimetres**

(mm). Unit part for the SI unit of millimetres. *Part Type*: units *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*: 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.

## **Measure, Method, or Attribute Set Header**

(mmaSet). The set for a measure, method, or attribute. Only applicable for categorical fields, and the categories that populate them. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## **Measure, method, or attribute sets**

(mmaSets). A set of categories. For example, site type has a list of different sites, such as a wastewater treatment plant, a septic tank, or a pumping station. Only used for the dictionary entries of parts. *Part Type*:

## Parts

partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## Millimho per centimeter

(mmhocm). Millimho per centimeter (mmho/cm) *Part Type*: units *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## Model

(model). Model number or version of the instrument. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 100 *Part Status*: active. First released: active. Last updated: 2.0.0.

## *Parts*

### **monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo)**

(monarchRNA). monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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: 2.2.0.

## **Months**

(months). A unit for indicating a length of time in months. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: na-Class *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.

## **Moore swab passive sample**

(moorSw). Moore swab passive sample. Use collectionPeriod to describe how many hours the Moore swab was used to collect the sample *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*

## 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.

## 1,000,000+ people

(more1mil). More than 1,000,000 people. *Part Type:* categories *Domain:* allDo *Speciment ID:* poSiSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Morning

(morn). Sample was collected at some point in the morning, early in the day. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Mozilla Public License 2.0

(mpl20). The licensing for the measure or data set is managed under the Mozilla Public License 2.0. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

## Parts

*Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale  
*Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/mlp-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.

### **Most probable number per 100 milliliters**

(mpn100mL). most probable number per 100 milliliter (MPN/100 mL)  
*Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Most probable number per milliliter**

(mpnmL). most probable number per milliliter (MPN/mL) *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

## Mpox

(mpox). The virus known as Mpox, previously also known as Monkey Pox. *Part Type:* measurements *Domain:* bio *Speciment ID:* poSaSpeci-

menSet *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*: gen-MissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.1.0.

## **MPox Clade I Group**

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

## **MPox Clade II Group**

(mpoxCldIIGrp). A group of measures/methods related to Mpox Clade II (formerly “Monkey Pox”). Used to describe the organism information for general measures. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxCldIIGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*:

## *Parts*

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

## **MPox Group**

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

## **Medium priority pathogen**

(mpp). A resistant organism of moderate concern, needing ongoing monitoring. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Metres per second**

(mps). metres per second. *Part Type*: units *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*: quantAggScale *Quality*

## Parts

*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.

## Metapneumovirus Group

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

## Mpox B6R Gene Target

(mpxB6R). Human MPox Virus (hMPXV) gene target. Envelope protein 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.

*Parts*

### **Clade I Mpox C3L Gene Target**

(mpxC3L). Human MPox Virus (hMPXV) Clade I gene target. hMPXV C3L primers and probe detect Clade I viruses. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxCldIGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Mpox Clade I**

(mpxCII). The virus known as Mpox, previously also known as Monkey Pox, Clade I virus type. *Part Type*: measurements *Domain*: bio *Speciment ID*: poSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxCldIGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quanttAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **Mpox Clade II**

(mpxCIII). The virus known as Mpox, previously also known as Monkey Pox, Clade II virus type. *Part Type*: measurements *Domain*: bio *Speciment ID*: poSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxCldIIGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA

## Parts

*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.

### **Mpox & Orthopox E9L-NVAR Gene Target**

(mpxe9lNVAR). Human MPox Virus (hMPXV) gene target for Orthopoxvirus DNA polymerase. CDC Assay detects all hMPXV clades and non-variola Orthopox viruses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

### **Mpox & Orthopox E9L-OPX3 Gene Target**

(mpxe9lOPX3). Human MPox Virus (hMPXV) gene target using the generic orthopox virus OPX3. Lower sensitivity for MPox. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## *Parts*

### **Mpox Clade I F3L Gene Target**

(mpxF3L). Human MPox Virus (hMPXV) Clade I gene target, F3L *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxCldIGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Mpox G2R-G Gene Target**

(mpxG2RG). Human MPox Virus (hMPXV) gene target using the G2R\_G primers and probe which detects all MPox Virus strains. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Mpox G2R-NML Gene Target**

(mpxG2RNML). Human MPox Virus (hMPXV) gene target using the G2R\_NML primers and probe which detects all MPox Virus strains. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mpoxCldIIGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA

## 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: 2.3.0.

### **Clade II Mpxo G2R-WA Gene Target**

(mpxG2RWA). Human MPox Virus (hMPXV) Clade II gene target, measured with G2R\_WA primers and probe to detects Clade II viruses. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxCldIIGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

### **Mpxo GT Molecular Gene Target**

(mpxGTmol). Human MPox Virus (hMPXV) gene target - this specific measure and gene target are proprietary to GT Molecular *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* mpoxGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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

### Measure report table Shorthand

(mr). The abbreviated short name used to reference the The table that contains information and details about a given measure table *Part Type*: shorthand *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.

### MrBayes Software

(mrBayes). A lineage or clade analysis software tool for bayesian inference of phylogeny, used for inferring clade relationships with high accuracy. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://nbisweden.github.io/MrBayes/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Methicillin-resistant Staphylococcus aureus (MRSA)

(mrsa). Methicillin-resistant Staphylococcus aureus (MRSA) *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: staphGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*:

## Parts

NA *Data Type*: seeUnitData *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.

## Measure set report table Shorthand

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

## ms2 coliphage

(ms2Col). Measure of the amount of ms2 coliphage. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: phageGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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

### **ms2 coliphage spike target**

(ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. *Part Type*: categories *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.

### **Millisiemen per centimeter**

(mScm). Millisiemens per centimeter (mS/cm) *Part Type*: units *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Matrix spike duplicate**

(msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum*

## *Parts*

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

### **Microsoft Public License**

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

### **Moore swab passive sample deprecated**

(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:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Major sewer pipeline**

(mSwrPpl). Major sewer pipeline *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.

## Mycobacterium tuberculosis

(mTuberculosis). Mycobacterium tuberculosis *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tuberculosisGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Mu

(mu). B.1.621 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **murine coronavirus**

(muCo). Measure of the amount of murine coronavirus. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: betaCoronaGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **murine coronavirus spike target**

(muCoMat). Murine coronavirus is used as the recovery efficiency control target. *Part Type*: categories *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.

### **Multiple fraction**

(mul). Multiple fractions were analyzed separately and aggregated together post-analysis. This fractionID is intended for use for archival data and should not be used for newly added new moving forward (2022). Please also specify in the notes section which fractions were used for the multiple fractions (ex. solid and liquid) to avoid loss of information. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

## **Mulan Permissive Software License, Version 2**

(mulanPSL20). The licensing for the measure or data set is managed under version 2 of the Mulan Permissive Software License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://choosealicense.com/licenses/mulanpsl-2.0/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## **Multi-Community-level Surveillance**

(multiComLev). The scope of the surveillance covers multiple communities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* anySpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Multiple Purpose

(multiple). A measure or sample taken for multiple purposes, not easily captured by the other purpose categories. Useful for parent samples where various subsamples will have different purposes/ *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## MultiQC

(multiQC). A QC pipeline tool for sequencing data that aggregates QC results from multiple sources (e.g., FastQC, SAMtools) into a single report, useful in large pipelines. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://seqera.io/multiqc/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Mumps

(mumps). Mumps *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: mumpsGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale

## *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.

## **Mumps Group**

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

## **Municipalities or communes**

(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.

## **Municipality**

(municip). A complete municipality, this specifies an entire metropolitan area, either a city, town, etc. *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*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Municipality-level Aggregation at Site

(muniLevel). Specifies that a sewershed/site represents an entire municipality. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Mutations class

(mutation). Measures and methods related to mutations. *Part Type*: classes *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: any-CompartmentSet *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*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.3.0.

## Parts

### **Mutation panels class**

(mutationPanel). Measures and methods related to a panel or list of more than one mutation from the same sequence read. *Part Type*: classes *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *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.

### **MilliVolt**

(mvolt). milliVolt (mV) *Part Type*: units *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Mycoplasma Group**

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

## Parts

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

## Mykrobe

(mykrobe). Mykrobe. Focus: Rapid detection of resistance, MLST, and serotyping. Applications: Mycobacterium tuberculosis and other pathogens. Features: Fast processing and species-specific database compatibility. *Part Type:* categories *Domain:* bio *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:* 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.

## N sars-cov-2 gene target

(n). N sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENE-PIO: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.

## *Parts*

### **Combined N1 and N2 sars-cov-2 gene target**

(n1n2). Combined N1 and N2 sars-cov-2 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Omicron Variant n211i mutation**

(n211i). Omicron Variant n211i mutation & gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **N50**

(n50). The length of the shortest read that, together with other reads, represents at least 50% of the nucleotides in a set of sequences. Provide the N50 value in Mb. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: basePairSet *Aggregation Scale*: quantAggScale

## Parts

*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.

### **Omicron Variant n679k mutation**

(n679k). Omicron Variant n679k mutation & gene target. *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.

### **Omicron Variant n856k mutation**

(n856k). Omicron Variant n856k mutation & gene target. *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.

## Parts

### Omicron Variant n969k mutation

(n969k). Omicron Variant n969k mutation & gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: omicronGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### Not applicable

(NA). The field for which the expected value is not a property of the described object. Missing value indicator for missing data with no explanation. *Part Type*: missingness *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Aggregation not applicable

(naAggr). Not applicable for aggregations. Used for parts for which an aggregation value is not applicable or appropriate. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*

## 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.

### Aggregation scale not applicable

(naAggrScale). Not application for aggregation sets. Used for parts for which an aggregation scale value is not applicable or appropriate. *Part Type:* aggregationScales *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Aggregation set not applicable

(naAggrSet). Not application for aggregation sets. Used for parts for which an aggregation set value is not applicable or appropriate. *Part Type:* aggregationSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### No amplification control

(nac). Denotes a no amplification control replicate sample. *Part Type:* categories *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment*

## *Parts*

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

## **Class not applicable**

(naClass). Class is not applicable. Use this for all parts that don't have classes (most non-measure or method parts) *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Compartment not applicable**

(naCompartment). Compartment not applicable. *Part Type:* compartments *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Compartment set not applicable**

(naCompartmentSet). Compartment not applicable. *Part Type*: compartmentSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Domain not applicable**

(naDomain). Not applicable. Use ‘not applicable’ when there is no domain for the part *Part Type*: domains *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Group not applicable**

(naGroup). Used when there is no group; ie. group is not applicable. Use ‘not applicable’ when there is no group for the part *Part Type*: groups *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

## **Name**

(name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity. 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.

## **English name for countries**

(nameEngl). English-language name of a given country. Preprogrammed into dictionary tables, not editable by users. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 75 *Part Status*: active. First released: active. Last updated: 2.1.0.

### **Official state name**

(nameOfficial). Official english-language name of a given state. Preprogrammed into dictionary tables, not editable by users. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 75 *Part Status*: active. First released: active. Last updated: 2.1.0.

### **Not a number**

(nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, ...) Missing values indicator for when a numeric value is expected but not given. *Part Type*: missingness *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Nomenclature not applicable**

(naNomenclature). Not applicable. Use ‘not applicable’ when there is no nomenclature for the part *Part Type*: nomenclatures *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*:

## *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: 2.0.0.*

## **NanoPlot**

(nanoPlot). A QC pipeline tool for sequencing data that does visualizations for quality assessment of long-read data, particularly from Oxford Nanopore. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: procGrp Class: software Nomenclature: software Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: https://github.com/wdecoster/NanoPlot Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## **Specimen not applicable**

(naSpecimen). Non applicable specimen. Use ‘not applicable’ when there is no specimen/set for the part *Part Type: specimens Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

### **Specimen set not applicable**

(naSpecimenSet). A specimen set for when specimen/specimen set is not applicable. Use ‘not applicable’ when there is no specimen/set for the part  
*Part Type*: specimenSets *Domain*: naDomain *Speciment ID*: naSpecimenSet  
*Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass  
*Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Native Name**

(natName). The native name of the language, i.e. what the language is called by its speakers. Part of the metedata for a languageID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **Unit not applicable**

(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*

## *Parts*

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

### **Unit set not applicable**

(naUnitSet). Not applicable for unit sets. *Part Type: unitSets Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: anyCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: categorical Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

### **NB.1.8.1 variant (Nimbus)**

(nb181V). The Nimbus variant of SARS-CoV-2 (NB.1.8.1), descendant of the recombinant variant XDV.1.5.1. *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: nimbusGrp Class: variant Nomenclature: variant Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale Quality Set: NA Reference Link: NA Data Type: 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.*

### **number of base-pairs sequenced**

(nBPSeq). The number of total base pairs generated by the sequencing process. Provide a numerical value (no need to include units). *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: sequence Nomenclature:*

## Parts

sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: base-PairSet *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.

## National Center for Biotechnology Information

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

## NCBI Format

(ncbiForm). Dataset was originally recorded and/or stored in NCBI format. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.ncbi.nlm.nih.gov/biosample/docs/packages/SARS-CoV-2.wwsurv.1.0/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Parts

### Nomenclature from the NCBI

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

### NCBI - notes

(ncbiNotes). NCBI notes *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

### NCBI's Pathogen Detection Isolates Browser

(ncbiPDIB). Database that tracks AMR in pathogens and provides resistance profiles for pathogens worldwide. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: database *Nomenclature*: database *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.ncbi.nlm.nih.gov/pathogens/isolates/> *Data Type*:

## *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.

### **number of contigs**

(nContig). The number of contigs (contiguous sequences) in a sequence assembly. Provide a numerical value. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

### **ncov-tools**

(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.

### **University of Illinois/NCSA Open Source License**

(ncsa). The licensing for the measure or data set is managed under the University of Illinois/NCSA Open Source License. *Part Type*: categories

## 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:* <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.

## National Database of Antibiotic Resistant Organisms (NDARO)

(ndaro). A database maintained by the USCDC with genomic data on AMR organisms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* [ncbi.nlm.nih.gov/pathogens/antimicrobial-resistance/](https://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.

## NEBNext Ultra II DNA Library Prep Kit

(nebnextUltraII). NEBNext Ultra II DNA Library Prep Kit by New England Biolabs. A high-efficiency library prep kit for low DNA input, ideal for whole-genome and target enrichment. *Part Type:* categories *Domain:* bio *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*

## *Parts*

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

### **New England Biolabs VarSKip V1a Long Primer Set**

(nebVarSkipV1aLong). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a long. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-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:* <https://github.com/nebulabs/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.

### **New England Biolabs VarSKip V1a short Primer Set**

(nebVarSkipV1aShort). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a short. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* any-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:* <https://github.com/nebulabs/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.

*Parts*

### **New England Biolabs VarSKip V2a Primer Set**

(nebVarSkipV2a). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2a. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **New England Biolabs VarSKip V2b Primer Set**

(nebVarSkipV2b). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2b. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Negative experimental control**

(negCon). A sample or experimental condition where the expected outcome should not occur, intended to check the original sample matrix for contamination, false positives, or unintended effects. An example would be testing for viral RNA or DNA in a sample known to be free of that virus.

## Parts

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

## Neighbourhood

(neigh). A municipal neighbourhood, this specifies a sub-section of a larger municipality. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Local administrative units or neighborhoods

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

*Parts*

### **Neighbouring relationship**

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

### **Neighbourhood-level Aggregation at Site**

(neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a 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.

### **Population of newly vaccinated persons**

(newVax). Population of newly vaccinated persons A unit used 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*:

## *Parts*

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

### **NextClade nomenclature**

(nextclade). Specifies variant or genetic nomenclature as set out by NextClade. *Part Type*: nomenclatures *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: na-Group *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Nextera XT DNA Library Preparation Kit**

(nexteraXT). Nextera XT DNA Library Preparation Kit by Illumina. A fast and efficient library prep kit for small genomes and amplicons, uses transposase-based fragmentation. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Nextstrain Software**

(nextstrain). A lineage or clade analysis software tool for real-time tracking of pathogen evolution, with tools for clade and lineage analysis. *Part Type*:

## Parts

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.

## Nanograms per liter

(ngL). nanograms per liter (ng/L) *Part Type*: units *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## NGMLR (Next-Generation Mapping and Long-Read Alignment)

(ngmlr). NGMLR (Next-Generation Mapping and Long-Read Alignment). A long-read specific mapper. Specialized for long-read platforms like PacBio and Nanopore. Best for: Structural variant analysis. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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/phires/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.

### **Normalized geometric mean**

(ngmn). Geometric mean, normalized. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Neisseria gonorrhoeae**

(nGonorrhoeae). Neisseria gonorrhoeae *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: gonococcusGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Next-Generation Sequencing (NGS) platforms or intruments**

(ngsInst). Next generation sequencer instruments and platforms. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*:

## *Parts*

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

## **Ammonia and Ammonium as Nitrogen**

(nh3nh4). Ammonia and Ammonium combined concentration, as Nitrogen  
*Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet  
*Compartment Set*: waterCompartmentSet *Group*: waterQualityGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

## **Ammonium Nitrogen**

(nH4N). Ammonium nitrogen concentration, as N. *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: waterQualityGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **Night**

(night). Sample was collected at night, between sunset and sunrise. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: timeClass

## Parts

*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.

### **niid\_2019-ncov\_n sars-cov-2 gene target**

(niid19). iid\_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.

### **SARS-CoV-2 Nimbus Variant Group**

(nimbusGrp). A group of measures/methods related to the SARS-CoV-2 Nimbus Variant. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* nimbusGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **Nano-molar**

(nM). the unit of nanomolar. *Part Type*: units *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### **No quality concerns**

(noConcern). A flag to indicate there is no quality concern about the measure or sample. *Part Type*: qualityIndicators *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.

### **Sample not labelled**

(noLabel). Sample had no label *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum*

## Parts

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

### No liquid concentration, liquid recombined with separated solids

(noliquid). No liquid concentration, liquid recombined with separated solids  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Nomenclature

(nomenclature). A classification system to report the measure class. Only applicable to variants, mutations, and diseases. Currently only used for class = variant, mutation, or disease. Valid options are currently restricted to ‘NextClade’, ‘Pangolin’, ‘WHO’, or ‘ICD’. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

### Nomenclatures

(nomenclatures). A classification system to report the measure class. See partID = nomenclatureID. *Part Type:* partType *Domain:* naDomain *Spec-*

## Parts

*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: 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.*

## No sample storage medium used

(none). No sample storage medium used *Part Type: categories 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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## No rain

(noRain). Qualitative category for the weather measure, specifying no rainfall for a given day. *Part Type: categories Domain: phy Speciment ID: siSpecimenSet Compartment Set: anyCompartmentSet 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.*

## Purpose is normalization

(norm). The purpose of a measure or sample is for normalization. *Part Type*: categories *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*: 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: 2.3.0.

## Normalization Calculation Type

(normalization). A transformation of data to have a mean of zero and a standard deviation of one, commonly used to compare values across different datasets or units. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## NORMAN

(norm). 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*: 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.*

## Norman Format

(normanForm). Dataset was originally recorded and/or stored in Norman format. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass 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.*

## NORMAN - notes

(normanNotes). Norman notes *Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 1000 Part Status: active. First released: active. Last updated: 2.0.0.*

## Norovirus

(noro). Norovirus. *Part Type: measurements Domain: bio Speciment ID: poSaSpecimenSet Compartment Set: anyCompartmentSet Group: noroGrp Class: allele Nomenclature: allele Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale: seeUnitAggScale*

## 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: 2.1.0.

### Norovirus G1

(noroG1). Norovirus genogroup 1 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Norovirus G2

(noroG2). Norovirus genogroup 2 *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* noroGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Norovirus GI Group

(noroGIGrp). A group of measures/methods related to norovirus GI. Used to describe the organism information for general measures. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

## *Parts*

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

## **Norovirus GII Group**

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

## **Norovirus Group**

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

## No Separation or Concentration

(noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. *Part Type*: categories *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Notes

(notes). A note used to describe details that are not captured in other attributes There is no recommended structure of a note. Use notes as needed. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Sample missing time stamp

(noTime). Sample is missing the autosampler time; incomplete metadata on collection. *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality*

## *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.*

## **Novoalign**

(novoalign). Novoalign. A specialized read mapper. Commercial aligner known for high accuracy. Best for: Applications requiring precise alignments. *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet 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.*

## **NovoPlasty**

(novoPlasty). A sequencing software that is an assembler tailored for organellar genomes (mitochondrial and chloroplast). *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: procGrp Class: software Nomenclature: software Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: <https://github.com/ndierckx/NOVOPlasty> Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

### **Number per 100 kilo-base-pairs**

(nPerKbp). This unit expresses the frequency of an event (such as a mutation, binding site, or feature) per 100,000 base pairs (kbp) of DNA or RNA. It normalizes counts across genomic regions of different lengths, making comparisons more meaningful. *Part Type*: units *Domain*: bio *Speciment 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.

### **Not reported**

(nr). A value could have been recorded, however, it was not. Missing value indicator for data that is absent because it was not reported. *Part Type*: missingness *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Not reported, Not applicable missing set**

(nrNAMissingnessSet). Not reported, Not applicable missing set. *Part Type*: missingnessSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## *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.

## **MinusRT**

(nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). *Part Type:* categories *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Sarbecovirus-specific N sars-cov-2 gene target**

(nSarbec). Sarbecovirus-specific N sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### SARS-CoV-2 nsp1 Gene target { #nsp1 }

(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.

### SARS-CoV-2 nsp10 Gene target { #nsp10 }

(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.

### SARS-CoV-2 nsp11 Gene target

(nsp11). SARS-CoV-2 nsp11 Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENEPIO:0100157 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **SARS-CoV-2 nsp15 Gene target**

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

### **SARS-CoV-2 nsp16 Gene target**

(nsp16). SARS-CoV-2 nsp16 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100172 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### **SARS-CoV-2 nsp2 Gene target { #nsp2 }**

(nsp2 ). SARS-CoV-2 nsp2 Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

*Parts*

*Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENE-PIO: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.

**SARS-CoV-2 nsp3 Gene target { #nsp3 }**

(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:* GENE-PIO: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.

**SARS-CoV-2 nsp4 Gene target { #nsp4 }**

(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:* GENE-PIO: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.

## *Parts*

### **SARS-CoV-2 nsp5 Gene target { #nsp5 }**

(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*: GENE-PIO: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.

### **SARS-CoV-2 nsp6 Gene target { #nsp6 }**

(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*: GENE-PIO: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.

### **SARS-CoV-2 nsp7 Gene target { #nsp7 }**

(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*: GENE-PIO: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.

### SARS-CoV-2 nsp8 Gene target { #nsp8 }

(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*: GENE-PIO: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.

### SARS-CoV-2 nsp9 Gene target { #nsp9 }

(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*: GENE-PIO: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.

### Non-template control

(ntc). Denotes a non-template control sample replicate. *Part Type*: categories *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

*Parts*

### **NTC Amplification Detected**

(ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. *Part Type*: qualityIndicators *Domain*: bio *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: 3.0.0.

### **Control-plate Flag - NTCs**

(ntcFlag). quality indicator for when there is observed amplification in the non-template controls (NTCs) of a PCR reaction. *Part Type*: qualityIndicators *Domain*: bio *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*: depreciated. First released: depreciated. Last updated: 3.0.0.

### **number of total reads**

(nTotRead). The total number of non-unique reads generated by the sequencing process. Provide a numerical value (no need to include units). *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## Parts

*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.

## No target present

(ntp). Denotes a sample replicate/control with no target present. *Part Type:* categories *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Nephelometric turbidity unit

(ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see “turbidity” under measureIDs). Nephelometric turbidity units (NTU) are based on white light (400–680nm) and 90° incident angle. *Part Type:* units *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

## *Parts*

### **Nuclisens automated magnetic bead extraction kit**

(nucAuto). Nucleic acid extraction performed using the nuclisens automated magnetic bead extraction kit. *Part Type:* categories *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.

### **nucleomag (ref. 744220.4) using kingfisher automated instrument**

(nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *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: 2.2.0.

### **Nuclisens manual magnetic bead extraction kit**

(nucManu). Nucleic acid extraction performed using the nuclisens manual magnetic bead extraction kit. *Part Type:* categories *Domain:* 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.

## Null

(null). A logical representation of a statement that is neither TRUE nor FALSE. Missing value indicator when the value is neither TRUE nor FALSE. *Part Type:* missingness *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## ISO 3166-1 numeric country code

(numCode). The ISO 3166-1 numeric code, a three-digit country code which is identical to that developed and maintained by the United Nations Statistics Division, with the advantage of script (writing system) independence, and hence useful for people or systems using non-Latin scripts. 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:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 3 *Maximum Length:* 3 *Part Status:* active. First released: active. Last updated: 2.1.0.

*Parts*

### **Number of NTCs per Run**

(numNTC). The number of no-template controls included in each PCR instrument run. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **number of unique reads**

(nUniRead). The number of unique reads generated by the sequencing process. Provide a numerical value (no need to include units). *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

### **National Wastewater Surveillance System**

(nwss). NWSS header *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness*

## 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.*

### US-CDC NWSS Format

(nwssForm). Dataset was originally recorded and/or stored in the US-CDC's NWSS format. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://covid.cdc.gov/covid-data-tracker/#wastewater-surveillance> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length: 0 Maximum Length: 50 Part Status:* active. First released: active. Last updated: 3.0.0.

### NWSS - notes

(nwssNotes). NWSS notes *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length: 0 Maximum Length: 1000 Part Status:* active. First released: active. Last updated: 2.0.0.

### NWSS - process

(nwssProcess). NWSS process *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:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Water

(nww). Non-wastewater, coming from any kind of water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## coronavirus OC43

(oc43). Measure of the amount of coronavirus OC43. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **oc43 spike target**

(oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. *Part Type*: categories *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.

### **Ocean, natural water body**

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

### **Other Collection depreciated**

(oColDep). Other type of collection method. Add description to collectionOther. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (<https://github.com/Big-Life-Lab/PHES-ODM/issues>), or at phesd\_odm@ohri.ca *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale

## Parts

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

## Odour Control Unit

(ocu). Odour Control Unit ventilation extends the life of a sewer by reducing the amount of maintenance the pipeline needs, making management of the network much more efficient. The filters used in the Odour Control Unit and ventilation stacks absorb gases such as hydrogen sulphide, which is a common source of odours from sewerage systems. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Office

(office). A workplace where administrative, managerial, or clerical tasks are performed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## SIL Open Font License 1.1

(ofl11). The licensing for the measure or data set is managed under the SIL Open Font License 1.1. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/ofl-1.1/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

## Original Data Format Set

(ogFormSet). The category set for recording the possible original data formats to be recorded in the originalFormat field in the datasets table. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: ogFormSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Lab Analysis

(ola). Offline laboratory analysis. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum*

## Parts

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

### Omicron BA.1

(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.

### Omicron BA.2

(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.

### Omicron BA.2.75

(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

## Parts

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

### Omicron BA.4

(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.

### Omicron BA.5

(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.

### SARS-CoV-2 Omicron Variant Group

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

## *Parts*

naClass *Nomenclature*: naClass *Ontology Reference*: [http://purl.obolibrary.org/obo/NCIT\\_C169076](http://purl.obolibrary.org/obo/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.

## **Onset date**

(onsDate). Earliest that symptoms were reported for this case. This data is often not known and reported. In lieu, episode is used. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: NA *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

## **Online Sensor**

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

## Ontology reference

(ontologyRef). Ontology reference for a part. This field contains a link to an existing ontology reference for the part. ODM content spans several existing ontologies. ODM does not strive to generate a new ontology, rather ODM seeks to harmonize and extend dictionaries for application in environmental and public health surveillance. *Part Type*: partSupport  
*Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass  
*Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 200 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Value out of range

(oor). Value is outside of the allowable range for quality control. *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Open license not otherwise described

(open). The licensing for the measure or data set is managed under an open license not otherwise described. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet

## 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.

## Orthophosphates

(ophos). Ortho-phosphate concentration. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* waterQualityGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Optical calibrator sample

(opt). Denotes a sample control or replicate used for optical calibration. *Part Type:* categories *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Surface water

(opWa). An outdoor accumulation of water either on the surface of the earth, no other additional details specified. *Part Type*: categories *Domain*: naDomain *Specimen 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Organization table Shorthand

(or). The abbreviated short name used to reference the The table that contains information about a laboratory. table *Part Type*: shortName *Domain*: naDomain *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: 2.2.2.

## Other residential building

(orb). Individual residential buildings or institutions not captured in other categories *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

## *Parts*

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

## **OR Boolean aggregation**

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

## **Sequence Order**

(order). The order a single calculation/data treatment takes within the full container pipeline/workflow. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

### SARS-CoV-2 orf10 Gene target

(orf10). SARS-CoV-2 orf10 Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENE-PIO: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.

### SARS-CoV-2 orf14 Gene target

(orf14). SARS-CoV-2 orf14 Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENE-PIO: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.

### ORF1a sars-cov-2 gene target

(orf1a). ORF1a sars-cov-2 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: allele *Nomenclature*: allele *Ontology Reference*: GENEPIO:0100156 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **ORF1ab sars-cov-2 gene target**

(orf1ab). ORF1ab sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* GENEPIO:0100155 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **ORF1b sars-cov-2 gene target**

(orf1b). ORF1b sars-cov-2 gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **SARS-CoV-2 orf3a Gene target**

(orf3a). SARS-CoV-2 orf3a Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100173 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation*

## Parts

*Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### SARS-CoV-2 orf3b Gene target

(orf3b). SARS-CoV-2 orf3b Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100174 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### SARS-CoV-2 orf6 (ns6) Gene target

(orf6). SARS-CoV-2 orf6 (ns6) Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100175 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### SARS-CoV-2 orf7a Gene target

(orf7a). SARS-CoV-2 orf7a Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet

## Parts

*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.

## SARS-CoV-2 orf7b (ns7b) Gene target

(orf7b). SARS-CoV-2 orf7b (ns7b) Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100177 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

## SARS-CoV-2 orf8 (ns8) Gene target

(orf8). SARS-CoV-2 orf8 (ns8) Gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100178 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### SARS-CoV-2 orf9b Gene target

(orf9b). SARS-CoV-2 orf9b Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENE-PIO:0100179 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### SARS-CoV-2 orf9c Gene target

(orf9c). SARS-CoV-2 orf9c Gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: GENE-PIO:0100180 *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### Organism

(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*

## *Parts*

*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.*

## **Organization ID**

(organizationID). A unique identifier for the organization to which the reporter is affiliated. *Part Type:* attributes *Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: genMissingnessSet Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 100 Part Status: active. First released: active. Last updated: 2.0.0.*

## **Organization table**

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

## **Organizations table column order**

(organizationsOrder). Specifies the order of the columns 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*: 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.

## Organization table required headers

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

## Organization level

(orgLevel). The geographic level of an organization. There are six levels based on International Standard Classification of Administrative Units (ISCU). *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: orgLevelSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: nrNAMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Parts

### Organization level set

(orgLevelSet). Categories of organization levels. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: any-CompartmentSet *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.

### Organization sector

(orgSector). The sector of an organization *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: orgSectorSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: nrNAMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Organization sector set

(orgSectorSet). Cateogries of organization sectors. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: any-CompartmentSet *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.

## Organization Type

(orgType). Specifies the type or purpose of a given organization. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* nrNAMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Organization type set

(orgTypeSet). The set for storing organization types. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* orgTypeSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Sample origin

(origin). An attribute of a sample specifying the origin. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* originSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum*

## *Parts*

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

## **Original Data Format**

(originalFormat). The original structure or model used to record and store the data. This helps indicate if data have been transformed or mapped into the ODM structure. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* ogFormSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Sample Origin set**

(originSet). The set for storing the valid categorical values of sample origin. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* originSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Oxidation reduction potential (ORP)**

(orp). Oxidation-reduction potential (ORP) measures the ability of a lake or river to cleanse itself or break down waste products, such as contaminants and dead plants and animals. *Part Type:* measurements *Domain:* bio

*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.

## OrthoFinder Software

(orthoFinder). OrthoFinder - For orthogroup identification and phylogenetic tree building, often useful in evolutionary clade studies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/davidemms/OrthoFinder> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Orthopox Virus Group

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

*Parts*

### **Open Science Foundation (OSF)**

(osf). Open Science Foundation project/data storage. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://osf.io> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Open Software License 3.0**

(osl30). The licensing for the measure or data set is managed under the Open Software License 3.0. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://choosealicense.com/licenses/osl-3.0/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### **Other Collection depreciated**

(otco). Other type of collection method. Add description to collectionOther. Deprecated as of version 2, please avoid use. Specify in type, or contact the PHES-ODM research team to add your specific item via a github issue (<https://github.com/Big-Life-Lab/PHES-ODM/issues>), or at phesd\_odm@ohri.ca *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category*

## Parts

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

## Other aggregation scale

(othAgg). Specifies an aggregation scale that can't be described as either "qualitative" or "quantitative". *Part Type:* aggregationScales *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Other

(other). Other Other category. A categorical response for several variables in version 1. Also accompanied by a free text field. Depreciated in version 2, with common text fields added as new categories in version 2.0.0 *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* NA *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated**. First released: depreciated. Last updated: 2.0.0.

## *Parts*

### **Other aggregation set**

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

### **Other aggregation deprecated**

(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: depreciated. Last updated: 2.0.0.

### **Other (or proprietary) Format**

(otherForm). Dataset was originally recorded and/or stored in a format not otherwise described. Please name (and optionally describe) the data format in the “notes” section when using this value. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment*

## Parts

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

## Access to other prov deprecitated

(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: depreciated. Last updated: 2.0.0.

## Other report table set

(otherReportTableSet). Additional tables that form the full data model. *Part Type: dictSets Domain: naDomain Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

## Parts

### Variants Other

(otherV). Used for reporting variants detected for which a specific measureID doesn't already exist. The ODM team will periodically migrate collected responses in this category into set measureIDs. Please write in an official name for the new variant that was detected, and specify which nomenclature you're using with the nomenclatureID. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### Other Site - sample deprecated

(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*: NA *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.

### **Other Site - Site depreciated**

(otsisiDep). Other site type. Add description to typeOther *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: NA *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Other Unit depreciated**

(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: depreciated. Last updated: 2.0.0.

### **Value is an outlier**

(out). Value is an outlier and may be of questionable quality. *Part Type*: qualityIndicators *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## 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.

## Outbreak declaration

(outb). Public health action type used to indicate outbreak status. Given that when outbreaks occur, full data on case counts may not be available or completely accurate, using this measure indicates that case counts may be approximate. The datetime for the measure helps indicate that start and end periods for an outbreak. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* outbreakSet *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.

## End of Outbreak

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

## Outbreak - on-going

(outbOngoing). Indicates an outbreak is on-going. *Part Type*: categories  
*Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: na-  
CompartmentSet *Group*: naGroup *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: 3.0.0.

## Outbreak class

(outbreak). Measures and methods relating to public health outbreaks.  
*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*: **deprecated**. First released: depreciated. Last updated: 3.0.0.

## Outbreak declaration Value Set

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

*Parts*

### **Declared outbreak or Outbreak start**

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

### **Overlapping relationship**

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

### **Delta Variant p100I mutation**

(p100l). Delta Variant p100l mutation & gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: deltaGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Omicron Variant p13l mutation**

(p13L). Omicron Variant p13l mutation *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Delta Variant p2046l mutation**

(p2046l). Delta Variant p2046l mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Delta Variant p2287s mutation**

(p2287s). Delta Variant p2287s mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* deltaGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet

## *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.

## **Omicron Variant p3395h mutation**

(p3395h). Omicron Variant p3395h mutation & gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA  
*Data Type:* seeUnitData *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.

## **Delta Variant p681r**

(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.

## Parts Look-up table Shorthand

(pa). The abbreviated short name used to reference the Look up table containing all parts in of the data model. *table Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *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.

## polymerase activation

(pAct). Describes the polymerase activation cycle in a PCR process. *Part Type:* categories *Domain:* bio *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: 2.2.0.

## Paired Layout

(pairLay). Specifies the paired layout for a sequencing method *Part Type:* categories *Domain:* bio *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:*

## *Parts*

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

## **Pangolin nomenclature**

(pangolin). Specifies variant or genetic nomenclature as set out by the Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin). *Part Type*: nomenclatures *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Pangolin Software**

(pangolinSoft). A lineage or clade analysis software tool used for lineage assignment in SARS-CoV-2 and other viral genomes. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/cov-lineages/pangolin> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Papillomavirus Group**

(papillomavirusGrp). A group of measures/methods related to papillomaviruses. Used to describe the organism information for general measures.

## Parts

*Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* papilomavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## Paraxanthine (PARA)

(para). A metabolite of the common central nervous system stimulant caffeine, measured 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.

## Parainfluenza Group

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

## Parts

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

## Parapoxvirus Orf Virus Spike Target

(parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* 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: 2.2.0.

## Parent dataset ID

(parDatasetID). The datasetID that is a parent to another datasetID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Parent sample ID

(parent). If this sample has been pooled into one big sample for analysis this indicates the sample of the larger pooled sample. *Part Type:* attributes *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:* genMissingnessSet *Minimum Value:* NA  
*Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* **deprecated.** First released: depreciated. Last updated: 2.0.0.

### Parent Site ID

(parSiteID). The siteID that is a parent to another siteID; usually the sub-site will be contained in the parentSite. An example would be surface testing in a LTC facility. The LTC facility would be the parentSiteID, and the various rooms/surfaces would be the sub-sites, or child-sites. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet  
*Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA  
*Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Part description

(partDesc). The description of the part. Provides description of the part, used for translation. *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: active. Last updated: 2.0.0.

## *Parts*

### **Part identifier**

(partID). The unique identify of any entity within the dictionary. Every entity in the ODM has a partID. The partID must be unique with no duplicates. partIDs are short. partIDs that are constructed by different part attributes can be up 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 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, ovid-pr (allele, variant or protein) or units and aggregations (i.e. covid-al-N1-mean-cpl representing ovid allele N1, mean observation of viral copies per litre of effluent). A similar approach to naming subComponent is 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.

### **Part instruction**

(partInstr). Additional notes and instructions on how a part is used and/or defined. *Part Type*: partSupport Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality

## Parts

*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.*

### Parts Look-up table

(parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. pa *Part Type: tables Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: lookup Nomenclature: lookup Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

### Parts table column order

(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 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*

### **Parts table required headers**

(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.

### **Part Support**

(partSupport). Parts designed to support the metadata definition of other parts in the parts table. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Part types**

(partType). Part types describe the purpose or use of the part. Enivornment 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*: partType *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:* 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.

### Part type input (wide table)

(partTypeInput). The partID for the part type being used in a wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* 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: 2.2.0.

### Part type name (wide table)

(partTypeName). The part type being used in a wide name. *Part Type:* attributes *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: 2.2.0.

### Passive Sample - General

(passiveGen). Used to specify a passive sampling method not otherwise specified was used to collect the sample. *Part Type:* categories *Domain:*

## *Parts*

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

## **Pasteurized sample**

(pasteur). Binary indicator for whether a sample was pasteurized as part of its processing. *Part Type:* methods *Domain:* bio *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## **Pathogenwatch**

(pathogenwatch). Pathogenwatch. Focus: Integrates MLST, serotyping, and resistance typing with a user-friendly interface. Applications: Primarily used for *Salmonella* and *Escherichia coli*. Features: Combines typing results with interactive visualization. *Part Type:* categories *Domain:* bio *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:* <https://next.pathogen.watch/> *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.

### **PATRIC/RAST Database**

(patricRast). Database that hosts resistance gene annotations within their microbial genome data resources. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* database *Nomenclature:* database *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* patricbrc.org *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **PBPfinder**

(pbfinder). PBPfinder. Used for typing and serotyping of Streptococcus pneumoniae through analysis of penicillin-binding proteins and capsular genes. *Part Type:* categories *Domain:* bio *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:* 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.

### **Phosphate Buffered Saline (PBS)**

(pbs). An isotonic solution for general sample preservation, used when immediate freezing is available. *Part Type:* categories *Domain:* naDomain

## Parts

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

## Primary Clarifier Effluent depreciated

(pceDep). Effluent obtained after primary clarifiers. Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* NA *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.

## Postal or Zip Code

(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.

## **qPCR Class**

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

## **PCR Action/Activity**

(pcrAct). Describes a given PCR cycle for delineating more method information. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: measGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: pcrActSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

## **PCR action/activity set**

(pcrActSet). The set capturing containing all of the valid methods for the PCR activity cycles. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: pcrActSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum*

## *Parts*

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

## **PCR Quanitification Cycles**

(pcrCycles). A count unit of how many Polymerase Chain Reaction (PCR) cycles it took to detect a real signal from a sample. Equivalent to the PCR cycle number at which a sample's reaction curve intersects the threshold line. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## **PCR method**

(pcrmeth). Description of the PCR method. Description of the PCR method used *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* measGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* pcrSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## **PCR quality set**

(pcrQualitySet). Quality set for PCR measures. *Part Type:* qualityInd Sets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:*

## Parts

anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: na-  
Class *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.

## PCR Sequencing Selection Method

(pcrSeq). Specifies the PCR selection method for sequencing, ie. that a pre-determined primer was used. Primer should be specified if this is selected. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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*: 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.

## PCR Method set

(pcrSet). The set capturing containing all of the valid methods for the PCR method. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: pcrSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## *Parts*

### **Primary Clarifier Sludge depreciated**

(pcs). Sludge produced by primary clarifiers. *Part Type*: categories *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*: NA *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.

### **Number of people**

(peeps). Unit specifying a number of people. *Part Type*: units *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Primary clarifier effluent**

(pEfflu). Effluent obtained after primary clarifiers *Part Type*: categories *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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Polyethyleneglycol (PEG) precipitation**

(peg). Peg precipitation *Part Type*: categories *Domain*: che *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **PEHaplo**

(pehaplo). A sequencing software that is an assembler that considers heterozygosity in diploid genomes. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/chjiao/PEHaplo> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Percent**

(perc). Percentage. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum*

## *Parts*

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

### **percent read contamination**

(percContam). The percent of the total number of reads identified as contamination (not belonging to the target organism) in a sequence dataset. Provide the percent contamination value (no need to include units). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

### **Percent unit set**

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

### **percent Ns across total genome length**

(percNLength). The percentage of the assembly that consists of ambiguous bases (Ns). Provide a numerical value (no need to include units). *Part Type:*

## Parts

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.

## Percent recovery

(percRec). Percent of the surrogate recovery for a recovery efficiency control assay (as a unit). Use this for reporting the results of any recovery control assay. *Part Type*: units *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: 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*: 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.

## Persons for square kilometre

(personPerKm). Persons per square kilometre. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## Parts

### Persons per square mile

(personPerMile). Persons per square mile. *Part Type*: units *Domain*: allDo Speciment ID: anySpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 3.0.0.

### PGAP (Prokaryotic Genome Annotation Pipeline)

(pgap). PGAP (Prokaryotic Genome Annotation Pipeline). Focus: Annotation pipeline that integrates MLST and antigen typing. Applications: Broad bacterial pathogens. Features: Provided by NCBI, designed for high-throughput workflows. *Part Type*: categories *Domain*: bio 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: NCBI: [https://www.ncbi.nlm.nih.gov/ref-seq/annotation\\_prok/](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.

### pH

(ph). pH measurement *Part Type*: measurements *Domain*: phy Speciment ID: siSaSpecimenSet Compartment Set: anyCompartmentSet Group: waterQualityGrp Class: pHClass Nomenclature: pHClass Ontology Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet Aggregation Scale:

## Parts

*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.*

## Public Health Actions Report Table Shortname

(pha). The abbreviated short name used to reference the table for recording information on public health actions. table *Part Type: shortName Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## PHA4GE Format

(pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: https://github.com/pha4ge/Wastewater\_Contextual\_Data\_Specification Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## *Parts*

### **Access to phac**

(phac). If this is ‘no’, the data will not be available to employees of the Public Health Agency of Canada - PHAC. If missing, data will be available to employees of the Public Health Agency of Canada - PHAC. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* booleanSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* depreciated. First released: depreciated. Last updated: 2.0.0.

### **Public Health Action ID**

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

### **Public Health Actions Report Table**

(phActions). Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. pha *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit*

## 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: 3.0.0.*

### Public health actions table column order

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

### Public health actions table required headers

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

### Public health advisory

(phAdvise). A public health action type wherein a public health advisory is disseminated to the public. *Part Type: categories Domain: naDomain Spec-*

## Parts

*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.

## Public Health Advisory Value Set

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

## PHAGE

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

## Bacteriophage Group

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

## PHAGE - notes

(phageNotes). PHAGE notes *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Phagotyping Results

(phagetype). The phagotyping 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*

## Parts

*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.

## Phandango

(phandango). Phandango. A visualization tool that integrates serotype predictions with phylogenetic analyses for population studies. Often used alongside other serotyping tools. *Part Type:* categories *Domain:* bio *Specimen 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:* 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.

## Pharmaceutical manufacturing plant

(pharmPl). An industrial building in which pharmaceutical drugs are synthesised and processed on an industrial scale. *Part Type:* categories *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **pH class**

(pHClass). Measures and methods relating to pH. *Part Type*: classes *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: any-CompartmentSet *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.

### **Public health emergency (outbreak)**

(phEmerg). Indicates a public health emergency from an outbreak. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Phenol chloroform**

(phenCl). Nucleic acid extraction performed using phenol chloroform. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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

### **PHES-ODM Version 1 Format**

(phesODMFormV1). Dataset was originally recorded and/or stored in PHES-ODM version 1 format. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.phes-odm.org> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **PHES-ODM Version 2 Format**

(phesODMFormV2). Dataset was originally recorded and/or stored in PHES-ODM version 2 format. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.phes-odm.org> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **PHES-ODM Version 3 Format**

(phesODMFormV3). Dataset was originally recorded and/or stored in PHES-ODM version 3 format. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.phes-odm.org>

## Parts

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

### **Pseudomonas virus phi6**

(phi6). Measure of the amount of pseudomonas virus phi6. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* phageGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **phi6 spike target**

(phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control target. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### **Country national phone prefix**

(phone). International dialing code for the country. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *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:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 75 *Part Status:* active. First released: active. Last updated: 2.1.0.

## **Total phosphorous**

(phos). Total phosphorous *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **Total Phosphates**

(phostot). Total phosphates *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## PHRED quality score

(phred). PHRED Quality Score For Sequencing *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Physical property

(phy). A physical property or object not characterized by life or chemistry. *Part Type*: domains *Domain*: phy *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## PhyloPhIAn Software

(phyloPhIAn). A lineage or clade analysis software tool, specialized in high-resolution phylogenetic analysis, typically used for microbial clade analysis. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://huttenhower.sph.harvard.edu/phylophlan/> *Data*

## *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.

## **PhyloSuite Software**

(phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://dongzhang0725.github.io/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **PhyML Software**

(phyML). A lineage or clade analysis software tool that builds phylogenetic trees using maximum likelihood methods, with clade confidence assessments. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://www.atgc-montpellier.fr/phymml/> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Physical class

(physical). Measures and methods related to generic physical properties. *Part Type*: classes *Domain*: phy *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.

## Picard MarkDuplicates

(picard). A deduplication method within the Picard suite that marks duplicate reads in BAM files based on mapped location. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://broadinstitute.github.io/picard/> (Picard toolkit includes MarkDuplicates) *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Pipeline ID

(pipelineID). A primary key linked to a single measure (may be used multiple times), it is the shorthand for the data transformation pipeline used. Serves as a data pipeline identifier. Can be used to link multiple data treatments together - rows of different related treatments will share the same pipelineID. *Part Type*: attributes *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: 3.0.0.

## PIQMie

(piqmie). A comprehensive QC and contamination assessment pipeline for metagenomic datasets and sequencing data. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## PiSeqQC

(PiSeqQC). A QC pipeline tool for sequencing data for microbiome and metagenomic sequencing data, including quality filtering and contaminant removal. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://sourceforge.net/projects/piseqqc/> (genomic QC) *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Primary key

(pK). Primary key for a table. All report tables have a primary key. Each row in a report table has unique identifier recorded in the primary key.  
*Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet  
*Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass  
*Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Plasmodium

(plasmodium). Plasmodium *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: malariaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Platanus

(platanus). A sequencing software that is an assembler, optimized for large, diploid genome assemblies, particularly plants. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/bioinformatics-i/platanus> link pending retrieval *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.

## Plumbing drain

(pluDra). An artificial channel which transports unwanted water or waste liquids away from their source, either to a more useful area, a receptacle, or into sewers or stormwater mains as waste discharge to be released or processed. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## PMMoV- and flow-normalized mean

(pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Mostly used for reporting specific alleles (N1, N2, E, etc.) *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

## PMMoV Group

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

## PMMoV-normalized mean

(pmmovNorm). Mean measure normalized to amount of PMMoV. Mostly used for reporting specific alleles (N1, N2, E, etc.) *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

## PMMoV Standardized

(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

## Parts

*Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: 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.*

### **PMMV forward primer (ABI)**

(pmmvABIFor). PMMV forward primer (ABI) *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: pmmovGrp Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet Aggregation Scale: 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.*

### **PMMV probe (ABI)**

(pmmvABIProbe). PMMV probe (ABI) *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: pmmovGrp Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet Aggregation Scale: 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.*

### **PMMV reverse primer (ABI)**

(pmmvABIRev). PMMV reverse primer (ABI) *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: pmmovGrp Class: pcr Nomenclature: pcr Ontology*

## Parts

*Reference: NA Category Set ID: NA Unit Set: unitlessUnitSet Aggregation Scale: 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.

## Polygon table Shorthand

(po). The abbreviated short name used to reference the The table that contains information about the geometry of a geographic area. table *Part Type: shortName Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active.* First released: active. Last updated: 2.2.2.

## Post-Grit depreciated

(pogr). Raw wastewater after a treatment plant's headworks. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: 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: NA 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

### Polygon License

(poLic). The license for the availability of the polygon shapefile. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: saSpecimenSet *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*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Policy and political sector or organization

(policy). Describes organizations whose core focus is on policy or political activity. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### Poliovirus Group

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

## Parts

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

## Polygon

(poly). A measure made on a compartment or property within a polygon. An example would be the population of a polygon; this specimen is used for measures at the polygon level, where site or population might not be entirely appropriate. *Part Type:* specimens *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Polygon ID

(polygonID). Unique identifier for the polygon. A polygon is a geographic area 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.

*Parts*

### **Polygon ID Object**

(polygonIDObject). The polygon ID Object in a polygon relationship. The polygon relationship should be read as “‘subject’ is ‘relationshipID’ to ‘object’”. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Polygon ID Subject**

(polygonIDSubject). The polygon ID subject in a polygon relationship. The polygon relationship should be read as “‘subject’ is ‘relationshipID’ to ‘object’”. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Polygon Relationships Table**

(polygonRelationships). Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. por *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:*

## Parts

*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.

### Polygon relationships table column order

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

### Polygon relationships table required headers

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

## Parts

### Polygon relationship ID

(polygonRelID). Unique identifier for each row in the polygon relationships table. Provisional PK. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Polygon table

(polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. po *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: programDescr *Nomenclature*: programDescr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Polygons table column order

(polygonsOrder). Specifies the order of the columns in a Polygons table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## Parts

*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.

### Polygon table required headers

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

### Polygon Population

(polyPop). An attribute of a polygon, which specifies the population of that polygon. A rough estimate of the number of human residents. *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.

### Polygon Relationship Set

(polyRelSet). Value set for polygon relationships. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* any-

## *Parts*

*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.

## **Polygon or site specimen set**

(polySiSpecimenSet). A specimen set that inculdes polygon or site specimen.  
*Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* polySiSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Polygon specimen set**

(polySpecimenSet). A specimen set that inculdes only a polygon specimen.  
*Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* polySpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Pooled

(pooled). Is this a pooled sample, and therefore composed of multiple child samples obtained at different sites *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: booleanSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: boolean *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Population

(pop). An measure or observation for a geographic area or population. Examples include human compartment measures such as case numbers, hospitalization rates for diseases or surface or air compartment measures such as snow coverage or ambient temperature. *Part Type*: specimens *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Populated area type set

(popAreaSet). Set of valid values used to describe the type of a populated area. *Part Type*: mmaSets *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: popGrp *Class*: popClass

## *Parts*

*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.

## **Populated area type**

(popAreaType). Type of populated area being sample (ie. urban, rural) *Part Type:* measurements *Domain:* allDo *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.

## **Population assessment method**

(popAs). Method for assessing the population count for a site/polygon. *Part Type:* methods *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* popMetSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## Population Class

(popClass). Measures and methods relating to population (ie. Measures of population, location). *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* populationUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* 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.

## Type of date for case reporting depreciated

(popDateTypeDep). Type of date used for confirmed cases. Typically, report or episode are reported. Onset and test date is not usually reported within aggregate data. *Part Type:* attributes *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* humanCompartmentSet *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:* 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.

## Population density

(popDensity). Measure of population density of a site. *Part Type:* measurements *Domain:* allDo *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*

## *Parts*

*Link:* NA *Data Type:* 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.

## **Population density unit set**

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

## **Population equivalents**

(popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a signle person would use. *Part Type:* units *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Population group**

(popGrp). A group of measures/methods related to population-level factors. Examples might be case numbers, hospitalization rates, etc. *Part*

*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.

## Population Interval Set

(popIntSet). The collection of categorical inputs for population interval measures. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* popIntSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Population assessment method set

(popMetSet). The set for valid inputs for the population assessment method. *Part Type:* mmaSets *Domain:* allDo *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* popGrp *Class:* popClass *Nomenclature:* popClass *Ontology Reference:* NA *Category Set ID:* popMetSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Parts

### **Population or polygon specimen set**

(poPolySpecimenSet). A specimen set that includes population or polygon specimen. *Part Type*: specimenSets *Domain*: naDomain *Speciment ID*: poPolySpecimenSet *Compartment Set*: naCompartmentSet *Group*: na-Group *Class*: 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.

### **Population Served**

(popServ). An measure of a site, which specifies the population of/population served by a given site. *Part Type*: measurements *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: siteFeat *Class*: popClass *Nomenclature*: popClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: populationUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeU-unitData *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.

### **Population Served - Interval**

(popServRange). Population served by a site, when reported as an interval. *Part Type*: measurements *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: siteFeat *Class*: popClass *Nomenclature*: popClass *Ontology Reference*: NA *Category Set ID*: popIntSet *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.*

### **Population unit set**

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

### **Polygon Relationships Table Short Name**

(por). The abbreviated short name used to reference the table for recording the relationships between polygons. table *Part Type: shortName Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.3.0.*

### **Porechop**

(porechop). A sequencing data processing application that is specifically designed for adapter trimming in Oxford Nanopore Technologies data. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet*

## Parts

*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.

## Port or Harbour

(port). A harbor is any sheltered body of water where boats or ships may moor or anchor. A port is an installation that has been built around a harbor with facilities for loading and unloading such vessels. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Population or sample set

(poSaSpecimenSet). A specimen set that inculdes population or sample specimen. *Part Type:* specimenSets *Domain:* naDomain *Speciment ID:* poSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Positive experimental control**

(posCon). A sample or experimental condition where the expected outcome is known to occur, intended to confirm that the experimental setup is working properly. An example would be a wastewater sample spiked with a known quantity of SARS-CoV-2 virus. *Part Type*: categories *Domain*: naDomain *Speciment ID*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Population or site set**

(poSiSpecimenSet). A specimen set that inculdes population or site specimen. *Part Type*: specimenSets *Domain*: naDomain *Speciment ID*: poSiSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Population specimen set**

(poSpecimenSet). A specimen set that inculdes only a population specimen. *Part Type*: specimenSets *Domain*: naDomain *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## *Parts*

*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.

## **PostgreSQL License**

(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.

## **Percent positive**

(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.

## **parts per million**

(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.

## PMMoV-CP

(ppmv). Pepper mild mottle virus capsid protein gene region *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* pmmovGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Percent positivity rate

(pprt). Percent positivity rate of tests conducted within a day in a given region. *Part Type:* units *Domain:* bio *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

## *Parts*

### **Percent primary sludge**

(pps). Percentage of total solids, for primary sludge. *Part Type*: units *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: 100 *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **parts per thousand**

(ppt). Parts per thousand. *Part Type*: units *Domain*: phy *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Protocol relationships table Shorthand**

(pr). The abbreviated short name used to reference the The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). table *Part Type*: shortName *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category 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.

### Precipitation (from solution)

(prec). The formation of a solid from a dissolved substance in a solution, typically induced by chemical reactions or changes in temperature/pH. *Part Type:* categories *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### Precipitation - general

(precip). General measure of precipitation, type not specified. *Part Type:* measurements *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* precipitationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* 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.

### Precipitation class

(precipitation). Measures and methods related to precipitation. *Part Type:* classes *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* precipitation *Nomenclature:*

## *Parts*

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.

## **Precipitation unit set**

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

## **Storage temperature prior to concentration**

(preConcTemp). The temperature at which a sample was stored between collection and concentration. *Part Type*: measurements *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: temperatureUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Storage time prior to concentration**

(preConcTime). Length of time for which a sample is stored between collection and concentration. *Part Type*: measurements *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: timeUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Predicted data**

(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.

### **Predictive Modeling Calculation Type**

(predictiveModels). A statistical or machine learning approach used to estimate future values or outcomes based on historical data patterns. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## 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: 3.0.0.

## Storage temperature prior to extraction

(preExtractTemp). The temperature at which a sample was stored between concentration and extraction. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## Storage time prior to extraction

(preExtractTime). Length of time for which a sample is stored between concentration and extraction. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## preQC (from Meraculous)

(preQC). A QC pipeline tool for sequencing data that evaluates data quality before assembly, particularly for large genomes. *Part Type:* categories

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

### **presampling activity**

(presampAct). A measure for recording any relevant activities that occur upstream of the sampling source. For example, recording that the river one is sampling from flows through farmland, or that filtration and/or sedimentation occurred at the wastewater treatment plant before the sample was collected. *Part Type:* measurements *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* presampSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

### **Presampling activity category set**

(presampSet). The set of valid input values for reporting pre-sampling activity. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* presampSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50

## *Parts*

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

### **Pre-sampling weather**

(preSampWeath). Weather leading up to, but not including, the day of sampling. *Part Type:* measurements *Domain:* allDo *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* weathSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

### **Pretreatment**

(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.

### **Primary clarifier**

(primClar). A large settling tank that removes solids and floating materials from wastewater before secondary treatment. *Part Type:* categories

## Parts

*Domain:* naDomain *Specimen ID:* naSpecimenSet *Compartment Set:* wa-  
terCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass  
*Ontology Reference:* ENVO:03501468 *Category Set ID:* NA *Unit Set:* naU-  
nitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:*  
NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maxi-  
mum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:*  
active. First released: active. Last updated: 3.0.0.

## Genetic primer

(primer). Method ID used for indicating the primer used for a PCR or sequencing assay. *Part Type:* methods *Domain:* bio *Specimen 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 *Min-  
imum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released:  
active. Last updated: 2.0.0.

## Genetic primer set

(primerSet). The set for genetic primers used in sequencing or PCR assays. *Part Type:* mmaSets *Domain:* bio *Specimen ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* primer-  
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 *Min-  
imum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

*Parts*

## **PRINSEQ**

(prinseq). A QC pipeline tool for sequencing data for assessing and filtering sequences based on complexity, quality scores, and GC content. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/prinseq/prinseq> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Prinseq-lite**

(prinseqLite). A sequencing data processing application that filters sequences based on complexity and removes low-quality reads. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://prinseq.sourceforge.net> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Private sector**

(priv). The category of organization type used for private sector or non-profit groups that are not otherwise captured by the academic category. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass

## Parts

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

## Private data - not for dissemination

(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.

## Protocols table Shorthand

(pro). The abbreviated short name used to reference the the table that contains the summary information and details about a given protocol. table  
*Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.2.

## *Parts*

### **Processing group**

(procGrp). A group of measures/methods related to processing samples for analysis. *Part Type*: groups *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Environmental survey or profiling**

(profil). Purpose of sampling/measure is to record characteristics and profile a given environment. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSpecimenSet *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Program description tables**

(programDescr). Tables used to describe surveillance and testing programs. Program description tables record metadata on the organizations, locations, and protocols. Information include the name, location, and other contact information. These tables are usually completed once and they are updated only when contact information changes. *Part Type*: classes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: programDescr *Nomenclature*:

## Parts

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.

## Prokka (with serotyping integration)

(prokka). Prokka (with serotyping integration) While primarily an annotation tool, Prokka outputs can be paired with databases for identifying serotypes of certain bacterial pathogens. *Part Type*: categories *Domain*: bio *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*: <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.

## Prokka + Roary Pipeline (Nextflow)

(prokkaRoary). Prokka + Roary Pipeline. Focus: Genome annotation (Prokka) with MLST and serotyping integration via Roary. Applications: Broad compatibility with bacterial pathogens. Features: Facilitates core-genome MLST and accessory gene analysis. *Part Type*: categories *Domain*: bio *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*: <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*

### **promega automated tna kit**

(promAuto). Nucleic acid extraction performed using the promega automated tna kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **promega wastewater large volume tna capture kit**

(promegaLVTNA). promega wastewater large volume tna capture kit *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **promega ht tna kit**

(promHt). Nucleic acid extraction performed using the promega ht tna kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **promega manual tna kit**

(promManu). Nucleic acid extraction performed using the promega manual tna kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **promega wastewater large volume tna capture kit**

(promWW). Nucleic acid extraction performed using the promega wastewater large volume tna capture kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Proportion of total**

(prop). Proportion as a precent of total. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: 100 *Minimum*

## Parts

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

## Proportion of variant in sample

(propV). Proportion of a variant as percent of total variants. *Part Type:* units *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* float *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* 100 *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

## Proteins class

(protein). Measures and methods related to proteins. *Part Type:* classes *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* protein *Nomenclature:* protein *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* 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.

## Protocol ID

(protocolID). A unique identifier for a given protocol. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data*

## Parts

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.

## Protocol ID container

(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.

## Protocol ID object

(protocolIDObj). The object of the relationship between one protocol and another protocol or step, within a given protocol ID container. Populate this field using Protocol ID (partID = protocolID). Together with ‘protocolIDSub’ or ‘stepIDSub’ and ‘relationshipID’, the protocol relationship is defined as: [protocolIDSubject or stepIDSubject] [relationshipID] [protocolIDObject or stepIDObject]. Ex: stepIDSubject precedes protocolIDObject. Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: genMissingnessSet Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum

## *Parts*

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

### **Protocol ID subject**

(protocolIDSub). The subject of the relationship between one protocol and another protocol or step, within a given protocol ID container. Populate this field using Protocol ID (partID = protocolID). Together with ‘protocolIDObj’ or ‘stepIDObj’ and ‘relationshipID’ the row of ‘protocolRelationships’ should say: [protocolIDSubject or stepIDSubject] [relationshipID] [protocolIDObject or stepIDObject]. Ex: stepIDSubject precedes protocolIDObject. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Protocol relationships table**

(protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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.

### Synthetic ID for the protocolRelationships table

(protocolRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the protocolRelationships table. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 2.2.0.

### Protocol relationships table column order

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

## Parts

### Protocol Relationship table required headers

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

### Protocol Relationships set

(protocolRelSet). set for valid values of relationshipID in the protocolRelationships table. Use only for protocolRelationships table relationshipID. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: protocolRelSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Protocols table

(protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. pro *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: programDescr *Nomenclature*: programDescr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation*

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

### Protocols table column order

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

### Protocols table required headers

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

### Protocol steps table

(protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. ps *Part Type: tables*

## Parts

*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.

## Protocol steps table column order

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

## Protocol steps table required headers

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

### Protocol table set

(protocolTableSet). Tables holding information on the methods used for sample collection or measurement. *Part Type*: dictSets *Domain*: naDomain *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Protocol version

(protocolVersion). Specifies the version of a method set. Version of the method set. Semantic versioning is recommended. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: genMissingnessSet *Minimum Value*: 1 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### Access to prov ha

(provHA). If this is ‘no’, this data will not be available to provincial health authorities. If missing, data will be available to provincial health authorities. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: booleanSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale

## Parts

*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: depreciated. Last updated: 2.0.0.

## Provisional report

(provisional). A provisional or interim 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.

## Province-level Aggregation at Site

(provLevel). Specifies that a sewershed/site represents a sub-national state, province, or region. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Protocol steps table Shorthand

(ps). The abbreviated short name used to reference the The table for collecting metadata on individual steps in a protocol, methodological process, or assay. table *Part Type*: shortName *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.2.

## Pseudomonas

(pseudomonas). Pseudomonas *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: pseudomonasGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Pseudomonas Group

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

## *Parts*

*Reference Link:* NA *Data Type:* varchar *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.

### **Primary clarifier sludge**

(pSludge). Sludge produced by primary clarifiers *Part Type:* categories *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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Pumping station**

(pStat). Pumping station *Part Type:* categories *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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Post-grit**

(pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but prior to a primary clarifier) *Part Type:* categories *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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Practical salinity unit

(psu). practical salinity unit (PSU) *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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.

## Pretreatment description - deprecated

(ptDescDep). If preTreatment then describe the treatment that was performed. Deprecated in version 2, please do not use. Use pretreatment methodID and specify further in summary and/or notes, if necessary. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* 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:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* **deprecated**. First released: deprecated. Last updated: 2.0.0.

## Parts

### **Number of positive tests**

(ptot). Number of positive tests conducted within a day in a given region. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Public Administration**

(pubAdm). An organisation type that describes governmental organizations that manage or administer programs. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Public Authority**

(pubAuth). An organization type describing a public agency with authority over a given domain. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*:

## Parts

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

### Public health agency

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

### Access to public

(public). If this is ‘no’, this data will not be available to the public. If missing, data will be available to the public. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: booleanSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: boolean *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

### PubMLST

(pubMLST). PubMLST. Focus: Web-based platform for MLST and serotyping analyses. Applications: Neisseria, Campylobacter, Salmonella, and more. Features: Combines curated databases with user-uploaded sequences. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment*

## Parts

*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:* <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.

## Puro virus

(puro). Measure of the amount of puro virus. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* lentiGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Puro virus spike target

(puroMat). Puro Virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Purpose

(purpose). The reason the measure or sample was taken. See allowed categories: report, quality control, validation study, test *Part Type*: attributes *Domain*: naDomain *Specimen 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.

## Purpose set

(purposeSet). Purpose set for a sample or measure. *Part Type*: mmaSets *Domain*: naDomain *Specimen ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: purposeSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Poliovirus type 2

(pv2). Poliovirus type 2 *Part Type*: measurements *Domain*: bio *Specimen 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

## *Parts*

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

### **Peptone Water with Glycerol**

(pwWg). A buffer solution/medium used in environmental sampling, especially for preserving microorganisms. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **q19e omicron-variant gene target**

(q19e). q19e omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **q493r omicron-variant gene target**

(q493r). q493r omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:*

anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **q498r omicron-variant gene target**

(q498r). q498r omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **q954h omicron-variant gene target**

(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*

### **Quality assurance method**

(qaqc). Quality assurance and quality control method. Description of the quality control steps taken *Part Type*: methods *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *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*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **QC3**

(qc3). A comprehensive QC pipeline for NGS sequencing data that provides summary statistics on sequence quality and contamination. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: [https://github.com/nhoffman/seq\\_qa\\_tools](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.

### **Quality Control Method**

(qcMethod). Method for 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*: NA *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data*

## Parts

*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.

## Quality concerns

(qf1). A flag to indicate there is a quality concern, not otherwise specified.  
*Part Type:* qualityIndicators *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.

## qiagen allprep dna/rna kit

(qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## qiagen digital PCR

(qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.*

### **qiagen ez1 virus mini kit v2.0**

(qgEz1). Nucleic acid extraction performed using the qiagen ez1 virus mini kit v2.0. *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet 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.*

### **qiagen allprep powerfecal dna/rna kit**

(qgPwrFecal). Nucleic acid extraction performed using the qiagen allprep powerfecal dna/rna kit. *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet 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.*

### **qiagen allprep powerviral dna/rna kit**

(qgPwrViral). Nucleic acid extraction performed using the qiagen allprep powerviral dna/rna kit. *Part Type: categories Domain: bio Speciment ID:*

## Parts

saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **qiagen powerwater kit**

(qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **qiagen qiaamp buffers with epoch columns**

(qgQiAmp). Nucleic acid extraction performed using the qiagen qiaamp buffers with epoch columns. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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*

### **qiagen rneasy kit**

(qgRNeasy). Nucleic acid extraction performed using the qiagen rneasy kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **qiagen rneasy powermicrobiome kit**

(qgRNeasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **qiagen allprep dna/rna kit**

(qiAllprep). qiagen allprep dna/rna kit *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeUnitAggrScale *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.

### **qiagen qiaamp dsp viral rna mini kit**

(qiampDSP). qiagen qiaamp dsp viral rna mini kit *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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: 2.2.0.

### **QIAseq FX DNA Library Kit**

(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. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Quantitative Real-Time PCR**

(qpcr). Real-time PCR, also called ‘quantAggScale’ PCR *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*:

## *Parts*

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

## **qPCR instruments (quantitative PCR)**

*(qPCRinst). A quantitative PCR instrument, to detect and quantify specific  
DNA/RNA targets. Part Type: categories Domain: naDomain Speciment  
ID: naSpecimenSet Compartment Set: naCompartmentSet Group: na-  
Group Class: naClass Nomenclature: naClass Ontology Reference: NA  
Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale  
Quality Set: NA Reference Link: 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.*

## **qProfiler2**

*(qProfiler2). A QC pipeline tool for sequencing data that produces reports  
with detailed QC metrics for aligned and unaligned reads. Part Type: cat-  
egories 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://sourceforge.net/projects/qprofiler2/> Data Type: varchar Missing-  
ness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length:  
0 Maximum Length: 50 Part Status: active. First released: active. Last  
updated: 3.0.0.*

## Quality reports table Shorthand

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

## Qualitative

(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.

## Quality control

(qualityControl). A measure or sample taken for the purpose of quality control. Measures with this category are take to assess quality control. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference*

## *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.

## **Quality flag**

(qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample or measure. Types of quality flag vary on context; please see the qulaityFlagSet to be confirm. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

## **Quality indicators**

(qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts. *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* 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.

## Quality Indicator Set Header

(qualityIndSet). The quality set that corresponds to a given part. Only applicable for samples and measures. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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.

## Quality indicator sets

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## Quality report ID

(qualityReportID). A unique identifier for a given quality report. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA

## Parts

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

## Quality reports table

(qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. qr *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Quality rerpots table column order

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

## Quality report table required headers

(qualityReportsRequired). Specifies the columns required in the Quality Reports table. *Part Type:* tableSupport *Domain:* naDomain *Speciment ID:*

## 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.

## Quantitative

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

## Quarantine recommendation

(quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Parts

### R squared

(r2). R-squared value of the calibration curve. Used for storing calibration curve information, potentially also applicable for other curve types. *Part Type*: units *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### r203m delta-variant gene target

(r203m). r203m delta-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### R346T Mutation

(r346t). The FLiT/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*

## Parts

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

### Raindance digital PCR

(rainDper). Describes a PCR analysis done using Raindance's digital PCR technology. *Part Type:* categories *Domain:* bio *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.

### dPCR Rain Percentage

(rainPerc). The percentage of droplets tha fall between the major positive and negative population in digital droplet PCR. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* percentUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### Rainy

(rainy). Qualitative category for the weather measure, specifying a rainy day. *Part Type:* categories *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *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.

## **Random sampling surveillance program**

(randomSurv). A surveillance sampling strategy in which baseline is established at the beginning of a study or project by the selection of sample units via random sampling. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Random sequencing selection method**

(ranSeq). Specifies the random selection method for sequencing No primer set should be used if this is selected. *Part Type:* categories *Domain:* bio *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.

## Ratio

(ratio). Ratio (unitless) Report as a real number or fraction. i.e 10:2 ratio is reported as 5. The specifics of the ratio (the numerator and the denominator) are described in the measure. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Raw data

(raw). Raw data, without adjustment or additional treatment. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Raw wastewater

(raws). Raw wastes water sample *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.*

## Raw Sequence Data Processing Method

(rawSeqProc). The software/library/pipeline used to process the raw sequencing data. *Part Type: methods Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: sequence Nomenclature: sequence Ontology Reference: NA Category Set ID: rawSeqProcSet Unit Set: naUnitSet Aggregation Scale: qualAggScale Quality Set: 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.*

## Raw Sequence Data Processing Method Set

(rawSeqProcSet). The category set of valid input 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.*

## Raw sewage at site

(rawWW). Wastewater without any form of treatment *Part Type: categories 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: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

### **Raw sewage downstream from a site**

(rawWWdown). Downstream from a site. See partType = rawWWup. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: 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.*

### **Raw sewage upstream from a site**

(rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjuctiion with downstream sample. For example, if the site is a long-term care home, but ther is not access to the building or property cleanout. Use two sameple, one sample upstream and one sample downstream. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: 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: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

## Parts

### RaxML Software

(raxML). A lineage or clade analysis software tool, popular for rapid maximum likelihood-based phylogenetic tree building with clade assignment.  
*Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://cme.h-its.org/exelixis/web/software/raxml/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### IP2 rdrp sars-cov-2 gene target

(rdrpIP2). IP2 rdrp sars-cov-2 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: 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.

### IP4 rdrp sars-cov-2 gene target

(rdrpIP4). IP4 rdrp sars-cov-2 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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: 2.0.0.

### **Sequencing read mapping software name**

(readMapper). The name of the bioinformatics software tool used to align short DNA or RNA sequence reads (obtained from high-throughput sequencing technologies like Illumina, PacBio, or Oxford Nanopore) to a reference genome or transcriptome. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* readMapperSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

### **Sequencing read mapping software set**

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

## *Parts*

### **Date sample received**

(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.

### **Recombinant Lineage Variant**

(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.

## Recovered patients

(recov). Units for describing a population measure of patients who have recovered from a given disease. Unit for a population or disease measure to explain population-level clinical effects. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Redundans

(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.

## Refugee camp

(refCamp). A temporary, often makeshift shelter for persons displaced by war, political oppression, or for religious beliefs. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Reference link

(refLink). Link to the reference material for a part. May link to literature on a method, measure, etc. Link to standard operating procedure for a measure or part. Part reference is a reference to a technical document that describes the part in detail. The reference could be a URL, DOI, or reference to a 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.

## Regular Pathogen Surveillance

(regular). A measure or sample taken for surveillance or epidemiology. A ‘regular’ measure is the default. Missing data will be recoded to this purpose. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Regular reports table set**

(regularReportTableSet). Tables used for daily reporting of new measurements and information on sample collection. *Part Type:* dictSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Relationship between entities**

(relationshipID). Attribute for specifying the relationship between a sample subject and object. Together with ‘sampleIDSubject‘ and ‘sampleRelID‘, a row of the ‘sampleRelationships‘ should say: [sampleIDSubject] is a [sampleID] of [sampleIDObject] *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* relSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### **Measure relevance end date**

(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:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass

## Parts

*Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *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: 2.3.0.

## Measure relevance start date

(relDateStart). The start date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* 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:* datetime *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.3.0.

## Relative humidity

(relHum). The unit of relative humidity, or the air-water mixture. The ratio of the partial pressure of water vapor in the mixture to the equilibrium vapor pressure of water over a flat surface. of pure water at a given temperature. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* humid *Nomenclature:* humid *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* relHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Relative humidity unit set**

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

### **Relationship Not Reported**

(relNR). A relationship ID used in relationship tables across the ODM when two entities are related or connected in some way, but the actual nature of that relationship is not clear or reported. This is mostly used when mapping data from other data formats wherein protocol relationships (for example) do not report clear temporal relationships or order to method steps. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **General Relationship Set**

(relSet). set for valid values of relationshipID across all fields and tables. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: relSet

## Parts

*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.

## Representative grab sample

(repGrab). A single large representative grab sample. Deprecated in version 2, please do not use. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* NA *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.

## Replicate Type set

(replicateSet). The set for storing valid categorical values of replicate type. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* replicate-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.

## replicate number

(repNum). The replicate number for a Ct or Cq value - used for specifying out a protocol standard curve. Only applies and used for aggregated

standard curves, or curves that are used across multiple plates. Otherwise, these details can be captured in a measure report and specified by measure index. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standardCurve *Nomenclature*: standardCurve *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

## Primary reporting authority ID

(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.

## *Parts*

### **Secondary reporting authority ID**

(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 *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.

### **Reportable**

(reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied. *Part Type:* attributes *Domain:* naDomain *Specimen 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.

## Report date

(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.

## Reporter ID deprecated

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

## Reporter table deprecated

(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 - deprecated *Part Type:*

## *Parts*

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.

## **Report table input (wide table)**

(reportTableInput). The short name for the listed source table. *Part Type*: attributes *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: 2.2.0.

## **Report table name (wide table)**

(reportTableName). The report table that the wide name calls from. *Part Type*: attributes *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: 2.2.0.

## Replicate Type

(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? *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.

## Reservoir

(res). An artificial body of water, often contained by a dam, constructed for the purpose of water storage. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Resuspend COSCa filter collection

(resCosca). Nucleic acid extraction via resuspension of a sample collected using the COSCa ball method. See partID = cosca for additional details. *Part Type*: categories *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *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.

## **Research sector or organization**

(research). Describes organizations whose focus is on research generation.  
*Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet  
*Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA  
*Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## **Research purposes**

(researchPurp). Purpose of sampling/measure is for research. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **ResFinder Database**

(resFinderDbase). 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*

## Parts

*Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* genepi.food.dtu.dk/resfinder *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## ResFinder Tool

(resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* amrGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/genomicepidemiology/resfinder> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Residents per square kilometre

(resPerKm). Residents per square kilometre. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 0 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

## *Parts*

### **Residents per square mile**

(resPerMile). Residents per square mile. *Part Type*: units *Domain*: allDo Speciment ID: poSpecimenSet *Compartment Set*: naCompartmentSet Group: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Restaurant**

(restaurant). A commercial establishment that prepares and serves food and beverages to customers. *Part Type*: categories *Domain*: naDomain Speciment ID: naSpecimenSet *Compartment Set*: anyCompartmentSet 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.

### **Restricted data**

(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

## Parts

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

## Results tables

(results). Tables used to record samples, measures and quality reports. These tables are updated whenever a new sample is taken or a measure is reported. Quality reports are used to report quality assurance and quality control for samples and measures. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* results *Nomenclature:* results *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Resuspension method

(resuspension). Describes the method used for resuspending material. *Part Type:* methods *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* resusSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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*

### **Resuspension method set**

(resusSet). The set to describe valid categorical values for the resuspension method. *Part Type*: mmaSets *Domain*: phy *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standard-Conc *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.

### **Retained Element**

(retainedElement). The element retained after centrifugation, filtration, solid separation, etc. *Part Type*: methods *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *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.

### **Retained Element Set**

(retElSet). The set for enumerating the valid possible values of the retained element method. *Part Type*: mmaSets *Domain*: phy *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: retElSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical

## Parts

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

### Retention pond

(retPond). Retention pond *Part Type: categories 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: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

### Review of records

(rev). A review of records for determining site/polygon population. *Part Type: categories Domain: naDomain Speciment ID: poSiSpecimenSet Compartment Set: anyCompartmentSet 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.*

### Rickettsia

(rickettsia). Rickettsia *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: rickettsiaGrp Class: organism Nomenclature: organism Ontology Reference: NA Category Set ID: NA Unit Set: geneticUnitSet Aggregation Scale:*

## *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.*

## **Rickettsia Group**

(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.*

## **River, natural water body**

(river). River, natural water body *Part Type: categories 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: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

## **RNA Template**

(rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. *Part Type: categories Domain: bio Speciment ID: saSpecimenSet*

## Parts

*Compartment Set:* anyCompartmentSet *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.

## rRNA Depletion Method

(rnaDepl). Removal of background RNA for the purposes of enriching the genomic target. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## RNAlater

(rnaLater). A buffer solution/medium the stabilizes RNA and DNA in samples, effective for preserving nucleic acids in wastewater. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **Ribonuclease P (RNase P)**

(rnaseP). Ribonuclease P (RNase P) (usually measured as a human fecal indicator) *Part Type*: measurements *Domain*: bio *Speciment ID*: siSaS-SpecimenSet *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.

### **Road**

(road). A paved or unpaved pathway designed for vehicular and pedestrian travel. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Roadside**

(roadside). The area adjacent to a road, including sidewalks, shoulders, or drainage ditches. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: colGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: ENVO:01000447 *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.

### Role of contact

(role). Specifies the organizational role of a given contact. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Rotavirus

(rotavirus). Rotavirus *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rotavirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Rotavirus Group

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

## *Parts*

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.

## **Routine surveillance**

(routSurv). Standard, ongoing collection of public health data. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Rate per 100,000**

(rP100). Units for describing a population measure of a rate of case incidence per 100,000 people of a given disease. Unit for a population or disease measure to explain population-level clinical effects. *Part Type*: units *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Revolutions per minute (RPM)

(rpm). RPM stands for “Revolutions per minute.” This is how centrifuge manufacturers generally describe how fast the centrifuge is going. The rotor, regardless of its size, is revolving at that rate. *Part Type*: units *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

## Raw post-pasteurized wastewater

(rppw). Raw wastewater sample post-pasteurization *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

## Resistant strain identified

(rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness*

## *Parts*

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

### **Respiratory syncytial virus A and B combined**

(rsvAB). Human Respiratory Syncytial Virus Type A (RSV A) and Type B (RSV B). *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* [https://ontobee.org/ontology/NCIT?iri=http://purl.obolibrary.org/obo/NCIT\\_C184696](https://ontobee.org/ontology/NCIT?iri=http://purl.obolibrary.org/obo/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.

### **Respiratory syncytial virus A**

(rsvAMe). Human Respiratory Syncytial Virus Type A (RSV A). Refer to Group = ‘rsv‘ and ‘rsv‘ for measure that are apply to either RSV A or RSV B. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* rsvGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* [https://ontobee.org/ontology/NCIT?iri=http://purl.obolibrary.org/obo/NCIT\\_C184696](https://ontobee.org/ontology/NCIT?iri=http://purl.obolibrary.org/obo/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.

### **Respiratory syncytial virus B**

(rsvB). Human Respiratory Syncytial Virus Type B (RSV B). Refer to Group = ‘rsv‘ and ‘rsv‘ for measure that are apply to either RSV A or RSV B. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: rsvGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: [https://ontobee.org/ontology/NCIT?iri=http://purl.obolibrary.org/obo/NCIT\\_C184697](https://ontobee.org/ontology/NCIT?iri=http://purl.obolibrary.org/obo/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.

### **Respiratory syncytial virus (RSV) Group**

(rsvGrp). Human Respiratory Syncytial virus (RSV). Refer to Group = ‘rsvA‘ and ‘rsvB‘ for measure that are specific to RSV A or RSV B, respectively. *Part Type*: groups *Domain*: bio *Speciment ID*: poSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: rsvGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: [http://purl.obolibrary.org/obo/NCIT\\_C14267](http://purl.obolibrary.org/obo/NCIT_C14267) *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: 2.1.2.

### **Respiratory syncytial virus**

(rsvMe). Human Respiratory Syncytial virus (RSV), generic measure. Refer to Group = ‘rsvA‘ and ‘rsvB‘ for measure that are specific to RSV

## *Parts*

A or RSV B, respectively. *Part Type*: measurements *Domain*: bio *Specimen ID*: poSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: rsvGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: http://purl.obolibrary.org/obo/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.

## **RSV N-gene**

(rsvN). Human Respiratory syncytial Virus, N-gene region. *Part Type*: measurements *Domain*: bio *Specimen 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.

## **reverse transcription**

(rt). Describes the reverse transcription cycle in a PCR process. *Part Type*: categories *Domain*: bio *Specimen 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: 2.2.0.

## RT-qPCR instruments

(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.

## Rubella

(rubella). Rubella *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: rubellaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Rubella Group

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

## *Parts*

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

## **Rural**

(rural). Rural populated area type *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **s2083i omicron-variant gene target**

(s2083i). s2083i omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## **s371l omicron-variant gene target**

(s371l). s371l omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet

*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.

**s373p omicron-variant gene target**

(s373p). s373p omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

**s375f omicron-variant gene target**

(s375f). s375f omicron-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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*

### **s477n omicron-variant gene target**

(s477n). s477n omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Sample**

(sa). A measure made on a compartment or property from a sample of a substance. *Part Type*: specimens *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Salinity**

(salinity). Measurement of salinity/salt content *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: miscMeas *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*:

salinityUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

### **Salinity unit set**

(salinityUnitSet). Unit set for salinity measurements. *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*: salinityUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Salmonella**

(salmonella). Salmonella *Part Type*: measurements *Domain*: bio *Specimen 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.

### **Salmonella Group**

(salmonellaGrp). A group of measures/methods related to salmonella bacteria. Used to describe the organism information for general measures.

## Parts

*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.

## SalmonellaTypeFinder

(salTypeFin). SalmonellaTypeFinder A specialized tool for predicting Salmonella serotypes based on genomic data, similar to SeqSero. *Part Type:* categories *Domain:* bio *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:* Source: <https://bitbucket.org/genomicepidemiology/salmonellatypewriter> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Sample material

(saMaterial). Type of sample. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* colGrp *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.

### **Sample concentrate**

(samConc). Sample concentrate. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Sampling Event**

(sampleEvent). In settings where a person goes out and collects multiple samples, but more accurate location data is not recorded, this is used to group samples from that outing, or ‘sampling event’. Use for the shared sampling event as a single sample, all independent samples would be child samples of the event, with a ‘child’ relationship ID. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Sample ID**

(sampleID). Unique identifier for a sample. Suggestion:siteID-date-index. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## *Parts*

*Set:* naUnitSet *Aggregation Scale:* 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.

## **Sample ID object**

(sampleIDObject). Populated by ‘sampleID‘ - this specifies the object of a sample relationship. Use ‘sampleID‘ for this field. Together with ‘sampleIDSub‘ and ‘relationshipID‘ the row of the ‘sampleRelationships‘ should say: [sampleIDSubject] is a[relationshipID] of [sampleIDObject] *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Sample ID subject**

(sampleIDSubject). Populated by ‘sampleID‘ - this specifies the subject of a sample relationship. Use ‘sampleID‘ for this field. Together with ‘sampleIDSub‘ and ‘relationshipID‘ the row of the ‘sampleRelationships‘ should say: [sampleIDSubject] is a[relationshipID] of [sampleIDObject] *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA

## Parts

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

### Sample material set

(sampleMatSet). set for the types of material that can be found in a sample. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sampleMatSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### Sample quality set

(sampleQualitySet). Quality set for a sample. *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* 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.

### Sample relationships table

(sampleRelationships). Table for recording the relationships between samples. Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for

## Parts

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.*

## Synthetic ID for the sampleRelationships table

(sampleRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the sampleRelationships table. *Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: genMissingnessSet Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 2.2.0.*

## Sample relationships table column order

(sampleRelationshipsOrder). Specifies the order of the columns in a Sample Relationships table. *Part Type: tableSupport Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 1 Maximum Value: NA Minimum Length: NA*

## *Parts*

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

### **Sample relationships table required headers**

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

### **Sample relationships set**

(sampleRelSet). set for valid values of relationshipID in the sampleRelationships table. Use only for sampleRelationships table relationshipID. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sampleRelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Sample report table**

(samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water

## *Parts*

or liquid), air, or surface area taken from a site. Samples can be combined, split, stored and reused. The ‘Sample relationships’ (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. sas *Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: results *Nomenclature*: results *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Sample shed**

(sampleShed). A geographic area, physical space, or structure. A sample is taken from a sampleshed for a representative measurement of a substance(s). Examples: Airplane, Long-term care home, Neighbourhood, University campus, Municipality *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: colGrp *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.

## **Samples table column order**

(samplesOrder). Specifies the order of the columns in a Samples table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit*

## Parts

*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.

## Sample table required headers

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

## Collection other deprecated

(sampleTypeOther). Description for other type of method not listed in collection. depreciated. *Part Type:* methods *Domain:* naDomain *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:* 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.

## SAMtools rmdup

(samRmdup). A deduplication method that identifies and removes PCR duplicates based on alignment data. *Part Type:* categories *Domain:* naDo-

## Parts

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.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.

## SAMtools

(samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.htslib.org/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Sample volume

(samVol). The volume of a given sample. *Part Type*: measurements *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: volumeUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: 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.

## Sapovirus

(sapovirus). Sapovirus *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sapovirusGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## Sapovirus Group

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

## Sample relationships table Shorthand

(sar). The abbreviated short name used to reference the Table for recording the relationships between samples. table *Part Type*: shortName *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum*

## *Parts*

*Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.2.2.*

## **SARS-CoV-2**

(sarsCov2). A group of measures/methods related to the SARS-CoV-2 virus. SARS-CoV-2 measures have the following classes: proteins, alleles, variants, mutations, diseases. *Part Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* [http://purl.obolibrary.org/obo/NCIT\\_C169076](http://purl.obolibrary.org/obo/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.

## **Sample report table Shorthand**

(sas). The abbreviated short name used to reference the The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.2.

### Sample specimen set

(saSpecimenSet). A specimen set that inculdes only a sample specimen. *Part Type*: specimenSets *Domain*: naDomain *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Sparse coverage

(sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. If there are multiple issues to flag, use the multiple issues flag and explain the details in the notes section. *Part Type*: qualityIndicators *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.

### Secondary clarifier effluent depreciated

(sce). Effluent obtained after secondary clarifiers. Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: colGrp *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:* NA *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.

## **Standard curve frequency**

(scf). A method for specifying the frequency over which a standard curve (or ‘Master Curve’) is used. *Part Type:* methods *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: 2.0.0.

## **School**

(school). A school serving students in the kindergarten to 12th grade range *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **School closure**

(schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. *Part Type:* categories *Domain:* naDomain *Speci-*

## Parts

*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.

## **sciencell viral rna isolation kit**

(sciencellRNA). sciencell viral rna isolation kit *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeU-unitAggScale *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.

## **Sequencing script version set**

(scriptSet). The set for script versions *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* scriptSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Parts

### **Genetic sequencing script version**

(scriptVersion). Used to specify the script or script version used to extract summary information (i.e. coverage and mutation frequency statistics, etc.) from the sequencing output. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: proc-Grp *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.

### **Secondary clarifier sludge deprecated**

(scsDep). Sludge produced by secondary clarifiers. Deprecated in version 2, please do not use. Duplicate of the sampleMat categories - refer to those. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: NA *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.

### **Standard deviation**

(sd). Standard deviation. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar

## Parts

*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.

### Normalized standard deviation

(sdn). Standard deviation, normalized. *Part Type: aggregations Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: seeUnitVal Maximum Value: seeUnitVal Minimum Length: NA Maximum Length: NA Part Status: active.*  
First released: active. Last updated: 2.0.0.

### Sludge dryer

(sDryer). A facility or equipment used to reduce moisture content in wastewater sludge for easier handling and disposal. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: waterCompartmentSet 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.

### Sterile Distilled Water with Sodium Thiosulfate

(sDWwST). Sterile Distilled Water with Sodium Thiosulfate - Used to neutralize chlorine for microbiological analysis in wastewater samples. *Part Type: categories Domain: naDomain Speciment ID: saSpecimenSet*

## Parts

*Compartment Set:* anyCompartmentsSet *Group:* naGroup *Class:* naClass  
*Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* 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.

## Sets look-up table Shorthand

(se). The abbreviated short name used to reference the Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. table *Part Type:* shortName *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentsSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *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.

## Sea, natural water body

(sea). Sea, natural water body *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentsSet *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.

## **Secondary clarifier**

(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*: waterCompartmentSet *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.

## **Seconds**

(seconds). The unit of time, seconds. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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.

## **See unit (aggregation scales)**

(seeUnitAggScale). A value for aggregation scale to be used when the aggregation scale depends on that specified in the parts list entry for the unit. When you encounter this value, see the unit being used for that entry and follow that aggregation scale entry. *Part Type*: 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

## Parts

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

## See unit (data type)

(seeUnitData). The data type entry when the data type for a given entry is specified by the unit used. Only used for measures, which is where the data type entry is used to validate the entry in the value field. For these cases, however, the data type is more dependant on the unit than the measure , and so this entry directs users to consult the data type of the unit.

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

## See unit (value)

(seeUnitVal). A value for maximum or minimum value in the dictionary, use when the maximum or minimum value is determined by the unit. Used for measures when the constraints on maximum and minimmum value are specified by the unit, not the measure. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* 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.

## Secondary clarifier effluent

(sEfflu). Effluent obtained after secondary clarifiers *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: wa-terCompartmentSet *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.

## Access to self

(self). If this is ‘no’, this data will not be shown on the portal when this reporter logs in. If missing, data will be available to this reporter. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmen-tSet *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: depreciated. Last updated: 2.0.0.

## Semi-solid

(semSol). A state of matter consisting of molecules in a non-rigid structure that can retain its shape and volume but that is not resistant to such change. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSaSpecimenSet

## *Parts*

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

## **Date sample was sent**

(sentDate). Date that the sample was sent from the collection site to the lab. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* datetime *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Septic tank wastewater**

(septage). Wastewater from within a septic tank *Part Type:* categories *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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Septic tank

(septTnk). Septic tank *Part Type*: categories *Domain*: naDomain *Specimen 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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Sequence Assembly Software

(seqAss). The name of the software/toolkit/pipeline used for assembling sequences from reads. *Part Type*: methods *Domain*: bio *Specimen 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*: 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.

## sequence assembly length

(seqAssLen). The length of the genome generated by assembling reads using a scaffold or by reference-based mapping. Provide a numerical value (no need to include units). *Part Type*: measurements *Domain*: bio *Specimen 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.*

## **Sequence Assembly Software Set**

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

## **Sequence Contaminated**

(seqContam). Sequence is contaminated. *Part Type: qualityIndicators Domain: bio 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: 2.3.0.*

## **SeqKit rmdup**

(seqKitRmdup). A deduplication method that works within SeqKit for duplicate removal in FASTA/FASTQ files. *Part Type: categories Domain:*

naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/shenwei356/seqkit> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## SeqKit stats

(seqKitStats). Part of SeqKit, a QC pipeline tool for sequencing data that providing a summary of sequence metrics like length, GC content, and quality. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://bioinf.shenwei.me/seqkit/usage/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Sequencing Layout

(seqLay). The layout of genetic material used in sequencing. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: seqLaySet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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*

### **Sequencing Layout set**

(seqLaySet). The set for the layout of genetic material used in sequencing. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: seqLaySet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **SeqMan Pro (Lasergene)**

(seqManPro). Sequencing software that is for de novo sequence assembly and consensus calling. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.dnastar.com/software/lasergene/> (homepage) — happy to fetch exact link *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Sequencing QC Pipeline**

(seqQC). The quality control pipeline for sequencing or PCR data. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: seqQCSets *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *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: 3.0.0.

### Sequencing QC Pipeline Set

(seqQCSet). The category set of valid innput values for the software/library/pipeline used to do quality checks on sequencing or PCR data. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqQCSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

### Sequencing quality set

(seqQualitySet). Quality set for sequencing measures *Part Type:* qualityIndSets *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* 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.

### Sequencing selection method

(seqSel). The primer sequence selection method used in sequencing. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment*

## Parts

*Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* 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.

## Sequencing selection method set

(seqSelSet). The set for the selection method used in sequencing *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seqSelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## SeqSero2

(seqSero2). SeqSero2. Specifically designed for Salmonella serotyping using raw sequence reads, assemblies, or even complete genomes. Provides results based on antigenic formulas or serotype names. *Part Type:* categories *Domain:* bio *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:* <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:*

## *Parts*

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

### **Sequencing Strategy**

(seqStrat). The sequencing strategy used for an analysis. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: seqStratSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

### **Sequencing Strategy set**

(seqStratSet). The set for the sequencing strategy used for an analysis *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: seqStratSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **seqtk**

(seqtk). A lightweight sequencing data toolkit for FASTQ and FASTA manipulation, including trimming and subsampling. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*:

## Parts

software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/lh3/seqtk> (homepage of tool) *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## SeqTyping

(seqTyping). SeqTyping. Focus: Simultaneous MLST and serotyping for Escherichia coli and Salmonella. Applications: Integrated with bacterial genome typing databases. Features: Compatible with short-read sequencing data. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Genetic sequences class

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

### **serial dilution**

(serDil). Describes a serial dilution process for standard curve generation for PCR. *Part Type*: categories *Domain*: bio *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: 2.2.0.

### **Serial dilution**

(serialDilution). The serial dilution method for assessing inhibition. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Serotyping Method**

(seroMeth). The method used to determine the serovar. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: sequence *Nomenclature*: sequence *Ontology Reference*: NA *Category Set ID*: seroMethSet *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

## **Serotyping Method Set**

(seroMethSet). The set of categorical inputs for populating the the serotyping method field. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* seroMethSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **SerotypeFinder**

(serotypeFin). SerotypeFinder. A web-based tool that predicts serotypes for Escherichia coli and other bacteria by detecting genes encoding O-antigens and H-antigens. Developed by the Center for Genomic Epidemiology. *Part Type:* categories *Domain:* bio *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:* Web tool: <https://cge.cbs.dtu.dk/services/SerotypeFinder/> CLI: [https://github.com/Papos92/ecoli\\_serotyper](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.

## Serological Variant (Serovar)

(serovar). The serovar of the organism. Only include this information if it has been determined by traditional serological methods or a validated in silico prediction tool e.g. SISTR. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: miscMeas *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

## Sewer Sediments Deprecated

(seseDep). Sediments obtained in sewer. *Part Type*: categories *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*: NA *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

## Composite Set ID

(setCompID). A composite ID generated by concatenating the ‘setID’ and ‘partID’ of a given row in the sets table. This allows for a unique primary key and robust relational database structure. *Part Type*: attributes *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: 2.2.2.

## Set ID

(setID). The unique identifier of a value set. A set is a group of units, attributes, categories, specimens, or compartments that can be used for a measure, method or attribute. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Sets look-up table

(sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. *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.

### Sets table column order

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

### Sets table required headers

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

### Settled solids

(settsol). Amount of settled solids from a wastewater sample. May be a volume or a weight, see the unitID for a given measure row for details on a given sample. *Part Type*: measurements *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: physical *Nomenclature*: physical *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: volumeUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

## **Set type**

(setType). The type of set. i.e. quality set, aggregation set, unit set *Part Type:* partSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

## **Severity indicator**

(severity). An indicator of the severity or seriousness of a quality flag. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sevSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Severity set**

(sevSet). A set for severity indicators. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* sevSet *Unit Set:* naUnitSet *Aggregation*

## Parts

*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.

## Sewage equivalent

(sewEq). Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## Sewer network file link deprecated

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

## Parts

### **Sewage travel time**

(sewTrTi). A measure of sewage travel time, often approximate, from sewage source to the sampling site. *Part Type*: measurements *Domain*: phy Speciment ID: siSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: siteFeat *Class*: physical *Nomenclature*: physical *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: timeUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Shaker agitation speed**

(shaker). The speed/agitation 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.

### **Shasta**

(shasta). A sequencing software that is a fast assembler optimized for nanopore long-read data. *Part Type*: categories *Domain*: naDomain Speciment ID: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://paoloshasta.github.io/shasta/>

## Parts

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

## Sampleshed set

(shedSet). The set for all valid values of sampleshed. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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.

## Shigella

(shigella). Shigella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* shigellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Shigella Group

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

## *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.

## **Ship**

(ship). A cruise ship or other ship. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **Shipped on ice**

(shipOnIce). Was the sample kept cool while being shipped to the lab *Part Type*: methods *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: booleanSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

## ShortBRED Software

(shortBRED). Software tool that screens for known AMR genes in shotgun metagenomic sequencing data. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://huttenhower.sph.harvard.edu/shortbred/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Short names

(shortName). Shortened names for tables and other important parts for use in wide names. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Read Lengths Shorter Than Expected

(shortRead). Read lengths are shorter than expected. *Part Type*: qualityIndicators *Domain*: bio *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*:

## *Parts*

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

## **Shorthand or Short Name Set Type**

(shortSets). Sets used to group together short names for tables or part types in ODM. *Part Type*: partType *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.

## **Short Name Set**

(shrtNameSet). The abbreviated short name used to reference the The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (indivduals). *Part Type*: shortSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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.

## **Sites table Shorthand**

(si). The abbreviated short name used to reference the The table that contains information about a site; the location where an environmental

## Parts

sample was taken. 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: 2.2.2.

## Sickle

(sickle). A sequencing data processing application that is a quality-based trimming tool for Illumina data with single-end and paired-end support. *Part Type*: categories *Domain*: naDomain *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://github.com/najoshi/sickle> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Single

(sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. *Part Type*: aggregations *Domain*: naDomain *Specimen 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

## *Parts*

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

### **Single Layout**

(sinLay). Specifies the single layout for a sequencing method *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* na-Class *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Singleplex, probe-based, one-step RT-qPCR**

(sinProbeOne). Describes a PCR method that is singleplex, probe-based, and one-step RT-qPCR. *Part Type:* categories *Domain:* 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:* 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.

### **Site or sample specimen set**

(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:*

## Parts

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.

## Site specimen set

(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.

## Salmonella In Silico Typing Resource (SISTR)

(sist). Salmonella In Silico Typing Resource (SISTR). Used for in silico serotyping of *Salmonella enterica* based on whole-genome sequencing. Combines genomic data with the traditional White-Kauffmann-Le Minor serotyping scheme. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: na-Group *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](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.

*Parts*

## **Site**

(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.

## **Site ID default**

(siteDef). Used as default when a new sample is created by this reporter. See ID in Site table. Deprecated in version 2, please do not use. Just populate standard SiteID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: deprecated. Last updated: 2.0.0.

## **Site features group**

(siteFeat). A group of environmental measures/methods and those pertaining to the features of a site. *Part Type*: groups *Domain*: allDo *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: siteFeat *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category*

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

## Site ID

(siteID). Unique identifier for the location where a sample was taken. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Level of Aggregation of a Sampling Site

(siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type of region is represented by the base sewershed. This can be used to pool together or average results across similar sewersheds, and avoid trying to average different scales of sewershed together without a correction for size. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* siteLevelSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

*Parts*

### **Site Level Category Set**

(siteLevelSet). The category set containing all valid entries for the siteLevel field. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: siteLevelSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Site measure ID**

(siteMeasureID). Unique identifier for wide table only. Use when all measures are performed on a single sample. Depreciate in version 2. siteMeasures *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: depreciated. First released: depreciated. Last updated: 2.0.0.

### **Sites table**

(sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an 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*:

## Parts

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.

## Sites table column order

(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.

## Sites table required headers

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

*Parts*

## **Site Type**

(siteType). Type of site or institution where sample was taken. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: colGrp *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.

## **Site set**

(siteTypeSet). set for the type of sampling site. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: siteTypeSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Skewer**

(skewer). A sequencing data processing application that is a fast tool for adapter trimming and quality trimming in Illumina data. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: https://github.com/relipmoc/skewer *Data Type*: varchar *Missingness Set*:

## 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.

### Skimmed milk flocculation

(skimMilkFloc). Skimmed milk flocculation *Part Type*: categories *Domain*: che *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### Slow-flowing

(slFlow). A quality of a body of water wherein there is a slow flow. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSaSpecimenSet *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Sample Limit of Detection (LOD)

(slod). The minimum level of a target within a sample that would be consistently detectable considering all sample processing steps, from sample concentration leading up to and including amplification and quantification

## *Parts*

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.

## **slope**

(slope). Slope value of the calibration curve. Used for storing calibration curve information, potentially also applicable for other curve types. *Part Type*: units *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Wastewater Sludge - non-specified**

(sludgeNS). Sample material is wastewater sludge - whether primary, secondary or other is unspecified. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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

## 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.*

### Slurry

(slur). An quality in which the fluid like material is more viscous due to the suspension of insoluble solid particles. *Part Type: categories Domain: naDomain Speciment ID: siSaSpecimenSet 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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

### Siemens per meter

(sm). Siemens per meter (S/m) *Part Type: units Domain: phy Speciment ID: siSaSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: quantAggScale Quality Set: NA Reference Link: NA Data Type: integer Missingness Set: NA Minimum Value: 0 Maximum Value: NA Minimum Length: NA Maximum Length: NA Part Status: active. First released: active. Last updated: 3.0.0.*

### SMALT

(smalt). SMALT. A highly parallelized mapper. High-speed aligner for genomic DNA reads. Best for: Applications requiring flexibility with non-standard parameters. *Part Type: categories Domain: bio Speciment ID:*

## Parts

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

## **SMARTer ThruPLEX Plasma-seq Kit**

(smarterThruPLEX). SMARTer ThruPLEX Plasma-seq Kit by Takara Bio. A library prep kit optimized for low-input DNA, including cell-free DNA for liquid biopsy studies. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Skim Milk–Glycerol Medium**

(smgm). A buffer solution/medium that protects bacteria in environmental samples, preventing freeze-thaw damage. *Part Type*: categories *Domain*: naDomain *Speciment ID*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Smoothing Calculation Type**

(smoothing). A technique used to reduce short-term fluctuations in data to better reveal underlying trends or patterns, such as using moving averages or splines. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Snap**

(snap). Snap. A highly parallelized mapper. Ultrafast, designed for genomic and RNA-seq applications. Best for: Large-scale sequencing projects. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/amplab/snap> (alignment tool) *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **SNAPP Software**

(snapp). A lineage or clade analysis software tool in BEAST for species delimitation and clade analysis in population genomics. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*:

## *Parts*

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.

## **Sewer network file link depreciated 2**

(snfl). Link to a file that has any detailed information about the sewer network associated with the site (any format). Depreciate in version 2. This attribute has been changed to referenceLink. Use po\_referenceLink to specify polygon link to sewer network file. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

## **Snowy**

(snowy). Qualitative category for the weather measure, specifying a snowy day. *Part Type*: categories *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Soap2

(soap2). Soap2. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <http://soap.genomics.org.cn/soap2.html> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Soap3

(soap3). Soap3. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: Reference: <http://soap.genomics.org.cn> (includes SOAP3 info) *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## SOAPdenovo

(soapDenovo). A sequencing software that is an assembler for short-read data, suited to large and complex genomes. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology*

## *Parts*

*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.

## **Social distancing measures**

(socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Software Class**

(software). Measures and methods related to software. *Part Type:* classes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Solid fraction (general)**

(sol). Solid fraction of a sample. *Part Type*: categories *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.

### **Solid Fraction (Dry)**

(solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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: 2.3.0.

### **Solids/Pellet retained**

(solid). The solids or pellet is retained after solid separation/centrifugation. *Part Type*: categories *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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

## *Parts*

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

## **Solid**

(solidMat). The state in which a substance has no tendency to flow under moderate stress; resists forces (such as compression) that tend to deform it; and retains a definite size and shape. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSaSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Solid seperation**

(solidSep). Process used to separate solid and liquid phases of the sample. Solid seperation is used either prior to or in the absence of the concentration method specified in ‘methodConc’. *Part Type:* methods *Domain:* allDo *Speciment ID:* saSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* solidSeparationSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

### Solid separation set

(solidSeparationSet). set for the separation of solids. *Part Type*: mmaSets *Domain*: phy *Speciment ID*: naSpecimenSet *Compartment Set*: any-CompartmentSet *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.

### Solid fraction (Wet)

(solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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: 2.3.0.

### SortMeRNA

(sortMeRNA). A sequencing data processing application that is used for ribosomal RNA filtering in metatranscriptomic data. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/sortmerna/sortmerna> *Data Type*: varchar *Missingness*

## *Parts*

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

## **Wide name source**

(source). The database or table sourced for the wide name. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* 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: 2.2.0.

## **Source Code**

(sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps. It is possible to record the full code as text, or to record it as a URL to where code is stored. Likely a different URL than the refLink field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Source Protocol ID**

(sourceProtocol). A protocol that served as a basis for another protocol. This may be due to version changes, or a referencing a protocol that was later adapted. Populate with protocolID. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Protocol step source ID**

(sourceStep). Specifies the protocol step which serves as a basis for a given protocol step. Populate with a protocol step ID (stepID). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Sovereign status of a country**

(sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory. Preprogrammed into dictionary tables, not editable by users. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Parts

*Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* 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.

## SPAdes

(spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://cab.spbu.ru/software/spades/> (via SPbU) — can confirm official mirror *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Specific humidity

(specHum). Measure for specific humidity, the unit is the ratio of the mass of water vapour and the mass of total air. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* siteFeat *Class:* humid *Nomenclature:* humid *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* specHumidUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Specific humidity unit set

(specHumidUnitSet). Unit set for specific humidity. *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*: 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.

### Specifies

(specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Use only for protocolRelationships table relationshipID. *Part Type*: categories  
*Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: na-  
*CompartmentSet Group*: naGroup *Class*: naClass *Nomenclature*: naClass  
*Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Specimen

(specimen). The substance or thing upon which the observation was made. Specimens include: site, sample, person and population. *Part Type*: attributes  
*Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass  
*Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data*

## *Parts*

*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.

## **Specimen input (wide table)**

(specimenInput). The partID for the specimen being used in a wide name. *Part Type:* attributes *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: 2.2.0.

## **Specimen name (wide table)**

(specimenName). The specimen referenced for the wide name. *Part Type:* attributes *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: 2.2.0.

## **Specimens**

(specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See partID = specimenID. *Part Type:* partType *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: 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.*

## Specimen Set Header

(specimenSet). An identification of a set of specimens that can be applied for a measure or method. *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: 2.2.2.*

## Specimen sets

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen. *Part Type: partType 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.*

## Parts

### Spectrophotometers or fluorometers

(spectroFluoro). Spetrometer and fluorometer instruments; may be used to assess concentration and purity (e.g., NanoDrop<sup>TM</sup>, Qubit<sup>TM</sup>). *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: 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.

### Speed class

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

### Speed Unit Set

(speedUnitSet). Unit set for reporting speeds (centrifugation speed, etc.) *Part Type*: unitSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: speedUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum*

## Parts

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

### Sucrose Phosphate Glutamate (SPG) Buffer

(spg). A buffer solution/medium that stabilizes viruses, including in wastewater samples, by preventing RNA degradation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartments *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* 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.

### Spike matrix and recovery

(spike). The spike matrix and recovery method for assessing inhibition. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartments *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.

### Spike Concentration

(spikeConc). Concentration of the recovery efficiency target in a spike matrix and recovery assay. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartments *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA

## Parts

*Category Set ID:* NA *Unit Set:* geneticUnitSet *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.

## SARS-CoV-2 Spike gene (orf2)

(spikeGene). SARS-CoV-2 Spike gene (orf2) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* GENEPIO:0100154 *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

## Spike material

(spikeMat). Material into which the recovery efficiency control target is spiked. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* spikeMatSet *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

### Spike material set

(spikeMatSet). set for spikeMat (aterial into which the recovery efficiency control target is spiked). *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: spikeMatSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Recovery efficiency spike target

(spikeTarget). Method specifying the recovery efficiency control target. This matches on to the the spike material method ID. Should typically be indexed as a step proceeding the spikeMaterial methodID step. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: spikeTargetSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

### Recovery efficiency spike target set

(spikeTargetSet). The set capturing containing all of the valid categories for the recovery efficiency control (or spike) target. *Part Type*: mmaSets *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*:

## *Parts*

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.

## **Sample spilled**

(spill). Sample contents spilled from container. *Part Type*: qualityIndicators *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.

## **Spring**

(spr). A surface landform which provides an egress for groundwater or steam to flow out of the ground. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Sequence Read Archive (SRA)**

(sra). Sequence Read Archive (SRA). *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.ncbi.nlm.nih.gov/sra/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **SRST2 Software**

(srst2). Software tool for analyzing antimicrobial resistance using short read sequences. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/katholt/srst2> or <https://katholt.github.io/srst2/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **SSAKE**

(ssake). A sequencing software that is a simple de novo assembler for highly overlapping short reads. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale

## Parts

*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.

## Streptococcus Serotyping Tool (SSI)

(SSI). Streptococcus Serotyping Tool (SSI) A web-based platform for serotyping Streptococcus pneumoniae based on capsular polysaccharide synthesis loci. *Part Type:* categories *Domain:* bio *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:* 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.

## Secondary clarifier sludge

(sSludge). Sludge produced by secondary clarifiers *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* wa-terCompartmentSet *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.

## **Social services shelter**

(sss). Other type of social services shelter *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **Stabilization pond**

(stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment to reduce the organic content and remove pathogens from wastewater. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Stagnant**

(stag). A quality of a body of water wherein it has no current or flow. *Part Type*: categories *Domain*: naDomain *Speciment ID*: siSaSpecimenSet *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

## Parts

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

## Statistical Analysis of Metagenomic Profiles (STAMP) Software

(stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <http://kiwi.cs.dal.ca/Software/STAMP> or <https://beikolab.cs.dal.ca/software/STAMP> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Standard for Data Adjustment

(standard). A field where one can categorically record the standard to which something is being standardized (ie. PMMoV, Crassphage, Flow, etc.) or smoothed (ie. bayesian smoothing, central average smoothing, 7-days, time, etc.). *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* allStandardSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Standard concentrations class**

(standardConc). Measures and methods relating to standard concentrations. *Part Type*: classes *Domain*: phy *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.

### **Standard curve class**

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

### **Standardization Calculation Type**

(standardization). A method used to scale data to a common range or distribution, often to enable fair comparisons across different variables, time periods, or locations. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale

## Parts

*Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

## Staphylococcus Group

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

## STAR (Spliced Transcripts Alignment to a Reference)

(star). STAR (Spliced Transcripts Alignment to a Reference). A general-purpose read mapper. Fast aligner designed for RNA-seq, supports spliced alignment. Best for: Transcriptome data analysis. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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/alex-dobin/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.

## StarAMR Software

(starAMR). Software tool that is used to detect AMR genes in genome assemblies. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: amrGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://www.rcac.purdue.edu/software/staramr> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Departments, states, or provinces

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

## State, Province, or Region

(stateProvReg). The state, province, or region where a site or organization is located; part of the address. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*:

## *Parts*

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

## **Status**

(status). Whether the part is still active and can be used in the most current ODM version. Values are ‘active’ or ‘inactive’. The status of the part or list. ‘active’ means the part is used in the dictionary version. ‘inactive’ means the part has been retired and not longer used in the version. *Part Type*: partSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: statusSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Status set**

(statusSet). A set for partID = Status to indicate whether a part is in current use or not. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: statusSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Standard sample

(std). Denotes a standard sample replicate. *Part Type*: categories *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Standard concentration unit set

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

## Standard Curve Calculation Method

(stdCurveMet). Describes the specific approach used for calculating a standard curve. *Part Type*: methods *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: measGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: stdCurveSet *Unit Set*: unitlessUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum*

## Parts

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

## Standard Curve Calculation Set

(stdCurveSet). The set capturing containing all of the valid methods for the PCR standard curve calculations. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* standardCurve *Nomenclature:* standardCurve *Ontology Reference:* NA *Category Set ID:* stdCurveSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## Shiga-toxin-producing Escherichia coli (STEC)

(stec). Shiga-toxin-producing Escherichia 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.

## Storage temp

(sTemp). Temperature that the sample is stored at in Celsius. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment*

## Parts

*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.

## Protocol Step ID

(stepID). The unique identifier for a specific protocol step. Protocol Steps are the component parts of a larger protocols, the latter being linked to specific measure reports. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Step ID Object

(stepIDObj). The object of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Populate this field using Protocol Step ID (partID = stepID). Together with ‘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*

## *Parts*

*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.

## **Step ID Subject**

(stepIDSub). The subject of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Populate this field using Protocol ID (partID = stepID). Together with ‘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.

## **Method step parent ID**

(stepProvenanceID). A method step that served as a basis for another method step. This may be due to version changes, or a referencing a method set that was later adapted. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar

## Parts

*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.

## Protocol step version

(stepVer). Specifies the version of a given protocol step. Version of the method step. Semantic versioning is recommended. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Standard Error

(stEr). The standard error of a series of measurements. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.2.0.

## Stercobilin

(stercobilin). Stercobilin is a tetrapyrrolic bile pigment and is one end-product of heme catabolism. It is the chemical responsible for the brown color of human feces and was originally isolated from feces in 1932. *Part*

## Parts

*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.

## Sample Storage Medium

(stoMed). The medium used to store a sample before final analysis. *Part Type:* methods *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* sequence *Nomenclature:* sequence *Ontology Reference:* NA *Category Set ID:* stoMedSet *Unit Set:* naUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## Sample Storage Medium Set

(stoMedSet). The set of valid categorical inputs for the stoMed field. *Part Type:* mmaSets *Domain:* bio *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* stoMedSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Stormy Weather

(stormy). Stormy weather *Part Type*: categories *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Sewer network file blob

(storTempDef). A file blob that has any detailed information about the sewer network associated with the site (any format). Deprecated in version 2, please do not use. Refer to WKT and EPSG instead. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: blob *Missingness Set*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 65535 *Part Status*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

## Storage time

(stoTim). Length of time that a sample was in storage. *Part Type*: measurements *Domain*: allDo *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: timeClass *Nomenclature*: timeClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: timeUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: float *Missingness Set*: genMissingnessSet *Minimum*

## Parts

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

## Stream

(str). A watercourse which is linear and flows across the solid portion of a planetary surface. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Strain ID

(strainID). The strain identifier for a given organism. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* miscMeas *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* qualAggScale *Quality Set:* 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.

## StrainPhlAn Software

(strainPhlAb). A lineage or clade analysis software tool within MetaPhlAn for strain-level lineage analysis from metagenomic data. *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://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.

## **Streptococcus Group**

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

## **Streptococcus pneumoniae**

(strepPneu). Streptococcus pneumoniae *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: strepGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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

### Sodium Thiosulfate Solution

(sts). A buffer solution/medium that neutralizes residual chlorine in wastewater samples, ensuring microbial viability. *Part Type*: categories *Domain*: naDomain *Speciment ID*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Summary worksheet Shorthand

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

### Subread

(subread). Subread. A general-purpose read mapper. Includes the subread-align algorithm for mapping DNA and RNA reads. Best for: High-throughput data with a balance of speed and accuracy. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*:

## Parts

anyCompartmentSet *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.

## Subsample (General)

(subSamp). A general replicate type for a subsample not otherwise defined. Use when additional details about the replicate are not available. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Suburban

(suburban). Suburban populated area type *Part Type*: categories *Domain*: naDomain *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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*

### **Sub-variant or lineage**

(subVar). A unit used to report a specific genetic lineage, or to specify that a reported variant is a sub-variant of another. Combine in a measure report if necessary. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: miscMeas *Class*: variant *Nomenclature*: variant *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Sucralose**

(suc). Sucralose (usually measured as a human fecal chemical indicator) *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: stdConcentrationUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Rolling sum of previous 14 days**

(sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: poSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology*

## Parts

*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.

## Summary

(summ). Short description of the assay and how it is different from the other assay methods. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 1000 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Summary worksheet

(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.

*Parts*

## **Sunny**

(sunny). Qualitative category for the weather measure, specifying a clear and sunny day. *Part Type*: categories *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **SureSelect XT HS2 DNA Library Preparation Kit**

(sureSelectXThs2). SureSelect XT HS2 DNA Library Preparation Kit by Agilent. A high-sensitivity library prep kit with target capture capabilities. *Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Surface compartment**

(surf). A measure or observation made from a substance on a surface. *Part Type*: compartments *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: surfaceCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum*

## Parts

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

### Other surface

(surface). Surface other than floor or desk. See also categories for floor and desk. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* surfaceCompartmentSet *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.

### Surface compartment set

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

### Surface and water compartment set

(surfaceWaterCompartmentSet). A compartment set for measures and methods in the surface or water compartments. *Part Type:* compartmentSets *Domain:* allDo *Speciment ID:* anySpecimenSet *Compartment Set:*

## *Parts*

*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.

## **Surface swab**

(surfSw). Surface swab. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* surfaceCompartmentSet *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.

## **Surveillance alert**

(survAlert). A public health action type wherein authorities have made a decision about surveillance and communicated the alert. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Surveillance Alert Value Set**

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

## **Surveillance Level**

(survLevel). The scale or level of surveillance being done at a site. Ie. Is it institutional, is it only for a single building, or is it for a whol municipality. Mostly for use when a polygon is not reported. But situations of community surveillance, ideally a polygon should also be supplied. *Part Type*: measurements *Domain*: allDo *Speciment ID*: poSpecimenSet *Compartment Set*: naCompartmentSet *Group*: miscMeas *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: survLevelSet *Unit Set*: naUnitSet *Aggregation Scale*: qualAggScale *Quality Set*: 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.

## **Surveillance Level Set**

(survLevelSet). The list of valid categories for the survLevel measure. *Part Type*: mmaSets *Domain*: allDo *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: popGrp *Class*: popClass *Nomenclature*:

## *Parts*

*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.*

## **Sewage truck**

(swgTrck). Sewage truck *Part Type: categories Domain: naDomain Specimen 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: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.0.0.*

## **Swift 2S Turbo DNA Library Kit**

(swift2STurbo). Swift 2S Turbo DNA Library Kit by Swift Biosciences. A fast library prep kit workflow with robust performance for low-input DNA. *Part Type: categories Domain: bio Specimen 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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## Sewer sediment

(swrSed). Sediments obtained in sewer *Part Type*: categories *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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Sewer catchment area

(swrSet). Sewer catchment area. *Part Type*: categories *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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Synthetic sample

(synthetic). A synthetic or artificially generated sample. Synthetic samples are artificially created by mixing known quantities of target substances or organisms with clean water, often in a laboratory setting. These samples are used as controls, benchmarks, or calibration standards during the analysis process to ensure accurate and reliable results. For instance, a synthetic sample containing a known concentration of a specific pollutant might be used to calibrate analytical equipment or to test the efficiency of a new detection method. *Part Type*: categories *Domain*: naDomain *Speciment ID*:

## *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.

## **t19r delta-variant gene target**

(t19r). t19r delta-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **t3646a delta-variant gene target**

(t3646a). t3646a delta-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **t547k omicron-variant gene target**

(t547k). t547k omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **t9i omicron-variant gene target**

(t9i). t9i omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **Tables**

(tables). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. An example of a table is ‘site’ a collection of attributes such as site name and address to describe where environment samples are taken. PHES-ODM has report tables, but users can create their own tables as well. *Part Type*: partType *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:* 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.

## **Table column set**

(tableSet). The set for valid inputs in table columns. These categories are used in the parts list for columns named after tables to indicate the position and function of a given part in the entity relationship diagram of the data model. *Part Type:* mmaSets *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* tableSet *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* categorical *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Table Support**

(tableSupport). Parts designed to support the metadata definition of tables in the parts table. *Part Type:* partType *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

### **TaqPath N sars-cov-2 gene target**

(taqpatN). TaqPath N sars-cov-2 mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **TaqPath S sars-cov-2 gene target**

(taqpatS). TaqPath N sars-cov-2 mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Targeted surveillance program**

(targetSurv). A surveillance sampling strategy in which an aspired outcome is explicitly stated. *Part Type*: categories *Domain*: allDo *Speciment ID*: poSiSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Targetted surveillance initiated**

(targSurv). Monitoring focused on a specific population, location, or risk factor. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Taxonum Software**

(taxonum). Taxonum - 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.

## **Total Dissolved Solids (TDS)**

(tds). Total dissolved solids *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet

## Parts

*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.

## Technical replicate

(techRep). A sample that comes from the same biological or environmental source (e.g., the same extracted DNA, the same RNA aliquot, or the same water sample). Helps detect inconsistencies due to pipetting errors, instrument fluctuations, or reagent inconsistencies, rather than biological variation. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Sample temperature

(temp). Temperature of the sample measured in degrees Celcius *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* waterQualityGrp *Class:* temperature *Nomenclature:* temperature *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.*

### **Temperature class**

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

### **Temperature unit set**

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

### **Template Sheet Set**

(templateSheetSet). Worksheets in the full generic ODM surveillance template (all tables). *Part Type: dictSets Domain: naDomain Speciment ID: saSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality*

## 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.*

### Template Set

(tempSet). The organizing set for templates. *Part Type: mmaSets Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: anyCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: tempSet Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: categorical Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.2.0.*

### Nucelic Acid Template Type

(tempType). Specifies whether a PCR or sequencing used RNA or DNA as the template for the reaction. *Part Type: methods Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: standardConc Nomenclature: standardConc Ontology Reference: NA Category Set ID: tempSet Unit Set: naUnitSet Aggregation Scale: qualAggScale Quality Set: 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.*

### Nucleic acid template volume

(tempVol). The volume of DNA or RNA template used for PCR. *Part Type: measurements Domain: bio Speciment ID: saSpecimenSet Compartment*

## Parts

*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.*

## Airport terminal

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

## Test date

(tesDate). Date that the covid-19 test was performed. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: NA 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.*

### **Number of tests performed**

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

### **Protocol testing**

(testing). A measure or sample taken to test a new method. These measures are typically used for internal lab uses and not reported to external partners. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Tetracycline Anti-microbial resistance Group**

(tetAMRGrp). The group for measures and methods pertaining to tetracycline-related anti-microbial resistance. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: tetAMRGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: genMissingnessSet *Minimum Value*: NA

## Parts

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

### **TetW Tetracycline-resistance gene target**

(tetW). The tetW tetracycline anti-microbial resistance gene target. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tetAMRGrp *Class:* allele *Nomenclature:* allele *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

### **Thermal cyclers**

(thermCyc). A thermal cycler instrument, used to perform temperature-controlled reactions for PCR. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **thermo magmax microbiome ultra nucleic acid isolation kit**

(thermMag). Nucleic acid extraction performed using the thermo magmax microbiome ultra nucleic acid isolation kit. *Part Type:* categories *Domain:*

## Parts

bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## **thermo magmax viral/pathogen nucleic acid isolation kit**

(thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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: 2.2.0.

## **Threat designation**

(threatDes). A public health action type wherein a threat level is determined and communicated by authorities. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: threatDesSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: 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*

### **Threat designation Value Set**

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

### **Public health threat targeted by action**

(threatTarget). The pathogen or variant for which the designation or action is being taken. Populated by a ‘measurement’ part type. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: 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.

### **ThruPLEX DNA-seq Kit**

(thruPLEX). ThruPLEX DNA-seq Kit by Takara Bio. A low-input library prep kit with fast, three-step protocol. *Part Type*: categories *Domain*: bio *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

## 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.

### Transport hub - General

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

### Time class

(timeClass). Measures and methods relating to time. *Part Type:* classes *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* timeClass *Nomenclature:* timeClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* timeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* 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.

### Time proportional sample

(timePr). A time proportional composite sample generally collected by an autosampler. Use collectionPeriod to describe how many hours the sample was taken. *Part Type:* categories *Domain:* naDomain *Speciment ID:*

## *Parts*

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

## **Time standardized**

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

## **Time unit set**

(timeUnitSet). The unit set for measures of time. *Part Type*: unitSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: any-CompartmentSet *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.

## Total Kjeldahl Nitrogen

(tkn). A measure of Total Kjeldahl Nitrogen; ie. the sum of nitrogen bound in organic substances, nitrogen in ammonia (NH<sub>3</sub>-N) and in ammonium (NH<sub>4</sub><sup>+</sup>-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.

## Country code top-level domain

(tld). The internet top-level domain generally used or reserved for a country, sovereign state, or dependent territory identified with a country code. Preprogrammed into dictionary tables, not editable by users. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 3 *Maximum Length*: 3 *Part Status*: active. First released: active. Last updated: 2.1.0.

## Total Nitrogen

(tn). Total nitrogen concentration, as N. *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: waterQualityGrp *Class*: standardConc *Nomenclature*:

## Parts

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

## TopHat

(tophat). TopHat. A general-purpose read mapper. An older RNA-seq aligner, splicing-aware. Replaced by HISAT2 in most workflows. Best for: Historical RNA-seq studies. *Part Type*: categories *Domain*: bio *Specimen ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.

## Total amount or count - the sum

(total). The total number or final count of cases, or other defined metric. Aggregation for a population or disease measure to explain population-level clinical effects. *Part Type*: aggregations *Domain*: naDomain *Speciment ID*: poSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

### Time Proportional 24hr sample

(tp24s). A time proportional 24-hour composite sample generally collected by an autosampler. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: NA *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.

### Treponema pallidum

(tPallidum). Treponema pallidum *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: treponemaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### Translation look-up table Shorthand

(tr). The abbreviated short name used to reference the Look up table for translations of the description, label, and instruction for all parts. table *Part Type*: shortName *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference*

## 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: 2.2.2.

## Traditional Serotyping methods

(tradSero). Traditional Serotyping methods used for serotyping. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Train

(train). A series of railroad cars moved as a unit by a locomotive or by integral motors. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## Synthetic ID for the translations table

(translationID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the translations table. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet

## 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.

## Translation look-up table

(translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. tr *Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Translation table column order

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

## Parts

### Translation table required headers

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

### Transportation vehicle - general

(transp). A vehicle, i.e. a mobile machine, transporting people or cargo, of a type not otherwise specified. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### Passive (trap) sampling

(trap). A composite sampler that passively collects a sample without use of electricity or a battery. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 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.*

### **Travel ban**

(travBa). A restriction prohibiting travel to or from specific locations. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

### **Travel hub surveillance - general**

(travelSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored. *Part Type: categories Domain: allDo Speciment ID: poSiSpecimenSet 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: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

### **Travel warning**

(travWa). A notice advising against travel to certain areas due to health risks. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID:*

## *Parts*

*NA Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA  
*Reference Link:* 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.

## **Treated**

(treat). A quality which denotes an altered state of an item resulting from purposeful interventions or processes. *Part Type:* categories *Domain:* naDomain *Speciment ID:* siSaSpecimenSet *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Treatment ID**

(treatmentID). A unique identifier for a single calculation/data treatment, a single data treatment identifier. Can be grouped together into a pipeline, which are then linked to a measure. This is done by having all related treatments share the same pipelineID, and specifying the order of the treatments in the pipeline using the order field. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **TreeTime Software**

(treeTime). A lineage or clade analysis software tool for phylodynamic analysis, often for molecular clock dating and clade assignment. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: [https://evol.bio.lmu.de/\\_statgen/software/treetime/](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.

## **Treponema Group**

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

## **Trichomonas Group**

(trichomonasGrp). A group of measures/methods related to trichomonas bacteria. Used to describe the organism information for general measures. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: trichomonasGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA

## Parts

*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.

## TrimGalore!

(trimGalore). A QC pipeline tool for sequencing data that integrates Cutadapt and FastQC to assess sequence quality and remove adapters in one step. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/FelixKrueger/TrimGalore> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Trimmomatic

(trimmomatic). A sequencing data processing application that trims adapters and low-quality bases from Illumina sequencing reads. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://www.usadellab.org/cms/?page=trimmomatic> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Trinity

(trinity). A sequencing software that is an assembler designed specifically for RNA-seq data, creating transcriptome assemblies. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/trinityrnaseq/trinityrnaseq> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## TE Buffer (Tris-EDTA)

(trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. *Part Type*: categories *Domain*: naDomain *Speciment ID*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Wastewater Triturator

(triturator). The location where wastewater transportation vehicles unload wastewater. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *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: 2.2.3.*

### **trizol, zymo mag beads w/ zymo clean and concentrator**

(trizol). Nucleic acid extraction performed using the trizol, zymo mag beads w/ zymo clean and concentrator method. *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet 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.*

### **trizol, garnet bead beating, alcohol precipitation**

(trizolEtOH). trizol, garnet bead beating, alcohol precipitation *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet Group: procGrp Class: pcr Nomenclature: pcr Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet 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: 2.2.0.*

### **trizol and RNA purification kit**

(trizolRNA). trizol and RNA purification kit *Part Type: categories Domain: bio Speciment ID: saSpecimenSet Compartment Set: anyCompartmentSet*

## Parts

*Group:* procGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA  
*Category Set ID:* NA *Unit Set:* naUnitSet *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: 2.2.0.

## Train Station

(trStat). A place on a railroad line where trains regularly stop so that passengers can get on or off. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## TRUE

(TRUE). Boolean data type = TRUE Use only “TRUE” (case sensitive) *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* boolean *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 4 *Maximum Length:* 4 *Part Status:* active. First released: active. Last updated: 2.3.0.

*Parts*

### **TruSeq DNA PCR-Free Library Prep Kit**

(truseqDNA). TruSeq DNA PCR-Free Library Prep Kit by Illumina. A high-quality library prep kit without PCR amplification, reducing bias.  
*Part Type*: categories *Domain*: bio *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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **Total solids concentration**

(ts). Total solids concentration *Part Type*: measurements *Domain*: che *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: waterQualityGrp *Class*: standardConc *Nomenclature*: 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.

### **Tryptic Soy Broth (TSB)**

(tsb). Tryptic Soy Broth (TSB) - A nutrient-rich medium for bacterial survival, sometimes used for short-term storage. *Part Type*: categories *Domain*: naDomain *Speciment ID*: saSpecimenSet *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*

## 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.

### Total suspended solids

(tss). Total suspended solids *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.

### Concentration of total suspended solids

(tssConc). Total suspended solids concentration of the wastewater. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* miscMeas *Class:* standard-Conc *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.

### Tuberculosis Group

(tuberculosisGrp). A group of measures/methods related to tuberculosis. Used to describe the organism information for general measures. *Part*

## Parts

*Type:* groups *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* tuberculosisGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

## Francisella tularensis (tularemia) Group

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

## Turbidity

(turb). A measure for the turbidity of water, or a liquid sample, quantifying the relative clarity or opacity 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.

## Turburdity class

(turbidity). Measures and methods relating to water and wastewater turbidity. *Part Type*: classes *Domain*: che *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.

## Turbidity unit set

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

## Trichomonas vaginalis

(tVaginalis). Trichomonas vaginalis *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: trichomonasGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

### **Tube weight empty**

(tWeighE). The weight of the tube used for analysis while empty. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

### **Tube weight full**

(tWeighF). The weight of the tube used for analysis while full of analyte. *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* procGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

### **Type other deprecate**

(tyOtDep). Description for other type of sample not listed in *Part Type:* methods *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*: 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: depreciated. Last updated: 2.0.0.

## Type other deprecate2

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

## University campus

(uCampus). University or 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*: anyCompartmentSet *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*

## **Ugene**

(uGene). Sequencing software that offers alignment and consensus sequence generation features. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://ugene.net/> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Micrograms per gram**

(ugG). Micrograms per gram *Part Type*: units *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

## **Micrograms per litre**

(ugL). Micrograms per litre *Part Type*: units *Domain*: allDo *Speciment ID*: siSaSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA

## Parts

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

### Micrograms per milligram

(ugmg). Concentration unit of micrograms per milligram. *Part Type:* units *Domain:* allDo *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* na-Class *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.

### Micro-litres

(uL). The unit of microlitres. *Part Type:* units *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.2.0.

### Ultracentrifuges

(ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Standard centrifuges are a separate instrument type option. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit*

## *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.*

## **Micromho per centimeter**

(umhocom). 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.*

## **Unique Molecular Identifier (UMI) Tagging**

(umiTag). A deduplication method that adds unique tags to individual DNA fragments, allowing identification and removal of duplicate reads. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: procGrp Class: software Nomenclature: software Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: <https://www.illumina.com/techniques/sequencing/ngs-library-prep/multiplexing/unique-molecular-identifiers.html> Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## **UMI-tools**

(umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/CGATOxford/UMI-tools> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## **Undisclosed or Not Provided**

(undisc). A value has been recorded, however it was not included in the dataset. Missing value indicator for data that has not been shared or disclosed with outside parties. *Part Type*: missingness *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Unicycler**

(unicycler). A sequencing software that is a hybrid assembler for bacterial genomes, combining short and long reads. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*:

## *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.

## **Unique sample**

(unique). A unique sample, not duplicated. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Unit**

(unit). The units of a measurement. Different units that are used to describe measurement values. Units are combined into UnitSetIDs. Please requests new units by creating an issue in the ODM repository. *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* 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.

### **Unit input (wide table)**

(unitInput). The partID for the unit being used in a wide name. *Part Type*: attributes *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: 2.2.0.

### **Unitless measure**

(unitless). A unit for unitless measures, like pH. *Part Type*: units *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*: 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.

### **Unitless unit set**

(unitlessUnitSet). Unit set for measurements that does not have units. *Part Type*: unitSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Parts

### Unit name (wide table)

(unitName). The unit referenced for the wide name. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: saSpecimenSet *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*: varchar *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.

## Units

(units). The unit of the measurement. Every measurement must have a unit. Meaning, ‘units’ are a mandatory field whenever a measurement is recorded. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

### Unit set

(unitSet). An idenification 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*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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.

## Unit sets

(unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of ‘yes’ and ‘no’; and set B could contain the values of ‘yes’, ‘no’, and ‘maybe.’ partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused. *Part Type*: partType *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: 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.

## Unknown sample

(unkn). Denotes an unknown sample replicate type. *Part Type*: categories *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*:

## *Parts*

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

## **The Unlicense**

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

## **Ultracentrifugation**

(untracent). Ultracentrifugation Should typically be linked to a lower limit, and some indication of data spread (ie. standard deviation), and a mean/median measure. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: 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.

## **Untreated**

(untreat). A quality which denotes an absence of purposeful intervention or processes on an item. *Part Type*: categories *Domain*: naDomain *Speci-*

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

### **Upper limit of a 95% confidence interval**

(upperCI95). Specifies the the upper limit of a 95% confidence interval. A catch-all category for upstream wastewater sampling sites, including major sewer pipelines and pumping stations. *Part Type:* aggregations *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* colGrp *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* seeUnitVal *Maximum Value:* seeUnitVal *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.0.0.

### **Upstream sites**

(upstream). A general site type for upstream wastewater sampling sites. *Part Type:* categories *Domain:* phy *Speciment ID:* siSaSpecimenSet *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:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## *Parts*

### **Urban**

(urban). Urban populated area type *Part Type*: categories *Domain*: naDomain *Speciment ID*: poSiSpecimenSet *Compartment Set*: anyCompartmentSet *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.

### **Ureaplasma**

(ureaplasma). Ureaplasma *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: ureaplasmaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### **Ureaplasma Group**

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

## Parts

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

### **Urobilin or urochrome**

(urobilin). Urobilin or urochrome is the chemical primarily responsible for the yellow color of urine. It is a linear tetrapyrrole compound that, along with the related colorless compound urobilinogen, are degradation products of the cyclic tetrapyrrole heme. *Part Type:* measurements *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* procGrp *Class:* standardConc *Nomenclature:* standardConc *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* stdConcentrationUnitSet *Aggregation Scale:* quantAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Micro-Siemens per centimetre**

(uSCm). Micro-siemens per centimetre. *Part Type:* units *Domain:* phy *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:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

*Parts*

### **Ultrafast Sample placement on Existing tRees (UShER) Software**

(usher). A lineage or clade analysis software tool that adds new genomes to an existing phylogenetic tree, widely used for SARS-CoV-2 clade assignment.  
*Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: procGrp *Class*: software *Nomenclature*: software *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://github.com/yatisht/usher> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### **U site measure ID**

(uSiteMeasureID). Unique identifier for each measurement for a site. *Part Type*: attributes *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*: **deprecated**. First released: depreciated. Last updated: 2.0.0.

### **Coordinated universal time (UTC) zone**

(utc). UTC – Time zone. Preprogrammed into dictionary tables, not editable by users. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category 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: 75 Part Status: active. First released: active. Last updated: 2.1.0.*

## Coordinated universal time (UTC) zone in daylight savings

(utcDST). Time zone during Daylight Saving Time. Preprogrammed into dictionary tables, not editable by users. *Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 75 Part Status: active. First released: active. Last updated: 2.1.0.*

## Utilities sector or organization

(utilities). Describes organization that manage or provide utilities services, whether water, gas, heat, etc. *Part Type: categories Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 30 Part Status: active. First released: active. Last updated: 2.2.0.*

## Parts

### **Universal Transport Medium (UTM)**

(utm). Universal Transport Medium (UTM) - Used for microbial preservation in various environmental samples, including wastewater. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **V1104L Mutation**

(v1104l). The FLiRT/SLip variant mutation V1104L *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flirtSLipGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **v2930l delta-variant gene target**

(v2930l). v2930l delta-variant mutation gene target *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* sarsCov2 *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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: 2.0.0.

### **Vacuum sludge sampling**

(vac). Instrument 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:* 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:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **Validation study**

(validationStudy). A measure 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.

### **Value Treatment**

(valTreat). A field which specifies what kinds of data treatments or the nature of the measurement value. The options are raw, derived, estimate, and predicted. *Part Type:* attributes *Domain:* naDomain *Speciment ID:*

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

## **Value treatment value set**

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

## **Value**

(value). Value of a measure, observation or attribute. Only used for the dictionary entries of parts. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 100 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **VanA-A Vancomycin-resistance gene target**

(vanAA). The VanA-A vancomycin anti-microbial resistance gene target. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: vanAMRGrp *Class*: allele *Nomenclature*: allele *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: <https://www.mediterranee-infection.com/accesressources/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.

### **Vancomycin Anti-microbial resistance Group**

(vanAMRGrp). The group for measures and methods pertaining to vancomycin-related anti-microbial resistance. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: vanAMRGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: quantAggScale *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.

### **Vancomycin resistance**

(vanc). Vancomycin resistant bacteria. *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: amrGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: bacteriaUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

## Variable character data type

(varchar). The data type for variable character data. Measured by sequencing. *Part Type:* dataTypes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Frequency of variants detected

(varFreq). A description of the frequency of 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.

## Variants class

(variant). Measures and methods relating to variants. *Part Type:* classes *Domain:* bio *Speciment ID:* poSaSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* variant *Nomenclature:* variant

## Parts

*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.

## Varicella

(varicella). Varicella *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* varicellaGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## Varicella Group

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

## *Parts*

### **Population with 1 dose of vaccine**

(vax1). The population with exactly 1 dose of vaccine, with the vaccine specified in the measure field. A unit used for 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.

### **Proportion of population with 1+ vaccine dose(s)**

(vax1p). Specifies the portion of the population with 1 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for 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.

### **Population with 1+ dose(s) of vaccine**

(vax1plus). The population with 1 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet

## Parts

*Group:* naGroup *Class:* 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.

### **Population with 2 or more doses of vaccine**

(vax2). The population with exactly 2 dose of vaccine, with the vaccine specified in the measure field. A unit used for 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.

### **Proportion of population with 2+ vaccine doses**

(vax2p). Specifies the portion of the population with 2 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for 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

### **Population with 2+ or more doses of vaccine**

(vax2plus). The population with 2 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for 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.

### **Population with 3 or more doses of vaccine**

(vax3). The population with exactly 3 dose of vaccine, with the vaccine specified in the measure field. A unit used for 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.

### **Proportion of population with 3+ vaccine doses**

(vax3p). Specifies the portion of the population with 3 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo Speciment ID: poSpecimenSet *Compartment Set:*

## Parts

naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: na-  
Class *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.

### **Population with 3+ or more doses of vaccine**

(vax3plus). The population with 3 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for 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.

### **Population with 4 or more doses of vaccine**

(vax4). The population with exactly 4 dose of vaccine, with the vaccine specified in the measure field. A unit used for 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*

### **Proportion of population with 4+ vaccine doses**

(vax4p). Specifies the portion of the population with 4 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* na-Class *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.

### **Population with 4+ or more doses of vaccine**

(vax4plus). The population with 4 or more doses of vaccine, with the vaccine specified in the measure field. A unit used for specifying a population-wide vaccination level measure. *Part Type:* units *Domain:* allDo *Speciment ID:* poSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* na-Class *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.

### **Change to Vaccine Schedule**

(vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass

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

## Velvet

(velvet). A sequencing software that is a de novo assembler optimized for short-read data, often used in microbial genomics. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/dzerbino/velvet> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## ODM V1 category

(version1Category). ODM V1 category *Part Type:* attributes *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* 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

### ODM V1 location

(version1Location). ODM V1 location *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### ODM V1 table

(version1Table). ODM V1 table *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### ODM version 1 to 2 changes

(version1to2Changes). Changes for part between ODM v1 and V2 *Part Type*: attributes *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## ODM V1 variable

(version1Variable). ODM V1 variable *Part Type*: attributes *Domain*: bio *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Vertical grab sampling

(vertGrb). 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 waste from a tank. *Part Type*: categories *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*: genMissingnessSet *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Vibrio

(vibrio). Vibrio *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: vibrioGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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: 2.2.0.

## **Vibrio Group**

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

## **Viral passage experiment**

(viralPass). A research sampling strategy in which samples are selected in order to perform a viral passage experiment. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Miscellaneous viruses group**

(virusMisc). A group of measures/methods related to miscellaneous viruses. The miscellaneous viruses are often measured for normalization or standardization and have only one measure or method. When a virus has many

## Parts

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*: 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*: genMissingness-Set *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: depreciated. First released: depreciated. Last updated: 2.2.0.

## Variant of concern

(voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for assigning this threat level. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Variant of interest

(voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA

## *Parts*

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

## **Size in volume**

(vol). Total volume of water or sludge sampled. Used for water or air testing *Part Type:* measurements *Domain:* phy *Speciment ID:* saSpecimenSet *Compartment Set:* airWaterCompartmentSet *Group:* colGrp *Class:* physical *Nomenclature:* physical *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* volumeUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* 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.

## **Volume proportional sample**

(volPr). A volume proportional sample generally collected by an autosampler. The sampling takes the same wastewater volume at variable time intervals, after a defined volume of wastewater has passed the sampling point. This is also called constant volume, variable time (CVVT). *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## Volume unit set

(volumeUnitSet). Unit set of volume 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*: 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.

## Volatile suspended solids

(vss). Volatile suspended solids *Part Type*: measurements *Domain*: phy *Speciment ID*: saSpecimenSet *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.

## Volatile suspended solids - ignition

(vssIg). A water quality measure, captured by via the loss on ignition of the mass of measured total suspended solids. This ignition generally takes place in an oven at a temperature of 550 °C to 600 °C. It represents the amount of volatile matter present in the solid fraction of the measured solution. *Part Type*: measurements *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: waterCompartmentSet *Group*: measGrp *Class*: standardConc *Nomenclature*: standardConc *Ontology*

## 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.

## **Vesicular stomatitis virus (VSV) target**

(vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *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.

## **VSV forward primer (ABI)**

(vsvABIFor). VSV forward primer (ABI) *Part Type:* categories *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* vsvGrp *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* unitlessUnitSet *Aggregation Scale:* 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.

## **VSV probe (ABI)**

(vsvABIProbe). VSV probe (ABI) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: vsvGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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.

## **VSV reverse primer (ABI)**

(vsvABIRev). VSV reverse primer (ABI) *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: vsvGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: unitlessUnitSet *Aggregation Scale*: 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.

## **Vesicular Stomatitis Virus (VSV) Group**

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

## *Parts*

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

### **Verotoxin-producing Escherichia coli (VTEC)**

(vtec). Verotoxin-producing Escherichia coli (VTEC) *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* ecoliGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Viral Transport Medium (VTM)**

(vtm). A buffer solution/medium the preserves viral samples during transport, commonly used for wastewater viral studies. *Part Type:* categories *Domain:* naDomain *Speciment ID:* 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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

### **variant under monitoring**

(vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat level. *Part Type:* categories *Domain:* naDomain *Speciment ID:*

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

## Water compartment

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

## water concentrating buffer (R2042-1)

(watConcBuff). water concentrating buffer (R2042-1) *Part Type*: categories *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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

### Water depreciated

(water). Non-wastewater, coming from any kind of water body. *Part Type*: categories *Domain*: allDo *Speciment ID*: anySpecimenSet *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*: depreciated. First released: depreciated. Last updated: 2.0.0.

### Water compartment set

(waterCompartmentSet). A compartment set for measures and methods in the water compartment. *Part Type*: compartmentSets *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: miscMeas *Class*: temperature *Nomenclature*: temperature *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: temperatureUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

### Water Quality Group

(waterQualityGrp). A group of measures/methods related to water quality. *Part Type*: groups *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: waterQualityGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum*

## Parts

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

### Water-based Transit Hub

(waterTH). A transport hub is a place where passengers and cargo are exchanged between water-based vehicles and/or between water-based transport modes. Used when not greater detail can be provided *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *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.

### Wastewater temperature

(watTemp). Temperature of the wastewater. *Part Type:* measurements *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* weather *Nomenclature:* weather *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* temperatureUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### Weather (time of sampling)

(weath). A measure for weather captured through qualitative categories; part of a larger suite of weather measures that may be useful when col-

## *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.

## **Weather class**

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

## **Weather set**

(weathSet). A set of the valid qualitative categories for the qualitative weather measure. *Part Type*: mmaSets *Domain*: phy *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: siteFeat *Class*: weather *Nomenclature*: weather *Ontology Reference*: NA *Category Set ID*: weathSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

## Weeks

(weeks). A unit of measuring time in weeks, or periods of seven days. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 3.0.0.

## Well

(well). A cylindrical hole, pit, or tunnel drilled or dug down to a depth from which water, oil, or gas can be pumped or brought to the surface. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: 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*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## West Nile

(westNile). West Nile *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: flavivirusGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: 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.

## Whole genome sequencing

(wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing *Part Type:* categories *Domain:* bio *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.

## WHO nomenclature

(who). Specifies variant or genetic nomenclature as set out by the World Health Organization. If there are multiple issues to flag, 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.

## Wide 95% interval

(wI). The 95% interval is too wide, low confidence in results. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* saSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomen-*

## 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.*

## Specified attribute (wide table)

(wideAttribute). Unique identifier for an attribute in a wide table only. *Part Type: attributes 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: 2.2.0.*

## Compartment set for wide names

(wideCompartmentSet). Compartment set for wide names. For wide names. *Part Type: compartmentSets Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: wideCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 50 Part Status: active. First released: active. Last updated: 3.0.0.*

## Parts

### Fraction set for wide names

(wideFractionSet). Fraction set for wide names. For wide names. *Part Type*: mmaSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: wideFractionSet *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

### Measure identification (wide table)

(wideMeasure). Unique identifier for a measure in a wide table only. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: 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*: 60 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Wide Name

(wideName). Unique identifier for wide table only. Use when all measures are performed on a single sample at the same time and same laboratory. Suggestion: siteID\_sampleID\_LabID\_reportDate\_ID. *Part Type*: attributes *Domain*: naDomain *Speciment ID*: 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.

### **Wide name table**

(wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field. *wn Part Type*: tables *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: lookup *Nomenclature*: lookup *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.0.0.

### **Wide name table order**

(wideNamesOrder). Column for indicating the order of the fields in the wide names table. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 1 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.2.0.

### **Wide name table required**

(wideNamesRequired). Column for indicating which fields in the wide names table are mandatory. *Part Type*: tableSupport *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet

## 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.

## Wide name type

(wideNameType). The type of wide name generated. Possible options are measure, protocol or attribute. *Part Type:* attributes *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: 2.2.0.

## Specified protocol (wide table)

(wideProtocol). Unique identifier for a protocol in a wide table only. *Part Type:* attributes *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: 2.2.0.

## Speciment set for wide names

(wideSpecimenSet). Speciment set for wide names. For wide names. *Part Type*: specimenSets *Domain*: naDomain *Speciment ID*: wideSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 2.2.0.

## Wind Speed

(wind). A measure for wind speed; part of a larger suite of weather measures that may be useful when collecting samples from outdoor sources. *Part Type*: measurements *Domain*: phy *Speciment ID*: siSpecimenSet *Compartment Set*: airCompartmentSet *Group*: siteFeat *Class*: speed *Nomenclature*: speed *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: windSpeedUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *Missingness Set*: gen-MissingnessSet *Minimum Value*: seeUnitVal *Maximum Value*: seeUnitVal *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## Wind speed unit set

(windSpeedUnitSet). Unit set for wind speed measurements. *Part Type*: unitSets *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: windSpeedUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: categorical *Missingness Set*: NA *Minimum*

## *Parts*

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

## **Whole Metagenome Sequencing**

(wms). A DNA sequencing assay that intends to provide information on the DNA sequences of multiple genomes (a metagenome) from different organisms present in the same input sample. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Wide name table Shorthand**

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

## **Sample stored incorrectly**

(wrongStorage). Sample was stored inappropriately. *Part Type:* qualityIndicators *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment*

## Parts

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

## Sample stored at wrong temperature

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

## World Sphere (W-SPHERE)

(wSphere). World Sphere header *Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: 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*

### wSphere Format

(wSphereForm). Dataset was originally recorded and/or stored in wSphere format. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: <https://sphere.waterpathogens.org/about> *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

### World Sphere (W-SPHERE) notes

(wSphereNotes). W-Shere notes *Part Type*: attributes *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*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 1000 *Part Status*: active. First released: active. Last updated: 2.0.0.

### Delta Variant wt214 gene target

(wt214). Delta Variant wt214 gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: deltaGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **Wastewater Treatment Agency**

(wta). An organization type that includes those organizations who manage wastewater treatment programs. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **WTDBG (aka wtdbg2)**

(wtdbg2). A sequencing software that is an assembler for long-read data that generates contigs rapidly. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* procGrp *Class:* software *Nomenclature:* software *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://github.com/ruanjue/wtdbg2> *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Do What The F\*ck You Want To Public License { #wtfpl }**

(wtfpl). The licensing for the measure or data set is managed under the Do What The 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.

## Wastewater Treatment Plant Operator

(wtpo). An organization type that includes those organizations who run and operate wastewater treatment facilities. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Whole Virome Sequencing

(wvs). A whole metagenome sequencing assay that intends to provide information on multiple genome sequences from different viruses present in the same input sample. *Part Type:* categories *Domain:* bio *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:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Weight for weight

(ww). weight for weight (% w/w) *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*: 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.

## Wastewater aerobic digestion

(wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. *Part Type*: categories *Domain*: bio *Specimen ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: GENEPIO:0101199 *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 50 *Part Status*: active. First released: active. Last updated: 3.0.0.

## Wastewater anaerobic digestion

(wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. *Part Type*: categories *Domain*: bio *Specimen ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: procGrp *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: GENEPIO:0101200 *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: naAggrScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum*

## Parts

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

### wastewater comminution process

(wwCominuated). wastewater comminution process occurred upstream of the sampling site. *Part Type: categories Domain: phy Speciment ID: siSaSpecimenSet Compartment Set: waterCompartmentSet Group: procGrp Class: naClass Nomenclature: naClass Ontology Reference: GENEPPIO: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.*

### Wastewater sludge removal

(wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. *Part Type: categories Domain: phy Speciment ID: siSaSpecimenSet Compartment Set: waterCompartmentSet Group: procGrp Class: naClass Nomenclature: naClass Ontology Reference: GENEPPIO: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.*

### Wastewater sludge dewatering

(wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. *Part Type: categories Domain: phy Speciment ID: siSaSpecimenSet Compartment Set: waterCompartmentSet Group: procGrp Class:*

## Parts

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.

### **Wastewater sludge drying**

(wwDry). Wastewater sludge drying occurred upstream of the sampling site. *Part Type*: categories *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Wastewater filtration**

(wwFilt). Wastewater filtration occurred upstream of the sampling site. *Part Type*: categories *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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*

### **Wastewater grit removal**

(wwGrit). Wastewater grit removal occurred upstream of the sampling site. *Part Type*: categories *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Wastewater microbial treatment**

(wwMic). Wastewater microbial treatment occurred upstream of the sampling site. *Part Type*: categories *Domain*: bio *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Wastewtaer primary sedimentation**

(wwPriSed). Wastewtaer primary sedimentation occurred upstream of the sampling site. *Part Type*: categories *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Wastewater screening process**

(wwScreen). Wastewater screening process occurred upstream of the sampling site. *Part Type*: categories *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Wastewater secondary sedimentation**

(wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. *Part Type*: categories *Domain*: phy *Speciment ID*: siSaSpecimenSet *Compartment Set*: waterCompartmentSet *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.

### **Wastewater treatment plant**

(wwtp). A general site type for wastewater treatment plants. Used as a catch-all category for industrial or municipal wastewater treatment plants that carry combined or sanitary sewage, or lagoons. *Part Type*: categories *Domain*: naDomain *Speciment ID*: naSpecimenSet *Compartment Set*: waterCompartmentSet *Group*: colGrp *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:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.0.0.

## **Wastewater treatment efficiency assessment**

(wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## **Back-up wastewater treatment site**

(wwtpBack). Indicates a wastewater treatment plant where multiple labs are or were sampling, and where secondary samples are being taken taken. Maps to units of either million gallons per day, or population equivalents. *Part Type:* categories *Domain:* phy *Speciment ID:* siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* siteFeat *Class:* capacity *Nomenclature:* capacity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *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.

### **Wastewater treatment plant designed capacity**

(wwtpCap). A measure for the designed capacity of a wastewater treatment plant, in terms of how much water it was designed to be able to hold and process. *Part Type:* measurements *Domain:* phy Speciment ID: siSpecimenSet *Compartment Set:* waterCompartmentSet *Group:* colGrp *Class:* capacity *Nomenclature:* capacity *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* capacityUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

### **Industrial wastewater treatment plant**

(wwtpInd). Industrial wastewater treatment plant *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* wa-terCompartmentSet *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.

### **Municipal wastewater treatment plant for combined sewage**

(wwtpMuC). Municipal wastewater treatment plant for combined sewage *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* 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:* NA

## Parts

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

### **Municipal wastewater treatment plant for sanitary sewage only**

(wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* naGroup *Class:* pcr *Nomenclature:* pcr *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *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.

### **Wastewater treatment**

(wwTrt). Wastewater treatment occurred upstream of the sampling site. *Part Type:* categories *Domain:* che *Speciment ID:* siSaSpecimenSet *Compartment Set:* waterCompartmentSet *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.

### **XEC Variant**

(xecV). The XEC variant of SARS-CoV-2, a subvariant of the Omicron strain. *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* omicronGrp *Class:* variant *Nomenclature:* variant *Ontology Reference:* NA *Category Set ID:*

## Parts

NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: 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.

## Relative Centrifugal Force (RCF) or x g units

(xg). RCF (Relative Centrifugal Force) denotes the degree of force exerted on a sample. RCF is quantified in multiples of the gravitational acceleration that is standard at the Earth's surface (x g). Thus, the terms RCF and XG are often used interchangeably in centrifugation protocols. *Part Type*: units *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: varchar *Missingness Set*: NA *Minimum Value*: NA *Maximum Value*: NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.2.0.

## y505h omicron-variant gene target

(y505h). y505h omicron-variant mutation gene target *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: sarsCov2 *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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*

## **Years**

(years). A unit for indicating a length of time in years. *Part Type*: units *Domain*: allDo *Speciment ID*: anySpecimenSet *Compartment Set*: naCompartmentSet *Group*: naGroup *Class*: naClass *Nomenclature*: naClass *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *Aggregation Scale*: quantAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: integer *Missingness Set*: NA *Minimum Value*: 0 *Maximum Value*: NA *Minimum Length*: NA *Maximum Length*: NA *Part Status*: active. First released: active. Last updated: 2.0.0.

## **Yersinia enterocolitica**

(yEnterocolitica). Yersinia enterocolitica *Part Type*: measurements *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: yersiniaGrp *Class*: organism *Nomenclature*: organism *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: geneticUnitSet *Aggregation Scale*: seeUnitAggScale *Quality Set*: NA *Reference Link*: NA *Data Type*: seeUnitData *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.

## **Yersinia Group**

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

## Parts

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

## Zenodo

(zenodo). Zenodo open data storage. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* <https://zenodo.org> *Data Type:* varchar *Missingness Set:* genMissingnessSet *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 50 *Part Status:* active. First released: active. Last updated: 3.0.0.

## Zika

(zika). Zika *Part Type:* measurements *Domain:* bio *Speciment ID:* saSpecimenSet *Compartment Set:* anyCompartmentSet *Group:* flavivirusGrp *Class:* organism *Nomenclature:* organism *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* geneticUnitSet *Aggregation Scale:* seeUnitAggScale *Quality Set:* NA *Reference Link:* NA *Data Type:* seeUnitData *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.

## zLib License

(zlib). The licensing for the measure or data set is managed under the zLib License. *Part Type:* categories *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality*

## *Parts*

*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.*

## **Zones look-up table Shorthand**

(zo). The abbreviated short name used to reference the Look up table for the possible sub-national region or zone inputs. table *Part Type: 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.*

## **English name of country sub-domains**

(zoneName). The english-language name for a given country sub-domain. Preprogrammed into dictionary tables, not editable by users. *Part Type: attributes Domain: naDomain Speciment ID: naSpecimenSet Compartment Set: naCompartmentSet Group: naGroup Class: naClass Nomenclature: naClass Ontology Reference: NA Category Set ID: NA Unit Set: naUnitSet Aggregation Scale: naAggrScale Quality Set: NA Reference Link: NA Data Type: varchar Missingness Set: NA Minimum Value: NA Maximum Value: NA Minimum Length: 0 Maximum Length: 75 Part Status: active. First released: active. Last updated: 2.1.0.*

## Zones look-up table

(zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field.

*zo Part Type:* tables *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* lookup *Nomenclature:* lookup *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:* NA *Minimum Length:* 0 *Maximum Length:* 30 *Part Status:* active. First released: active. Last updated: 2.1.0.

## Zones table column order

(zonesOrder). Specifies the order of the columns in the zones table.

*Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* integer *Missingness Set:* NA *Minimum Value:* 1 *Maximum Value:* NA *Minimum Length:* NA *Maximum Length:* NA *Part Status:* active. First released: active. Last updated: 2.1.0.

## Zones table required headers

(zonesRequired). Required headers in the zones table.

*Part Type:* tableSupport *Domain:* naDomain *Speciment ID:* naSpecimenSet *Compartment Set:* naCompartmentSet *Group:* naGroup *Class:* naClass *Nomenclature:* naClass *Ontology Reference:* NA *Category Set ID:* NA *Unit Set:* naUnitSet *Aggregation Scale:* naAggrScale *Quality Set:* NA *Reference Link:* NA *Data Type:* varchar *Missingness Set:* NA *Minimum Value:* NA *Maximum Value:*

## *Parts*

NA *Minimum Length*: 0 *Maximum Length*: 30 *Part Status*: active. First released: active. Last updated: 2.1.0.

### **zymo quick-rna viral kit #r1035**

(zymo1035). zymo quick-rna viral kit #r1035 *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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: 2.2.0.

### **zymo quick-rna viral 96 kit #r1041**

(zymo1041). zymo quick-rna viral 96 kit #r1041 *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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: 2.2.0.

### **zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)**

(zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit/ zymo environ water rna kit (cat. r2042). *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*:

Parts

anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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.

**zymo quick-rna fungal/bacterial miniprep #r2014**

(zymoQuick). Nucleic acid extraction performed using the zymo quick-rna fungal/bacterial miniprep #r2014 kit. *Part Type*: categories *Domain*: bio *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *Group*: procGrp *Class*: pcr *Nomenclature*: pcr *Ontology Reference*: NA *Category Set ID*: NA *Unit Set*: naUnitSet *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.

**zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)**

(zymoWatRNA). zymo environ water rna kit (cat. r2042) *Part Type*: categories *Domain*: phy *Speciment ID*: saSpecimenSet *Compartment Set*: anyCompartmentSet *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.



# Sets

New names:

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* `` -> `...392`  
* `` -> `...393`  
* `` -> `...394`  
* `` -> `...395`  
* `` -> `...396`  
* `` -> `...397`  
* `` -> `...398`  
* `` -> `...399`  
* `` -> `...400`  
* `` -> `...401`  
* `` -> `...402`  
* `` -> `...403`  
* `` -> `...404`
```

## Sets

```
* `` -> `...405`  
* `` -> `...406`  
* `` -> `...407`  
* `` -> `...408`  
* `` -> `...409`  
* `` -> `...410`  
* `` -> `...411`  
* `` -> `...412`  
* `` -> `...413`  
* `` -> `...414`  
* `` -> `...415`  
* `` -> `...416`  
* `` -> `...417`  
* `` -> `...418`
```

## Dictionary v3.0.0 Documentation v2.1.0

Sets are lists of categories and other parts. For example, **Collection category set** ([collectionCatSet](#)) contains a list of the different collection types including: **Moore swab**, **Grab sample**, **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.

## Aggregations

(aggregations). Statistical measures used to report a measure. Each measure reported as a number should be reported with an aggregation.

## Aggregations

The default aggregation is `$in`, which corresponds to a single measurement.

**AND Boolean aggregation** (`andBoo`). “AND” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Cumulative count** (`cuCo`). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Daily count** (`daiCo`). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**EpiWeek Mean** (`epiMean`). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Flow-normalized mean** (`floMean`). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Geometric mean** (`gmn`). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**See Header for Aggregation** (`hAg`). An indicator to show in a wide-name that aggregation information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Lower limit of a 95% confidence interval** (`lowerCI95`). Specifies the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Maximum value** (`maxVal`). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Arithmetic mean** (`me`). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Median** (`med`). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Normalized arithmetic mean** (`menr`). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Sets

**Minimum value** (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Aggregation not applicable** (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Normalized geometric mean** (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**OR Boolean aggregation** (orBoo). “OR” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Other aggregation deprecated** (otherDep). Other aggregation method. Add description to aggregationOther Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**PMMoV- and flow-normalized mean** (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**PMMoV-normalized mean** (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Standard deviation** (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Normalized standard deviation** (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Single** (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Standard Error** (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## *Aggregation scales*

**Rolling sum of previous 14 days** (sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Total amount or count - the sum** (total). The total number or final count of cases, or other defined metric. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Upper limit of a 95% confidence interval** (upperCI95). Specifies the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Aggregation scales**

(aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative.

**Aggregation scale not applicable** (naAggrScale). Not application for aggregation sets. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Other aggregation scale** (othAgg). Specifies an aggregation scale that can't be described as either "qualitative" or "quantitative". Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Qualitative** (qualAggScale). The qualitative aggregation scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quantitative** (quantAggScale). The "quantAggScale" aggregation scale. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See unit (aggregation scales)** (seeUnitAggScale). A value for aggregation scale to be used when the aggregation scale depends on that specified in the parts list entry for the unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

## Aggregation sets

(aggregationSets). Sets of aggregations. Examples of aggregation sets include logarithm, linear and boolean.

### Boolean aggregation set

(booleanAggrSet) Aggregation set for boolean. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**AND Boolean aggregation** (andBoo). “AND” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**OR Boolean aggregation** (orBoo). “OR” aggregation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Single** (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### Linear scale aggregation set

(linearAggrSet) The aggregation set that contains all aggregations that exist on the linear scale. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Cumulative count** (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Daily count** (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**EpiWeek Mean** (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Aggregation sets

**Flow-normalized mean** (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Lower limit of a 95% confidence interval** (lowerCI95). Specifies the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Maximum value** (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Arithmetic mean** (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Median** (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Normalized arithmetic mean** (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Minimum value** (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**PMMoV- and flow-normalized mean** (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**PMMoV-normalized mean** (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Standard deviation** (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Normalized standard deviation** (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Single** (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Sets

**Standard Error (stEr).** The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rolling sum of previous 14 days (sum14).** The rolling sum of case counts/some kind of count over the previous 14 days. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Total amount or count - the sum (total).** The total number or final count of cases, or other defined metric. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Upper limit of a 95% confidence interval (upperCI95).** Specifies the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Logarithmic scale aggregation set

(logAggrSet)The aggregation set that contains all aggregations that exist on the logarithmic scale (rather than linear or qualitative). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Flow-normalized mean (floMean).** Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Geometric mean (gmn).** Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Lower limit of a 95% confidence interval (lowerCI95).** Specifies the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Maximum value (maxVal).** Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Minimum value (minVal).** Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## *Aggregation sets*

**Normalized geometric mean** (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**PMMoV- and flow-normalized mean** (pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**PMMoV-normalized mean** (pmmovNorm). Mean measure normalized to amount of PMMoV. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Single** (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Standard Error** (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Upper limit of a 95% confidence interval** (upperCI95). Specifies the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Aggregation set not applicable**

(naAggrSet)Not application for aggregation sets. Used for parts for which an aggregation set value is not applicable or appropriate. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Aggregation not applicable** (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

### **Other aggregation set**

(otherAggrSet) Aggregation set used for unitless measures. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Cumulative count** (cuCo). The cumulative count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Daily count** (daiCo). The daily count of cases of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**EpiWeek Mean** (epiMean). The mean of all measures taken in one epiweek. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Flow-normalized mean** (floMean). Mean measure normalized to wastewater flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Geometric mean** (gmn). Geometric mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**See Header for Aggregation** (hAg). An indicator to show in a wide-name that aggregation information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Lower limit of a 95% confidence interval** (lowerCI95). Specifies the the lower limit of a 95% confidence interval. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Maximum value** (maxVal). Highest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Arithmetic mean** (me). Arithmetic mean. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Median** (med). Median. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Normalized arithmetic mean** (menr). Arithmetic mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## *Aggregation sets*

**Minimum value** (minVal). Lowest value in a range of values for a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Aggregation not applicable** (naAggr). Not applicable for aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Normalized geometric mean** (ngmn). Geometric mean, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Standard deviation** (sd). Standard deviation. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Normalized standard deviation** (sdn). Standard deviation, normalized. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Single** (sin). A value that is not an aggregate measurement (ie. not a mean, median, max or any other) and can be a replicate value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Standard Error** (stEr). The standard error of a series of measurements. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rolling sum of previous 14 days** (sum14). The rolling sum of case counts/some kind of count over the previous 14 days. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Total amount or count - the sum** (total). The total number or final count of cases, or other defined metric. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Upper limit of a 95% confidence interval** (upperCI95). Specifies the upper limit of a 95% confidence interval. Status: active. First released: 1.0.0. Last updated: 2.0.0.

*Sets*

## Attributes

(attributes). Attributes describe the who, where, when, and why of environmental surveillance. There are attributes for domain, specimen, compartment, or table. Attributes are one of the three main components or ways to report environment surviellence data. The other two components are measures and methods.

**Accessions Index ID** (accessIndexID). Provisional ID to act as a primary key for each row of the accessions table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Accession Number in Repository** (accessNum). The accession number for the data entry in the given data repository or hosting platform. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Public health action** (action). The specific public health action or designation being taken or applied. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Public health action datetime** (actionDT). The date and Time of the public health action. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Public Health Action Group ID** (actionGrpID). ID used for linking multiple public health actions together for a single action. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Public health action type** (actionType). The type of public health action being taken. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Analysis date** (aDate). Date the measurement was performed in the lab. Status: depreciated. First released: 1.0.0. Last updated: 2.1.0.

## *Attributes*

**Analysis date end** (aDateEnd). Date the measurement or analysis was completed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Analysis date start** (aDateStart). Date the measurement or analysis was started. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Address Line 1** (addL1). Line 1 (the street name, number and direction) for a given address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Address Line 2** (addL2). Line 2 (the unit number) for a given address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Address ID** (addressID). A unique identifier for an address. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Aggregation scale** (aggregationScale). A scale used for an aggregation. Only applicable for measures and units. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Aggregation** (aggregation). Statistical measures used to report a measure. Each aggregation has a corresponding value. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Aggregation input (wide table)** (aggregationInput). The partID for the aggregation being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Aggregation name (wide table)** (aggregationName). The aggregation referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Aggregation set** (aggregationSet). The aggregation set for a unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Alias depreciated** (aliasDep). ID of an assay that is the same or similar. A comma separated list. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

## Sets

**Alias ID depreciated** (aliasIDDep). Alias id Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Access to all org** (allOrgs). If this is ‘no’, this data will not be available to any partner organization. If missing, data will be available to the all organizations. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Assay method id default depreciated** (amDefDep). Used as default when a new measurement is created for this lab. See ID in AssayMethod table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Assay ID** (asID). Links with the AssayMethod used to perform the analysis. Use instrument.ID for measures that are not viral measures. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Attribute input (wide table)** (attributeInput). The partID for the attribute being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Attribute name (wide table)** (attributeName). The attribute referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Calculation Type** (calcType). A field to explain the purpose/nature of a single calculation/data treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Calculation ID** (calculationID). A unique identifier and primary key for every row of the calculations table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Capital city endonym** (capitalEndonym). The name locals use for their country’s capital. Status: active. First released: 2.1.0. Last updated: 2.1.0.

## Attributes

**Capital city exonym** (capitalExonym). The English name foreigners use for the country's capital. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**character length** (charLength). The number of characters used for the wide names. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**City** (city). The city where a site or organization is located; part of the address. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Class** (class). A unique identifier for a class, which is akin to a sub-group; it's a way of grouping parts within a given group. A group can have one or more classes to describe different parts of the class. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Collection Approximate Time Period** (collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Collection Date (time not included)** (collDate). Sample collection date, where time is reported in a separate field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Collection date time** (collDT). For grab samples this is the date, time and timezone the sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Collection date time end** (collDTEnd). For integrated time average samples this is the date, time and timezone the sample was finished being taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Collection date time start** (collDTStart). For integrated time averaged samples this is the date, time and timezone the sample was started being taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Collection number** (collNum). The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or

## Sets

passive sampling. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Collection period and number** (collNumPer). Composite collection number.period. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

**Collection period** (collPer). Collection period. The time period over which the sample was collected, in hours. Alternatively, use collectionStart and collectionEnd. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample collection type** (collType). The type of collection. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Column name depreciated** (columnNameDep). Name for the column. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Compartment** (compartment). The attribute identifying the substance from which where a sample was taken. For more information, see partID = compartment. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Compartment input (wide table)** (compartmentInput). The partID for the compartment being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Compartment name (wide table)** (compartmentName). The compartment referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Compartment Set Header** (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.

**Contact ID** (contactID). A unique identifier for a given contact person. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Contact name** (contactName). Contact person or group, for the lab. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

## Attributes

**Contact phone** (coPhone). Contact phone number, for the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Country** (country). The country where a site or organization is located; part of the address. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Country endonym** (countryEndonym). The name locals use for their country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Country exonym** (countryExonym). The English name foreigners use for the country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Covid-19 population measurement date** (cphDate). date of reporting for covid-19 measure. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Cphd ID** (cphid). Unique identifier for the table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Custody Contact ID** (custodyCont). A unique identifier for data custodians. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Data custodian ID** (custodyID). The data custodian of a database. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Host Data Repository or Bank** (dataHost). The external repository or database/bank in which a sequence (or other external data) is stored. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dataset creation date** (datasetDate). Specifies the date a given dataset was created. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Dataset ID** (datasetID). The name of the dataset that stores information for MeasureReport, SampleReport and other reporting tables. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Date** (dateDep). Date Status: depreciated. First released: 1.0.0. Last updated: 3.0.0.

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**Description** (descr). A detailed description of a measure, method, or attribute. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Access to details deprecated** (detailsDep). More details on the existing confidentiality requirements of this measurement. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Domain** (domain). Domain is the highest level of describing of a measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Contact email** (email). Contact e-mail address, for the lab. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**European Nucleotide Association Mapping Column** (enaMap). ENA header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**European Nucleotide Association (ENA) - notes** (enaNotes). ENA notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Enumeration for set values** (enumeration). The numeric value that corresponds to a given value in a set, defined in the sets table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**EpiWeek Number** (epiWeek). The number of the epi week in which a sample was collected, or to which a measure would apply. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**EpiWeek Start Date** (epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start date resolves the possible ambiguity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Year of the EpiWeek** (epiYear). The year in which the epi week is occurring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Equation** (equation). The equation used in the calculation/data treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Attributes

**File location of polygon** (fileLocation). The location of the file containing the geometry of the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**First name of contact** (firstName). Specifies the first name of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Fraction analyzed** (fraction). Fraction of the sample that is analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Fraction input (wide table)** (fractionInput). The partID for the fraction being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Fraction name (wide table)** (fractionName). The fraction analyzed referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Funder contact ID** (funderCont). A unique identifier for a funder. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Funding agency ID** (funderID). The funding agency of the dataset. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**European Petroleum Survey Group Coordinates** (geoEPSG). The unique EPSG code specifying a given geospatial area. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Latitude** (geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721) Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Longitude** (geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000) Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Type of geography** (geoType). Type of geography that is represented by the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Sets

**Well-known text** (geoWKT). Well-known text of the polygon Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Group** (group). Unique identifier for a group of measures. Mostly applicable for measures, methods, units, and aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Health Region for a Site** (healthRegion). A free-text variable for listing the health region for a given site. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Version of Data Hosting Platform/Repository** (hostVersion). The version of the data repository or hosting platform being used. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Index** (index). Index number in case the measurement was taken multiple times. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Instrument ID** (instrumentID). A unique identifier for an instrument. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Instrument Type** (insType). Type of instrument used to perform the measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Describe other instrument type, if applicable** (insTypeOth). Description of the instrument in case it is not listed in instrumentType. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**ISO639-1** (iso6391). The first part of the ISO 639 series of international standards for language codes. Part 1 covers the registration of two-letter codes. There are 183 two-letter codes registered as of June 2021. The registered codes cover the world's major languages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ISO639-2B** (iso6392B). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'B' specifies the bibliographic

## Attributes

code (B code). Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

**ISO639-2T** (iso6392T). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The ‘T’ specifies the terminological code (T code). Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ISO639-3** (iso6393). A set of international standards that lists short codes for language names. ISO 639-3 extends the ISO 639-2 alpha-3 codes with an aim to cover all known natural languages. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

**ISO639-6** (iso6396). A set of international standards that lists short codes for language names. ISO 639-6 builds off ISO639-3 with the use of four-letter codes, and allowing users to differentiate between variants of languages and language families, such as historical vs. revived versions of languages. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

**ISO 3166-1 alpha-2 country code** (isoCode). The ISO 3166-1 alpha-2 code, a two-letter country code which is also used to create the ISO 3166-2 country subdivision code and the Internet country code top-level domain. Status: active. First released: 2.1.0. Last updated: 3.0.0.

**ISO 3166-1 alpha-3 country code** (isoCodeX). The ISO 3166-1 alpha-3 code, a three-letter country code which may allow a better visual association between the code and the country names than the 3166-1 alpha-2 code. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**ISO 3166-2 code for country sub-domain** (isoZone). The ISO 3166-2 codes for the names of the principal subdivisions (e.g., provinces, states, departments, regions) of all countries coded in ISO 3166-1. Status: active. First released: 2.1.0. Last updated: 3.0.0.

## Sets

**Lab ID default deprecated** (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.

**Lab ID** (labID). Unique identifier for a laboratory. Status: depreciated. First released: 1.0.0. Last updated: 2.1.0.

**Language ID** (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.

**Language family** (langFam). Specifies the language family of a given language for translation and language tracking purposes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Language name** (langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**National language script** (langScript). The language(s) and script(s) used for the country's capital endonyms. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Last edited** (lastEdited). The date the entry was last updated. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Last name of contact** (lastName). Specifies the last name of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Link** (li). Link to an external reference that describes the geometry of the polygon. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**License** (license). The license of a dataset. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Access to local ha** (localHA). If this is 'no', the, data will not be available to local health authorities. If missing, data will be available to local health

## *Attributes*

authorities. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Manufacturer** (manufacturer). Manufacturer of an instrument. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure** (measure). A measurement or observation of any substance including a biological, physical or chemical substance. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Measure input (wide table)** (measureInput). The partID for the measure being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Measure license** (measureLic). Specifies the access and use licensing for a given single measurement. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure name (wide table)** (measureName). The measure referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Report ID** (measureRepID). Unique identifier for a measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Measure set report set ID** (measureSetRepID). Unique identifier that links together a group of related measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Method** (method). A procedure for collecting a sample or performing a measure. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Method input (wide table)** (methodInput). The partID for the method being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Method name (wide table)** (methodName). The method referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Sets

**Missingness Set** (missingnessSet). Missingness sets for measures, methods or attributes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure, Method, or Attribute Set Header** (mmaSet). The set for a measure, method, or attribute. Only applicable for categorical fields, and the categories that populate them. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Model** (model). Model number or version of the instrument. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**English name for countries** (nameEngl). English-language name of a given country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Official state name** (nameOfficial). Official english-language name of a given state. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Native Name** (natName). The native name of the language, i.e. what the language is called by its speakers. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**National Center for Biotechnology Information** (ncbi). NCBI header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NCBI - notes** (ncbiNotes). NCBI notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Nomenclature** (nomenclature). A classification system to report the measure class. Only applicable to variants, mutations, and diseases. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NORMAN** (norman). NORMAN header Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Attributes*

**NORMAN - notes** (normanNotes). Norman notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Notes** (notes). A note used to describe details that are not captured in other attributes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ISO 3166-1 numeric country code** (numCode). The ISO 3166-1 numeric code, a three-digit country code which is identical to that developed and maintained by the United Nations Statistics Division, with the advantage of script (writing system) independence, and hence useful for people or systems using non-Latin scripts. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**National Wastewater Surveillance System** (nwss). NWSS header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NWSS - notes** (nwssNotes). NWSS notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NWSS - process** (nwssProcess). NWSS process Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sequence Order** (order). The order a single calculation/data treatment takes within the full container pipeline/workflow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Organization ID** (organizationID). A unique identifier for the organization to which the reporter is affiliated. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Organization level** (orgLevel). The geographic level of an organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Organization sector** (orgSector). The sector of an organization Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Organization Type** (orgType). Specifies the type or purpose of a given organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sets

**Sample origin** (origin). An attribute of a sample specifying the origin. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Original Data Format** (originalFormat). The original structure or model used to record and store the data. This helps indicate if data have been transformed or mapped into the ODM structure. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Access to other prov deprecated** (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.

**Parent dataset ID** (parDatasetID). The datasetID that is a parent to another datasetID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Parent sample ID** (parent). If this sample has been pooled into one big sample for analysis this indicates the sample of the larger pooled sample. Status: depreciated. First released: 1.1.0. Last updated: 2.0.0.

**Parent Site ID** (parSiteID). The siteID that is a parent to another siteID; usually the sub-site will be contained in the parentSite. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Part type input (wide table)** (partTypeInput). The partID for the part type being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Part type name (wide table)** (partTypeName). The part type being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Postal or Zip Code** (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.

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**Access to phac** (phac). If this is ‘no’, the data will not be available to employees of the Public Health Agency of Canada - PHAC. If missing, data will be available to employees of the Public Health Agency of Canada - PHAC. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Public Health Action ID** (phActionID). Unique identifier for public health actions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PHAGE** (phage). PHAGE header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**PHAGE - notes** (phageNotes). PHAGE notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Country national phone prefix** (phone). International dialing code for the country. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Pipeline ID** (pipelineID). A primary key linked to a single measure (may be used multiple times), it is the shorthand for the data transformation pipeline used. Serves as a data pipeline identifier. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Polygon License** (poLic). The license for the availability of the polygon shapefile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Polygon ID** (polygonID). Unique identifier for the polygon. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Polygon ID Object** (polygonIDObject). The polygon ID Object in a polygon relationship. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Polygon ID Subject** (polygonIDSubject). The polygon ID subject in a polygon relationship. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Polygon relationship ID** (polygonRelID). Unique identifier for each row in the polygon relationships table. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Pooled** (pooled). Is this a pooled sample, and therefore composed of multiple child samples obtained at different sites Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Type of date for case reporting depreciated** (popDateTypeDep). Type of date used for confirmed cases. Typically, report or episode are reported. Onset and test date is not usually reported within aggregate data. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Protocol ID** (protocolID). A unique identifier for a given protocol. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol ID container** (protocolIDContainer). Unique identifier for the protocol and the steps and other protocols that make it up. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol ID object** (protocolIDObj). The object of the relationship between one protocol and another protocol or step, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol ID subject** (protocolIDSub). The subject of the relationship between one protocol and another protocol or step, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Synthetic ID for the protocolRelationships table** (protocolRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the protocolRelationships table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Protocol version** (protocolVersion). Specifies the version of a method set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Access to prov ha** (provHA). If this is ‘no’, this data will not be available to provincial health authorities. If missing, data will be available to provincial health authorities. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

## *Attributes*

**Pretreatment description - depreciated** (ptDescDep). If preTreatment then describe the treatment that was performed. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Access to public** (public). If this is ‘no’, this data will not be available to the public. If missing, data will be available to the public. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Purpose** (purpose). The reason the measure or sample was taken. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality flag** (qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample or measure. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality Indicator Set Header** (qualityIndSet). The quality set that corresponds to a given part. Only applicable for samples and measures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality report ID** (qualityReportID). A unique identifier for a given quality report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Date sample received** (recDate). The date the sample was received at the laboratory for analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Relationship between entities** (relationshipID). Attribute for specifying the relationship between a sample subject and object. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure relevance end date** (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.

## Sets

**Measure relevance start date** (relDateStart). The start date of the relevancy period of a measure - mostly for time-varrying metrics for sites or polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Primary reporting authority ID** (repOrg1). The primary or most responsible authority for rountine surveillance reports or findings, or where the site is located. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Secondary reporting authority ID** (repOrg2). The secondary, additional or alternative authority for rountine surveillance reports or findings, or where the site is located. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Reportable** (reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied. Status: active. First released: 2.0.0. Last updated: 2.1.0.

**Report date** (reportDate). The date a measure was reported. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Reporter ID depreciated** (reporterIDDep). Unique identifier for the person or organization that is reporting the data. Status: depreciated. First released: 1.1.0. Last updated: 2.0.0.

**Report table input (wide table)** (reportTableInput). The short name for the listed source table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Report table name (wide table)** (reportTableName). The report table that the wide name calls from. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Replicate Type** (repType). Attirbute of a sample, specifying whether the sample is unique, or a replicate. And if it is a replicate, what type of replicate is it? Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Attributes

**Role of contact** (role). Specifies the organizational role of a given contact. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample material** (saMaterial). Type of sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample ID** (sampleID). Unique identifier for a sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Sample ID object** (sampleIDObject). Populated by `sampleID` - this specifies the object of a sample relationship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample ID subject** (sampleIDSubject). Populated by `sampleID` - this specifies the subject of a sample relationship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Synthetic ID for the sampleRelationships table** (sampleRelationshipsID). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the sampleRelationships table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sample shed** (sampleShed). A geographic area, physical space, or structure. A sample is taken from a sampleshed for a representative measurement of a substance(s). Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Access to self** (self). If this is ‘no’, this data will not be shown on the portal when this reporter logs in. If missing, data will be available to this reporter. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Date sample was sent** (sentDate). Date that the sample was sent from the collection site to the lab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Composite Set ID** (setCompID). A composite ID generated by concatenating the ‘setID’ and ‘partID’ of a given row in the sets table. This allows

## Sets

for a unique primary key and robust relational database structure. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Set ID** (setID). The unique identifier of a value set. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Severity indicator** (severity). An indicator of the severity or seriousness of a quality flag. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sewer network file link deprecated** (sewerNetworkFileBLOB). Link to a file that has any detailed information about the sewer network associated with the site (any format). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Site ID default** (siteDef). Used as default when a new sample is created by this reporter. See ID in Site table. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Site ID** (siteID). Unique identifier for the location where a sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Level of Aggregation of a Sampling Site** (siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type of region is represented by the base sewershed. This can be used to pool together or average results across similar sewersheds, and avoid trying to average different scales of sewersheds together without a correction for size. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Site measure ID** (siteMeasureID). Unique identifier for wide table only. Use when all measures are performed on a single sample. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Site Type** (siteType). Type of site or institution where sample was taken. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sewer network file link depreciated 2** (snfl). Link to a file that has any detailed information about the sewer network associated with the site

## *Attributes*

(any format). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Wide name source** (source). The database or table sourced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Source Code** (sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Source Protocol ID** (sourceProtocol). A protocol that served as a basis for another protocol. This may be due to version changes, or a referencing a protocol that was later adapted. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol step source ID** (sourceStep). Specifies the protocol step which serves as a basis for a given protocol step. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sovereign status of a country** (sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Specimen** (specimen). The substance or thing upon which the observation was made. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Specimen input (wide table)** (specimenInput). The partID for the specimen being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Specimen name (wide table)** (specimenName). The specimen referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Specimen Set Header** (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.

## Sets

**Standard for Data Adjustment** (standard). A field where one can categorically record the standard to which something is being standardized (ie. PMMoV, Crassphage, Flow, etc.) or smoothed (ie. bayesian smoothing, central average smoothing, 7-days, time, etc.). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**State, Province, or Region** (stateProvReg). The state, province, or region where a site or organization is located; part of the address. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Protocol Step ID** (stepID). The unique identifier for a specific protocol step. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Step ID Object** (stepIDObj). The object of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Step ID Subject** (stepIDSub). The subject of the relationship between one protocol step and another step or protocol, within a given protocol ID container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Method step parent ID** (stepProvenanceID). A method step that served as a basis for another method step. This may be due to version changes, or a referencing a method set that was later adapted. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

**Protocol step version** (stepVer). Specifies the version of a given protocol step. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sewer network file blob** (storTempDef). A file blob that has any detailed information about the sewer network associated with the site (any format). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Summary** (summ). Short description of the assay and how it is different from the other assay methods. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## *Attributes*

**Public health threat targeted by action** (`threatTarget`). The pathogen or variant for which the designation or action is being taken. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Country code top-level domain** (`tld`). The internet top-level domain generally used or reserved for a country, sovereign state, or dependent territory identified with a country code. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Synthetic ID for the translations table** (`translationID`). A unique, autoincremental ID generated to produce a unique identifier and primary key for each row of the translations table. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Treatment ID** (`treatmentID`). A unique identifier for a single calculation/data treatment, a single data treatment identifier. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Type other depreciate2** (`tyOtDep2`). Description of the site when the site is not listed. See `siteType`. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Unit** (`unit`). The units of a measurement. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Unit input (wide table)** (`unitInput`). The partID for the unit being used in a wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Unit name (wide table)** (`unitName`). The unit referenced for the wide name. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Unit set** (`unitSet`). An idenfication of a set of units that can be used for a measure or method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sets

**U site measure ID** (uSiteMeasureID). Unique identifier for each measurement for a site. Status: depreciated. First released: 2.0.0. Last updated: 2.0.0.

**Coordinated universal time (UTC) zone** (utc). UTC – Time zone. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Coordinated universal time (UTC) zone in daylight savings** (utcDST). Time zone during Daylight Saving Time. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Value Treatment** (valTreat). A field which specifies what kinds of data treatments or the nature of the measurement value. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Value** (value). Value of a measure, observation or attribute. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 category** (version1Category). ODM V1 category Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 location** (version1Location). ODM V1 location Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 table** (version1Table). ODM V1 table Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM version 1 to 2 changes** (version1to2Changes). Changes for part between ODM v1 and V2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 variable** (version1Variable). ODM V1 variable Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Specified attribute (wide table)** (wideAttribute). Unique identifier for an attribute in a wide table only. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## *Classes*

**Measure identification (wide table)** (wideMeasure). Unique identifier for a measure in a wide table only. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wide Name** (wideName). Unique identifier for wide table only. Use when all measures are performed on a single sample at the same time and same laboratory. Suggestion: siteID\_sampleID\_LabID\_reportDate\_ID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wide name type** (wideNameType). The type of wide name generated. Possible options are measure, protocol or attribute. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Specified protocol (wide table)** (wideProtocol). Unique identifier for a protocol in a wide table only. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**World Sphere (W-SPHERE)** (wSphere). World Sphere header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**World Sphere (W-SPHERE) notes** (wSphereNotes). W-Sphere notes Status: active. First released: 1.0.0. Last updated: 2.0.0.

**English name of country sub-domains** (zoneName). The english-language name for a given country sub-domain. Status: active. First released: 2.1.0. Last updated: 2.1.0.

## **Classes**

(classes). A class is a collection of one or more related measures or methods within a group. A group can have one or more classes to describe different parts or the class.

**Alleles class** (allele). Measures and methods related to alleles. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sets

**Bacteria and Fungus Class** (bactFung). Measures and methods relating to bacteria. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Capacity class** (capacity). Measures and methods relating to capacity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Conductivity class** (conductivity). Measures and methods related to conductivity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Database and Data Repository Class** (database). Measures and methods related to databases and data repositories. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dilution Class** (dilution). Measures and methods relating to dilutions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Diseases (human) class** (disease). Measure and methods related to disease or infection in humans. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Flow class** (flowClass). Measures and methods related to flow. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Gas class** (gas). Measures and methods relating to gas and gases. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Humidity class** (humid). Measures and methods related to humidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Dictionary tables** (lookup). Tables to describe and support the ODM dictionary. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Mutations class** (mutation). Measures and methods related to mutations. Status: depreciated. First released: 2.0.0. Last updated: 2.3.0.

**Mutation panels class** (mutationPanel). Measures and methods related to a panel or list of more than one mutation from the same sequence read. Status: active. First released: 2.0.0. Last updated: 3.0.0.

## *Classes*

**Class not applicable** (naClass). Class is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Organism** (organism). Organism class Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Outbreak class** (outbreak). Measures and methods relating to public health outbreaks. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

**qPCR Class** (pcr). Measures and methods relating to qPCR. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**pH class** (pHClass). Measures and methods relating to pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Physical class** (physical). Measures and methods related to generic physical properties. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population Class** (popClass). Measures and methods relating to population (ie. Measures of population, location). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Precipitation class** (precipitation). Measures and methods related to precipitation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Program description tables** (programDescr). Tables used to describe surveillance and testing programs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Proteins class** (protein). Measures and methods related to proteins. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Results tables** (results). Tables used to record samples, measures and quality reports. Status: active. First released: 2.0.0. Last updated: 2.0.0.

*Sets*

**Genetic sequences class** (sequence). Measures and methods related to genetic sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Software Class** (software). Measures and methods related to software. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Speed class** (speed). Measures and methods relating to speed. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Standard concentrations class** (standardConc). Measures and methods relating to standard concentrations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Standard curve class** (standardCurve). Measures and methods relating to generating or recording a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Temperature class** (temperature). Measures and methods related to temperatures. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Time class** (timeClass). Measures and methods relating to time. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Turbidity class** (turbidity). Measures and methods relating to water and wastewater turbidity. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Variants class** (variant). Measures and methods relating to variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Weather class** (weather). Measures and methods relating to weather. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Compartments**

(compartments). The substance from which a sample was taken. For example, wastewater has component of “water”. Compartments are attributes of measures, methods, units, and aggregations.

**Air compartment** (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See Header for Compartment** (hCo). A indicator for wide-names that the compartment information is stored in a separate column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human compartment** (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Compartment not applicable** (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Surface compartment** (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Water compartment** (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Compartment sets**

(compartmentSets). Sets of compartments. Compartment sets are used to identify when a measure can be recorded for more than one compartment. For example, SARS-CoV-2 can be measured in people (humans), water, surface, or air.

Sets

### **Air compartment set**

(airCompartmentSet)A compartment set for measures and methods in the air compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Air compartment** (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Air and surface compartment set**

(airSurfaceCompartmentSet)A compartment set for measures and methods in the air or surface compartments. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Air compartment** (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Surface compartment** (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Air and water compartment set**

(airWaterCompartmentSet)A compartment set for measures and methods in the air or water compartments. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Air compartment** (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Compartment sets*

### **Any compartment set**

(anyCompartmentSet)A compartment set for measures and methods in any compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Air compartment** (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Surface compartment** (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Water compartment** (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Human compartment set**

(humanCompartmentSet)A compartment set for measures and methods in the human compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Human compartment** (hum). A measure or observation made about a human. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Compartment set not applicable**

(naCompartmentSet)Compartment not applicable. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Compartment not applicable** (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

### **Surface compartment set**

(surfaceCompartmentSet)A compartment set for measures and methods in the surface compartment. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Surface compartment** (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Surface and water compartment set**

(surfaceWaterCompartmentSet)A compartment set for measures and methods in the surface or water compartments. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Surface compartment** (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Water compartment** (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Water compartment set**

(waterCompartmentSet)A compartment set for measures and methods in the water compartment. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

**Water compartment** (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Compartment set for wide names**

(wideCompartmentSet)Compartment set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 3.0.0.

**Air compartment** (air). A measure or observation made from a substance in the air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See Header for Compartment** (hCo). A indicator for wide-names that the compartment information is stored in a separate column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Compartment not applicable** (naCompartment). Compartment not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Surface compartment** (surf). A measure or observation made from a substance on a surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Water compartment** (wat). A measure or observation made from a substance in the water, including wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Data types**

(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.

## Sets

**Binary Large Object (BLOB) data type** (blob). The data type for Binary Large Object (BLOB) data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Boolean data type** (boolean). The data type for boolean/binary data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Categorical data type** (categorical). The data type for categorical data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Date data type** (date). The data type for date data (does not include time). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Datetime data type** (datetime). The data type for date and time data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Float data type** (float). The data type for float data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Integer data type** (integer). The data type for integers. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See unit (data type)** (seeUnitData). The data type entry when the data type for a given entry is specified by the unit used. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Variable character data type** (varchar). The data type for variable character data. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Dictionary set type

(dictSets). Sets used to describe and group dictionary tables.

## **Airport Sheets Set**

(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.

**Airport lists worksheet** (airportLists). Parts lists used to generate airport and airplane data entry templates. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Airport Surveillance Template** (airportTemplate). The input template for airport and airplane surveillance in the EU. Status: active. First released: 2.0.0. Last updated: 2.1.0.

## **Contact table set**

(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.

**Address table** (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.

**Contact table** (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Organization table** (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in

## Sets

the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sites table** (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an 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.

## Crosswalk table set

(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.

**European Nucleotide Association Mapping Column** (enaMap). ENA header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**European Nucleotide Association (ENA) - notes** (enaNotes). ENA notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**National Center for Biotechnology Information** (ncbi). NCBI header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NCBI - notes** (ncbiNotes). NCBI notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NORMAN** (norman). NORMAN header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NORMAN - notes** (normanNotes). Norman notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**National Wastewater Surveillance System** (nwss). NWSS header Status: active. First released: 2.0.0. Last updated: 2.0.0.

*Dictionary set type*

**NWSS - notes** (nwssNotes). NWSS notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NWSS - process** (nwssProcess). NWSS process Status: active. First released: 2.0.0. Last updated: 2.0.0.

**PHAGE** (phage). PHAGE header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**PHAGE - notes** (phageNotes). PHAGE notes Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 category** (version1Category). ODM V1 category Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 location** (version1Location). ODM V1 location Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 table** (version1Table). ODM V1 table Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM version 1 to 2 changes** (version1to2Changes). Changes for part between ODM v1 and V2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ODM V1 variable** (version1Variable). ODM V1 variable Status: active. First released: 2.0.0. Last updated: 2.0.0.

**World Sphere (W-SPHERE)** (wSphere). World Sphere header Status: active. First released: 2.0.0. Last updated: 2.0.0.

**World Sphere (W-SPHERE) notes** (wSphereNotes). W-Sphere notes Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Sets

### **Dictionary reference table set**

(dictionaryRefTableSet)Reference or look-up tables. For example, the parts table describe all elements of the ODM, including tables, table headers, measures, methods, categories, and units. sets are collections of parts. For example, units can be grouped together in a unitSet. languages and translations support translations. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Countries look-up tables** (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Language Look-up table** (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Parts Look-up table** (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sets look-up table** (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Translation look-up table** (translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

*Dictionary set type*

**Zones look-up table** (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

## ERD table set

(erdTableSet)All tables listed in the Entity Relationship Diagram. The full ODM model is commonly referred to as “long” tables as it stores data with one measurement per row. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Address table** (addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (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.

**Contact table** (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Countries look-up tables** (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Dataset table** (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sets

**Instrument table** (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Language Look-up table** (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure report table** (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Measure set report table** (measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or 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.

**Organization table** (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Parts Look-up table** (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Polygon table** (polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

*Dictionary set type*

**Protocol relationships table** (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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.

**Protocols table** (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol steps table** (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Quality reports table** (qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Reporter table depreciated** (reportersDep). The table that contains information about a reporter of a sample, method, measure, or attribute. The short name for the table (partID) can be found in the instructions field. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Sample relationships table** (sampleRelationships). Table for recording the relationships between samples. Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in

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the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample report table** (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. Samples can be combined, split, stored and reused. The **Sample relationships** (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sets look-up table** (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sites table** (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an 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.

**Zones look-up table** (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

## Full dictionary sheets set

(fullDictionarySheetSet) Worksheets in the full Excel dictionary. The full dictionary is `ODM_full-dictionary.xlsx` Status: active. First

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Released: 2.0.0. Last updated: 2.0.0. <ul> <li> \*\*Address table\*\* <a href="/parts.html#addresses">(addresses)</a>. 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.  
</br>Status: active. First released: 2.0.0. Last updated: 2.0.0. </li> <li> \*\*Contact table\*\* <a href="/parts.html#contacts">(contacts)</a>. 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. </li> <li> \*\*Countries look-up tables\*\* <a href="/parts.html#countries">(countries)</a>. 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. </li> <li> \*\*Dataset table\*\* <a href="/parts.html#datasets">(datasets)</a>. 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. </li> <li> \*\*Instrument table\*\* <a href="/parts.html#instruments">(instruments)</a>. 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. </li> <li> \*\*Language Look-up table\*\* <a href="/parts.html#languages">(languages)</a>. 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. </li>

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**List worksheet** <a href="/parts.html#lists">(lists)</a>.
Parts lists for template dropdowns and other documentation.
</br>Status: active. First released: 2.0.0. Last updated:
2.0.0. </li> <li> **Measure report table** <a href="/parts.html#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. </br>Status: active. First
released: 1.0.0. Last updated: 2.0.0. </li> <li> **Measure
set report table** <a href="/parts.html#measureSets">(measureSets)</a>.
The table that identifies sets of measures. Examples of
measure sets include a set of replicates, dilutions (used
to generate a Ct curve) or varients that are identified in
a single sample. The short name for the table (partID) can
be found in the instructions field. </br>Status: active.
First released: 2.0.0. Last updated: 2.0.0. </li> <li>
**Organization table** <a href="/parts.html#organizations">(organizations)</a>.
The table that contains information about a laboratory.
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. </li> <li> **Parts Look-up
table** <a href="/parts.html#parts">(parts)</a>. 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. </li> <li> **Polygon table** <a href="/parts.html#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. </br>Status: active. First
released: 1.0.0. Last updated: 2.0.0. </li> <li> **Protocol
relationships table** <a href="/parts.html#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
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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. </li> <li> \*\*Protocols table\*\* <a href="/parts.html#protocols">(protocols)</a>. 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. </li> <li> \*\*Protocol steps table\*\* <a href="/parts.html#protocolSteps">(protocolSteps)</a>. 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. </li> <li> \*\*Quality reports table\*\* <a href="/parts.html#qualityReports">(qualityReports)</a>. 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. </li> <li> \*\*Sample relationships table\*\* <a href="/parts.html#sampleRelationships">(sampleRelationships)</a>. 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. </li> <li> \*\*Sample report table\*\* <a href="/parts.html#samples">(samples)</a>. The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other

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forms of water or liquid), air, or surface area taken from a site. Samples can be combined, split, stored and reused. The Sample relationships' (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sets look-up table** (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sites table** (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an 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.

**Summary worksheet** (summary). Summary sheet of the dictionary.xlsx file. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Translation look-up table** (translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wide name table** (wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Zones look-up table** (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found

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in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

### **List set**

(listSet)PartTypes that contain categories, sets, or lists. Used to generate documentation. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Aggregations** (aggregations). Statistical measures used to report a measure. Each measure reported as a number should be reported with an aggregation. The default aggregation is `sin`, which corresponds to a single measurement. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Aggregation scales** (aggregationScales). The scale of an aggregation set. Aggregation scales include quantitative and qualitative. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Attributes** (attributes). Attributes describe the who, where, when, and why of environmental surveillance. There are attributes for domain, specimen, compartment, or table. Attributes are one of the three main components or ways to report environment surviellence data. The other two components are measures and methods. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Classes** (classes). A class is a collection of one or more related measures or methods within a group. A group can have one more more classes to describe different parts or the class. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Compartments** (compartments). The substance from which a sample was taken. For example, wastewater has component of “water”. Compartments are attributes of measures, methods, units, and aggregations. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Data types** (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: 2.0.0.

**Domains** (domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature). Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Groups** (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. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measures** (measurements). The attribute to describe a part type of measures. All measures have `partType = “measure”`. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Methods** (methods). Procedures or steps for collecting samples or performing measures. For example, `methodExtract` is a method that describes the how a sample was extracted. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Missingness** (missingness). The part type for missingness values. Only used for the dictionary entries of parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Nomenclatures** (nomenclatures). A classification system to report the measure class. See `partID = nomenclatureID`. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Quality indicators** (qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Specimens** (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.

**Tables** (tables). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. An example of a table is `site` a collection of attributes such as site name and address to describe where environment samples are taken. PHES-ODM has report tables, but users can create their own tables as well. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Units** (units). The unit of the measurement. Every measurement must have a unit. Meaning, `units` are a mandatory field whenever a measurement is recorded. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Other report table set**

(otherReportTableSet)Additional tables that form the full data model. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Dataset table** (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Polygon table** (polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

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### **Protocol table set**

(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.

**Instrument table** (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Protocol relationships table** (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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.

**Protocols table** (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol steps table** (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Regular reports table set**

(regularReportTableSet)Tables used for daily reporting of new measurements and information on sample collection. Status: active. First Released:

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2.0.0. Last updated: 2.0.0.

**Measure report table** (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample report table** (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. Samples can be combined, split, stored and reused. The **Sample relationships** (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Template Sheet Set**

(templateSheetSet) Worksheets in the full generic ODM surveillance template (all tables). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Address table** (addresses). The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (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.

**Contact table** (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Dataset table** (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Instrument table** (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Language Look-up table** (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**List worksheet** (lists). Parts lists for template dropdowns and other documentation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure report table** (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Measure set report table** (measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or 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.

**Organization table** (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

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**Parts Look-up table** (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Polygon table** (polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Protocol relationships table** (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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.

**Protocols table** (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol steps table** (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Quality reports table** (qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample relationships table** (sampleRelationships). Table for recording the relationships between samples. Samples can be pooled or split. The

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sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample report table** (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. Samples can be combined, split, stored and reused. The **Sample relationships** (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sets look-up table** (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sites table** (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an 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.

## Domains

(domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen), physical measure (temperature).

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**All domains** (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.

**Biologic** (bio). A living organism or biological substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Chemical** (che). A chemical compound. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Domain not applicable** (naDomain). Not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Physical property** (phy). A physical property or object not characterized by life or chemistry. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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(groups). A collection of related measures. Used primary to group measurements and methods, this helps pare down the drop down list for a given measurement or methods.

**Acinetobacter Group** (acinetobacterGrp). A group of measures/methods related to acinebacter bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Adenovirus Group** (adenovirusGrp). A group of measures/methods related to Adenoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Anti-microbial resistance Group** (amrGrp). The group for measures and methods pertaining to anti-microbial resistant microbes (general). Status: active. First released: 2.1.0. Last updated: 2.1.0.

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**Anaplasma Group** (anaplasmaGrp). A group of measures/methods related to anaplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Astrovirus Group** (astrovirusGrp). A group of measures/methods related to astroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Babesia or Nuttallia Group** (babesiaGrp). A group of measures/methods related to babesia parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Bacteroides Group** (bacteroidesGrp). A group of measures/methods related to bacteroides bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Miscellaneous bacteria group** (bactMisc). A group of measures/methods related to miscellaneous bacteria. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Beta Coronavirus Group** (betaCoronaGrp). A group of measures/methods related to beta coronaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Beta-Lactamase Anti-microbial resistance Group** (bLacAMRGrp). The group for measures and methods pertaining to beta-lactamase-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Borrelia burgdorferi or Lyme Disease Group** (borreliaGrp). A group of measures/methods related to Borrelia burgdorferi or Lyme Disease. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Brucella Group** (brucellaGrp). A group of measures/methods related to brucella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Campylobacter Group** (campGrp). A group of measures/methods related to campylobacter bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Candida auris Group** (cAurisGrp). A group of measures/methods related to Candida auris. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Chikungunya Group** (chikungunyaGrp). A group of measures/methods related to chikungunya virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Chlamydia Group** (chlamydiaGrp). A group of measures/methods related to chlamydia bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Clostridium Group** (clostridiumGrp). A group of measures/methods related to clostridium bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Colistin Anti-microbial resistance group** (colAMRGrp). The group for measures and methods pertaining to colistin-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Collection group** (colGrp). A group of measurement-like attributes related to sample collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Cryptosporidium Group** (cryptosporidiumGrp). A group of measures/methods related to cryptosporidium parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SARS-CoV-2 Delta Variant Group** (deltaGrp). A group of measures/methods related to the SARS-CoV-2 Delta Variant. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Diphtheria Group** (diphtheriaGrp). A group of measures/methods related to the diphtheria bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Escherichia coli group** (ecoliGrp). A group of measures/methods related to Escherichia coli bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Enterovirus Group** (enterovirusGrp). A group of measures/methods related to enteroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Flavivirus (West Nile, Dengue, Zika) Group** (flavivirusGrp). A group of measures/methods related to flaviviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**FLiRT/SLip Variant Group** (flirtSLipGrp). The group for measures and methods pertaining to the FLiRT and SLip variants of SARS-CoV-2. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Influenza A Virus Group** (fluAGrp). A group of measures/methods related to Influenza A viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Influenza B Virus Group** (fluBGrp). A group of measures/methods related to Influenza B viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Influenza Virus General Group** (fluGrp). A group of measures/methods related to general influenza viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Gonococcus Group** (gonococcusGrp). A group of measures/methods related to gonococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Haemophilus Group** (haemophilusGrp). A group of measures/methods related to haemophilus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Hepatitis Group** (hepGrp). A group of measures/methods related to hepatitis viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Herpes Virus Group** (herpesGrp). A group of measures/methods related to herpes viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**HIV Group** (hivGrp). A group of measures/methods related to Human Immunodeficiency Virus (HIV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rhinovirus Group** (hrvGrp). A group of measures/methods related to rhinoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Integrase Anti-microbial resistance Group** (intAMRGrp). The group for measures and methods pertaining to integrase-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Klebsiella Group** (klebsiellaGrp). A group of measures/methods related to klebsiella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Legionella Group** (legionellaGrp). A group of measures/methods related to legionella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Lentivirus Group** (lentiGrp). A group of measures/methods related to lentiviruses, including viral vectors such as the Puro virus vector. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Listeria Group** (listeriaGrp). A group of measures/methods related to listeria bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Plasmodium or Malaria Group** (malariaGrp). A group of measures/methods related to plasmodium parasites or malaria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Measurement group** (measGrp). A group of measures that cannot be otherwise categorized. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measles Group** (measlesGrp). A group of measures/methods related to the measles virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Metabolite Group** (metaboliteGrp). A group of measures/methods related to metabolites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Miscellaneous attribute group** (miscAttr). A group of miscellaneous measurement-like attributes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Miscellaneous measure group** (miscMeas). A group of measures that cannot be otherwise categorized. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**MPox Clade I Group** (mpoxCldIGrp). A group of measures/methods related to Mpox Clade I (formerly “Monkey Pox”). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**MPox Clade II Group** (mpoxCldIIGrp). A group of measures/methods related to Mpox Clade II (formerly “Monkey Pox”). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**MPox Group** (mpoxGrp). A group of measures/methods related to Mpox (formerly “Monkey Pox”). Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Metapneumovirus Group** (mpvGrp). A group of measures/methods related to metapneumoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mumps Group** (mumpsGrp). A group of measures/methods related to the mumps virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mycoplasma Group** (mycoplasmaGrp). A group of measures/methods related to mycoplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Group not applicable** (naGroup). Used when there is no group; ie. group is not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2 Nimbus Variant Group** (nimbusGrp). A group of measures/methods related to the SARS-CoV-2 Nimbus Variant. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Norovirus GI Group** (noroGIGrp). A group of measures/methods related to norovirus GI. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Norovirus GII Group** (noroGIIGrp). A group of measures/methods related to norovirus GII. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Norovirus Group** (noroGrp). A group of measures/methods related to noroviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SARS-CoV-2 Omicron Variant Group** (omicronGrp). A group of measures/methods related to the SARS-CoV-2 Omicron Variant. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Orthopox Virus Group** (orthoGrp). A group of measures/methods related to orthopox viruses (excluding variola viruses). Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Papilomavirus Group** (papilomavirusGrp). A group of measures/methods related to papilomaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Parainfluenza Group** (parafluGrp). A group of measures/methods related to parainfluenza viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Bacteriophage Group** (phageGrp). A group of measures/methods related to bacteriophages. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**PMMoV Group** (pmmovGrp). A group of measures/methods related to the Pepper Mild Mottle Virus (PMMoV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Poliovirus Group** (polioGrp). A group of measures/methods related to polioviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population group** (popGrp). A group of measures/methods related to population-level factors. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Processing group** (procGrp). A group of measures/methods related to processing samples for analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Pseudomonas Group** (pseudomonasGrp). A group of measures/methods related to pseudomonas bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rickettsia Group** (rickettsiaGrp). A group of measures/methods related to rickettsia parasites. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rotavirus Group** (rotavirusGrp). A group of measures/methods related to rotaviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Respiratory syncytial virus (RSV) Group** (rsvGrp). Human Respiratory Syncytial virus (RSV). Status: active. First released: 2.0.0. Last updated: 2.1.2.

**Rubella Group** (rubellaGrp). A group of measures/methods related to the rubella virus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Salmonella Group** (salmonellaGrp). A group of measures/methods related to salmonella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sapovirus Group** (sapovirusGrp). A group of measures/methods related to sapoviruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SARS-CoV-2** (sarsCov2). A group of measures/methods related to the SARS-CoV-2 virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Shigella Group** (shigellaGrp). A group of measures/methods related to shigella bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Site features group** (siteFeat). A group of environmental measures/methods and those pertaining to the features of a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Staphylococcus Group** (staphGrp). A group of measures/methods related to staphylococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Streptococcus Group** (strepGrp). A group of measures/methods related to streptococcus bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Tetracycline Anti-microbial resistance Group** (tetAMRGrp). The group for measures and methods pertaining to tetracycline-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Treponema Group** (treponemaGrp). A group of measures/methods related to treponema bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Trichomonas Group** (trichomonasGrp). A group of measures/methods related to trichomonas bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Tuberculosis Group** (tuberculosisGrp). A group of measures/methods related to tuberculosis. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Francisella tularensis (tularemia) Group** (tularemiaGrp). A group of measures/methods related to Francisella tularensis. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Ureaplasma Group** (ureaplasmaGrp). A group of measures/methods related to ureaplasma bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Vancomycin Anti-microbial resistance Group** (vanAMRGrp). The group for measures and methods pertaining to vancomycin-related anti-microbial resistance. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Varicella Group** (varicellaGrp). A group of measures/methods related to varicella viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Vibrio Group** (vibrioGrp). A group of measures/methods related to vibrio bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Miscellaneous viruses group** (virusMisc). A group of measures/methods related to miscellaneous viruses. Status: depreciated. First released: 1.0.0. Last updated: 2.2.0.

**Vesicular Stomatitis Virus (VSV) Group** (vsvGrp). A group of measures/methods related to Vesicular Stomatitis Virus (VSV). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Water Quality Group** (waterQualityGrp). A group of measures/methods related to water quality. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Yersinia Group** (yersiniaGrp). A group of measures/methods related to yersinia bacteria. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## **Measures**

(measurements). The attribute to describe a part type of measures. All measures have partType = “measure”. mes

**a1306s delta-variant gene target** (a1306s). a1306s delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**a1918v delta-variant gene target** (a1918v). a1918v delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**a2710t omicron-variant gene target** (a2710t). a2710t omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**a63t omicron-variant gene target** (a63t). a63t omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**a67v omicron-variant gene target** (a67v). a67v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron Variant a67v del69 and del70 mutations** (a67vDel69Del70). Omicron Variant a67v mutation mutation, and del 69 and del70 mutations co-occurring Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Absolute humidity** (absHum). A measure of the total mass of water vapour present in the air per volume of air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Acinetobacter** (acinetobacter). Acinetobacter Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Adenovirus (F40/41)** (adenovirusF40). Adenovirus (F40/41) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Adenovirus 40** (adv40). Adenovirus serotype 40. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Adenovirus 41** (adv41). Adenovirus serotype 41. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Adenovirus F41 Fibre Gene Target** (advF41Fibre). Human Adenovirus Group F41 Fiber gene target Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Environmental temperature** (airTemp). Environmental temperature. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Alkalinity** (alkaline). Measure of alkalinity Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Assay Limit of Detection (LOD)** (alod). The minimum level of a target consistently detectable (e.g., with 95% probability) using the assay considering only the amplification and quantification steps of RT-qPCR. Status: active. First released: 2.2.0. Last updated: 3.0.0.

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**The number of ambiguous bases (Ns) normalized** (ambigNs). The number of ambiguous bases (Ns) normalized per 100 kilobasepairs (kbp). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Amplicon Size** (ampSize). The length of the amplicon generated by PCR amplification. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Anaplasma phagocytophilum** (aPhagocytophilum). Anaplasma phagocytophilum Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Arrival temperature** (arTemp). The temperature of a sample upon arrival at the laboratory for analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Astrovirus** (astrovirus). Astrovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Babesia** (babesia). Babesia Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Borrelia burgdorferi** (bBurgdorferi). Borrelia burgdorferi Status: active. First released: 2.2.0. Last updated: 2.2.0.

**bcov** (bcov). Measure of the amount of bovine coronavirus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Beta** (beta). B.1.351 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Cephamycin Beta-Lactamase-Resistance gene target** (blaCMY). Cephamycin Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**CTX-M Beta-Lactamase-Resistance gene target** (blaCTXM1). CTX-M Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Impenemase (IMP) Beta-Lactamase-Resistance gene target** (blaIMP). Impenemase (IMP) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase-Resistance gene target** (blaKPC). Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**New-Delhi Metallo- (NDM) Beta-Lactamase-Resistance gene target** (blaNDM). New-Delhi Metallo- (NDM) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**OXA-type Beta-Lactamase-Resistance gene target** (blaOXA48). OXA-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SHV Beta-Lactamase-Resistance gene target** (blaSHV). SHV-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**TEM Beta-Lactamase-Resistance gene target** (blaTEM). TEM-type Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase-Resistance-resistance gene target** (blaVIM). Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**5-Day carbonaceous biochemical oxygen demand** (bod5c). The quantity of oxygen utilized for the biochemical degradation of organic matter under standard laboratory procedures in five (5) days in the presence of a nitrification inhibitor, expressed in milligrams per litre (mg/l). Status: active. First released: 1.1.0. Last updated: 2.0.0.

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**5-day total biochemical oxygen demand** (bod5t). 5 day total biochemical oxygen demand. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Bovine respiratory syncytial virus group** (brsv). Bovine respiratory syncytial virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**BRSV-N** (brsvN). bovine respiratory syncytial virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Brucella** (brucella). Brucella Status: active. First released: 2.2.0. Last updated: 2.2.0.

**C28311T Omicron N1 Point Mutation** (c28311t). A measure of the C to T point mutation at position 28311 (C28311T) of the N1 probe, present in all Omicron sub-lineages. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Caffeine** (caff). Caffeine (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Calprotectin** (Calprotectin). Calprotectin is a calcium- and zinc-binding protein of the S-100 protein family which is mainly found within neutrophils and throughout the human body. The presence of calprotectin in faeces is a consequence of neutrophil migration into the gastrointestinal tissue due to an inflammatory process. Status: active. First released: 2.2.0. Last updated: 3.0.0.

**Campylobacter** (camp). Campylobacter. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Candida auris** (cAuris). The yeast species Candida auris, or C. auris. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Carbonaceous Biochemical Oxygen Demand** (cbod). A measure of the amount of oxygen required by microorganisms to break down organic carbon-based compounds in water over a specified period, typically five days at 20°C (CBOD). Unlike BOD (Biochemical Oxygen Demand), CBOD

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excludes oxygen demand from the oxidation of nitrogenous compounds (such as ammonia). It is used to assess organic pollution in wastewater and natural waters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Carbapenemase-encoding genes** (cbp). Carbapenemase-encoding genes. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Clostridium difficile** (cDiff). Clostridium difficile Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Corynebacterium diphtheriae** (cDip). Corynebacterium diphtheriae Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Centrifugation speed** (centSpeed). Centrifugation speed Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Chikungunya virus (CHIKV)** (chikv). Chikungunya virus (CHIKV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Chlamydia** (chlamydia). Chlamydia Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Campylobacter jejuni bacteria** (cJejuni). Campylobacter jejuni gene target/measurement Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Carbon Dioxide** (co2). A measure of an amount or concentration of carbon dioxide. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Chemical Oxygen Demand** (cod). Chemical oxygen demand. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Time from collection to storage** (col2Frdg). The amount of time between sample collection and the samples placement in stable storage/refrigeration. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Colistin resistance** (colis). Colistin-resistant bacteria. Status: active. First released: 2.1.0. Last updated: 2.1.0.

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**Concentration measure** (conc). Measurement of concentration (generalized) - designed for describing protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sample volume after concentration** (concVol). The total volume of a sample after the concentration step. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Water conductivity** (cond). Measurement of conductivity of sample or site. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**consensus genome length** (conGenLen). The length of the genome defined by the most common nucleotides at each position. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Covid-19** (cov). Covid-19 infection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2 measure** (cov2Me). Measure the amount of SARS-CoV-2 virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2-B.1.1.7** (covB117). Variant B.1.1.7 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**SARS-CoV-2-B.1.351** (covB135). Variant B.1.351 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**SARS-CoV-2-E** (covE). SARS-CoV-2 E gene. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**SARS-CoV-2 M Gene target** (covM). SARS-CoV-2 M gene (orf5) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2-N1** (covN1). SARS-CoV-2 nucleocapsid gene, allele 1. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**SARS-CoV-2-N2** (covN2). SARS-CoV-2 nucleocapsid gene, allele 2. Status: active. First released: 1.0.0. Last updated: 2.0.0.

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**SARS-CoV-2-N200** (covN200). SARS-CoV-2 nucleocapsid gene, amino acids 199-202. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2-N3** (covN3). SARS-CoV-2 nucleocapsid gene, allele 3. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**SARS-CoV-2-P.1** (covP1). Variant P.1 of the SARS-CoV-2 virus. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**SARS-CoV-2-RdRp** (covRdrp). SARS-CoV-2 RdRp gene. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**SARS-CoV-2 S Gene Target** (covS). S sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2 5' UTR Gene target** (covUTR5). SARS-CoV-2 5' UTR Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Clostridium perfringens** (cPerfrigens). Clostridium perfringens Status: active. First released: 2.2.0. Last updated: 2.2.0.

**crAssphage-N** (cra). crAssphage virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Creatinine** (crea). Creatinine (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Cryptosporidium** (cryptosporidium). Cryptosporidium Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Circulating vaccine-derived poliovirus type 2** (cVDPV2). Circulating vaccine-derived poliovirus type 2 Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number of cycles** (cyNum). The number of cycles of a PCR machine, or any other cycling process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**D339H Mutation** (d339h). The FLiT/SLip variant mutation D339H. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**d377y delta-variant gene target** (d377y). d377y delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**d3g omicron-variant gene target** (d3g). d3g omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**d63g delta-variant gene target** (d63g). d63g delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**d796y omicron-variant gene target** (d796y). d796y omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**d950n delta-variant gene target** (d950n). d950n delta-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ddcov\_e sars-cov-2 gene target** (ddcovE). ddcov\_e sars-cov-2 mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ddcov\_n sars-cov-2 gene target** (ddcovN). ddcov\_n sars-cov-2 mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron Variant 142-144 Deletion** (del142144). Omicron Variant 142-144 Deletion mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

**del143/145** (del143). 143 or 145 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Delta Variant 156-157 Deletion** (del156157). Delta Variant 156-157 Deletion mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

**del 157/158** (del157). 157 or 158 deletion delta-variant gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**del2084/2084** (del2084). 2084 or 2084 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**del212/212** (del212). 212 or 212 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron Variant 142-14431-33 Deletion** (del3133). Omicron Variant 142-14431-33 Deletion mutation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**del3674/3676** (del3674). 3674 or 3676 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**del69/70** (del6970). 69 or 70 deletion omicron-variant mutation gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Delta** (delta). B.1.617.2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Dengue Virus Type 1** (den1). Dengue virus, Type 1, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue Virus Type 2** (den2). Dengue virus, Type 2, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue Virus Type 3** (den3). Dengue virus, Type 3, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue Virus Type 4** (den4). Dengue virus, Type 4, general measurement Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue** (dengue). Dengue virus, general measurement Status: active. First released: 2.2.0. Last updated: 2.2.0.

**depth of coverage threshold** (depCovThresh). The threshold used as a cut-off for the depth of coverage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Detected Lineage or Clade Name** (detLinClade). The measurement for reporting detected lineage or clade information - used as an “other” for measurements not already captured in the ODM structure. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Dilution factor** (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.

**Point dilutions** (dillute). Exact concentration or dilutions for generating a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Dissolved oxygen** (dissOxy). Measure of dissolved oxygen in liquid medium Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DNA Fragment Length** (dnaFragLen). The length of the DNA fragment generated by mechanical shearing or enzymatic digestion for the purposes of library preparation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue Virus E Gene** (dnvE). Dengue Type 2-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue Virus NS5 Gene** (dnvNS5). Dengue Type 1-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dengue Virus prM Gene** (dnvprM). Dengue Type 3 and 4-specific gene target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Duration time of a method** (duration). The duration of time for a given method as described in protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**e156g delta-variant gene target** (e156g). e156g delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**e484a omicron-variant gene target** (e484a). e484a omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Enteropathogenic Escherichia coli (EAEC)** (eaec). Enteropathogenic Escherichia coli (EAEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Epstein–Barr virus (EBV)** (ebv). Epstein–Barr virus (EBV), formerly known as Human gammaherpesvirus 4 Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Escherichia coli** (ecoli). Concentration of bacteria that are passed through the faecal excrement of humans, livestock and wildlife Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Enterohemorrhagic Escherichia coli (EHEC)** (ehec). Enterohemorrhagic Escherichia coli (EHEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Enteroinvasive Escherichia coli (EIEC)** (eiec). Enteroinvasive Escherichia coli (EIEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Enterovirus** (enterovirus). Enterovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rainfall** (envRnF). Rainfall, i.e. amount of precipitation in the form of rain. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Ground snow depth** (envSnwD). Total depth of snow on the ground. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Snowfall** (envSnwF). Snowfall, i.e. amount of precipitation in the form of snow. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Enteropathogenic Escherichia coli (EPEC)** (epec). Enteropathogenic Escherichia coli (EPEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sarbecovirus-specific E sars-cov-2 gene target** (eSarbec). Sarbecovirus-specific E sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ESBL-encoding genes** (esbl). Extended-spectrum beta-lactamase-encoding genes. Status: active. First released: 2.1.0. Last updated: 2.1.0.

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**Estimated frequency of reads** (estFreqReads). Estimated frequency of reads in a sequencing assay Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Enterotoxigenic Escherichia coli (ETEC)** (etec). Enterotoxigenic Escherichia coli (ETEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SARS-CoV-2 exoN gene (nsp14)** (exoNnsp14). SARS-CoV-2 exoN gene (nsp14) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Extraintestinal pathogenic Escherichia coli (ExPEC)** (expec). Extraintestinal pathogenic Escherichia coli (ExPEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Extraction Recovery Percent** (extractRecov). The percentage of spiked in or endogenous compound used to assess extraction recovery of nucleic acids. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Extraction volume of sample** (exvol). Extraction volume of sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**F456L Mutation** (f456l). The FLiRT/SLip variant mutation F456L. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Male-specific (F+) coliphage - general** (fColiphage). Male-specific (F+) coliphage - general Status: active. First released: 2.2.0. Last updated: 2.2.0.

**F+ DNA coliphage** (fDNA). F+ DNA coliphage Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Fecal coliform count** (fecalCol). Measure of prevalence of fecal coliform bacteria Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Final volume** (finVol). The final volume of a testing solution or sample. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**FLiRT Variants** (flirtV). FLiRT is the name given to an entire family of COVID-19 subvariants that are gaining dominance. They've evolved from the JN.1 subvariant. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Flow rate** (floRate). Wastewater volumetric flow rate at the sample collection location over the 24-hr period during which the sample was collected. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Flow volume** (flowVol). Volume of influent. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Influenza virus measure** (flu). General influenza virus measure Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Influenza A virus** (fluA). Influenza A virus. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Influenza virus A1** (fluA1). Influenza virus A1 type Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Influenza virus A1 and A2 combined** (fluA1A2c). Measure of influenza virus A1 and A2 combined, usually due to single fluorescence channel. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**influenza virus A2** (fluA2). influenza virus A2 type Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Influenza virus B** (fluB). Influenza virus B type Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Influenza A H5 hemagglutinin gene** (fluH5hema). Measure of the H5 hemagglutinin gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Influenza A M gene** (fluIAVm). A measure of the M gene found in Influenza A viruses (IAV). The virus has segmented RNA genome and 7th segment, M gene, encodes 2 proteins. M1 is a matrix protein and M2 is

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a membrane protein. The M gene may be involved in determining host tropism. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Influenza A N1 neuraminidase gene** (fluN1neur). Measure of the N1 neuraminidase gene from the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**F-Specific RNA bacteriophages** (fRNABact). A measure for amount of F-Specific RNA bacteriophages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**F+ RNA coliphage** (fRNAColi). F+ RNA coliphage Status: active. First released: 2.2.0. Last updated: 2.2.0.

**F-Specific RNA bacteriophages, G2** (frnaG2). A measure for amount of G2 F-Specific RNA bacteriophages. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Field sample temperature** (fst). Temperature that the sample is stored at while it is being sampled. This field is mainly relevant for composite samples which are either kept at ambient temperature or refrigerated while being sampled. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Francisella tularensis** (fTularensis). Francisella tularensis Status: active. First released: 2.2.0. Last updated: 2.2.0.

**g215c delta-variant gene target** (g215c). g215c delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**g339d omicron-variant gene target** (g339d). g339d omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**g496s omicron-variant gene target** (g496s). g496s omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**g662s delta-variant gene target** (g662s). g662s delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Gamma** (gam). P.1 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**genome completeness** (genComplete). The percentage of expected genes identified in the genome being sequenced. Missing genes indicate missing genomic regions (incompleteness) in the data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**H5N1 avian influenza A virus (IAV)** (h5n1). General measurement for the Highly Pathogenic Avian Influenza Virus (HPAIV), the H5N1 Influenza A Virus (IAV) subtype. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Haemophilus ducreyi** (hDucreyi). Haemophilus ducreyi Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SARS-CoV-2 hel gene (nsp13)** (hel). SARS-CoV-2 hel gene (nsp13) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Hepatitis A** (hepA). Hepatitis A Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Hepatitis B** (hepB). Hepatitis B Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Hepatitis C** (hepC). Hepatitis C Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Hepatitis E** (hepE). Hepatitis E Status: active. First released: 2.2.0. Last updated: 2.2.0.

**hep g armored rna** (hepGRna). Measure of the amount Hepatitis G Armored RNA. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**HF183 Bacteroides 16S** (hf183). Human-Specific HF183 Bacteroides 16S rRNA Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**5-hydroxyindoleacetic acid (5-HIAA)** (hiaa5). 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.

**Haemophilus influenzae** (hInfluenzae). Haemophilus influenzae Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Immunodeficiency Virus (HIV)** (hiv). Human Immunodeficiency Virus (HIV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**See Header for Measure** (hMe). An indicator to show in a wide-name that measure information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Metapneumovirus (HMPV)** (hmpv). Human Metapneumovirus (HMPV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Parainfluenza Virus (HPIV)** (hpiv). Human Parainfluenza Virus (HPIV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Papiloma Virus (HPV)** (hpv). Human Papiloma Virus (HPV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Rhinovirus (HRV)** (hrv). Human Rhinovirus (HRV) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Rhinovirus (HRV) A** (hrvA). Human Rhinovirus (HRV) A Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Human Rhinovirus (HRV) B** (hrvB). Human Rhinovirus (HRV) B Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Human Rhinovirus (HRV) C** (hrvC). Human Rhinovirus (HRV) C Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Herpes Simplex Virus** (hsv). Herpes Simplex Virus Status: active. First released: 2.2.0. Last updated: 2.2.0.

**i1566v omicron-variant gene target** (i1566v). i1566v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**i3758v omicron-variant gene target** (i3758v). i3758v omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**i82t delta-variant gene target** (i82t). i82t delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Ibuprofen** (ibu). Ibuprofen (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Industrial input** (indusIn). Percentage of total wastewater input coming from industrial sources. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Influent equilibration** (influEqui). Binary indicator for whether a site stores influent wastewater prior to treatment to equilibrate flow rates. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Inhibition measure** (inhibMe). Parameter to report whether or not inhibition was detected in the sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Omicron Variant ins214epe Insertion** (ins214epe). Omicron Variant ins214epe Insertion mutation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Integrase Class I gene target** (integraseCl1). Integrase anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Combined ip2 and ip4 sars-cov-2 gene target** (ip2ip4). Combined ip2 and ip4 sars-cov-2 gene target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**JN.1.7 Variant** (jn17V). The JN.1.7 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**JN.1 Variant** (jn1V). The JN.1 variant is a subvariant of Omicron variant BA.2.86, and contains several mutations that are associated with escape from vaccine-mediated immune protection. The source of the FLiRT variants of SARS-CoV-2. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**k856r omicron-variant gene target** (k856r). k856r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Klebsiella pneumoniae** (klebsiellaPneu). Klebsiella pneumoniae Status: active. First released: 2.2.0. Last updated: 2.2.0.

**KP.1.1 Variant** (kp11V). The KP.1.1 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**KP.1 Variant** (kp1V). The KP.1 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**KP.2 Variant** (kp2V). The KP.2 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**KP.3.1.1 Variant** (kp311V). The KP.3.1.1 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**KP.3 Variant** (kp3V). The KP.3 variant of SARS-CoV-2, one of the FLiRT variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Omicron Variant l24s mutation** (l24s). Omicron Variant l24s mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

**l452r delta-variant gene target** (l452r). l452r delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**L455S Mutation** (l455s). The FLiRT/SLip variant mutation L455S. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**l981f omicron-variant gene target** (l981f). l981f omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Lachnospiraceae (Lachno3)** (lachno3). Human-associated bacteria in the family Lachnospiraceae (Lachno3), often used as microbial source tracking markers for human fecal pollution tracking in environmental waters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lambda** (lambda). C.37 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**LB.1 Variant** (lb1V). The LB.1 variant of SARS-CoV-2,similar to other FLiRT variants but with an additional mutation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Legionella** (legionella). Legionella Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Listeria** (listeria). Listeria Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Limit of Blank (LOB)** (lob). The highest concentration of a target analyte (DNA or RNA) that can be expected in a blank sample (a sample with no target DNA/RNA) while still considering the sample as negative. Defines the upper limit of “noise” or background signal that should not be confused with a true positive. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Limit of detection (LOD)** (lod). Limit of detection, ie. the minimum level of a genetic target. Status: active. First released: 1.1.0. Last updated: 3.0.0.

**Limit of detection (LOD) - sewage** (lodSewa). Limit of detection, ie. the minimum level of a genetic target, for sewage samples. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Limit of quantification (LOQ)** (loq). Sample limit of quantification (LOQ) is defined as “the concentration of a target that can be quantified with an acceptable level of precision when present in a sample” (Ahmed et al., 2021). Status: active. First released: 1.1.0. Last updated: 3.0.0.

**LP.8.1 Variant** (lp81V). The LP.8.1 variant of SARS-CoV-2, a Omicron subvariant of JN.1, and FLiRT variant. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Omicron Variant LPPA24S mutation** (lppa24s). Omicron Variant LPPA24S mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sample Material Characteristics** (matChar). A site measurement for describing the qualitative characteristics of the sample material in situ (ie. The material from which the sample is collected. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Concentration Factor** (mCF). Concentration Factor (CF) is the degree to which the concentration observed in the final qPCR assay volume has been magnified compared to concentration of the analyte in the original

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sample (see Box 2.1 Protocol). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MCR-1.1 Colistin-resistence gene target** (mcr11). The MCR-1.1 colistin anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Measles** (measles). Measles Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Other Measure** (measOth). Other measure, not otherwise specified in measures. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Other Measure Description** (meOthDe). Description of other measure (measOtherDesc). Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Effective Sample Size/Volume** (mESV). Effective Sample Size/Volume (ESV) is the amount of the original sample size/volume that was actually analyzed in a qPCR reaction (see Box 2.1 Protocol) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mycoplasma genitalus** (mGenitalus). Mycoplasma genitalus Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Murine Hepatitis Virus** (mhv). A measure for amount of murine hepatitis viurs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**minimum post-trimming read length** (minPTLength). The threshold used as a cut-off for the minimum length of a read after trimming. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Method Limit of Detection (LOD)** (mlod). The minimum level of a target necessary for its consistent detection considering all sample processing steps as in the definition of SLOD), but considering biases attributable to method losses. The MLOD is experimentally determined

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using a rigorous and iterative testing approach and it is sensitive to the recovery surrogate used and the sample matrix encountered. Status: active. First released: 2.2.0. Last updated: 3.0.0.

**Mpox** (mpox). The virus known as Mpox, previously also known as Monkey Pox. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Mpox B6R Gene Target** (mpxB6R). Human MPox Virus (hMPXV) gene target. Envelope protein gene CDC Assay; selective for MPXV. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Clade I Mpox C3L Gene Target** (mpxC3L). Human MPox Virus (hMPXV) Clade I gene target. hMPXV C3L primers and probe detect Clade I viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mpox Clade I** (mpxClI). The virus known as Mpox, previously also known as Monkey Pox, Clade I virus type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mpox Clade II** (mpxClII). The virus known as Mpox, previously also known as Monkey Pox, Clade II virus type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mpox & Orthopox E9L-NVAR Gene Target** (mpxe9lNVAR). Human MPox Virus (hMPXV) gene target for Orthopoxvirus DNA polymerase. CDC Assay detects all hMPXV clades and non-variola Orthopox viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mpox & Orthopox E9L-OPX3 Gene Target** (mpxe9lOPX3). Human MPox Virus (hMPXV) gene target using the generic orthopox virus OPX3. Lower sensitivity for MPox. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mpox Clade I F3L Gene Target** (mpxF3L). Human MPox Virus (hMPXV) Clade I gene target, F3L Status: active. First released: 2.3.0. Last updated: 2.3.0.

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**Mpox G2R-G Gene Target** (mpxG2RG). Human MPox Virus (hMPXV) gene target using the G2R\_G primers and probe which detects all MPox Virus strains. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mpox G2R-NML Gene Target** (mpxG2RNML). Human MPox Virus (hMPXV) gene target using the G2R\_NML primers and probe which detects all MPox Virus strains. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Clade II Mpox G2R-WA Gene Target** (mpxG2RWA). Human MPox Virus (hMPXV) Clade II gene target, measured with G2R\_WA primers and probe to detects Clade II viruses. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mpox GT Molecular Gene Target** (mpxGTmol). Human MPox Virus (hMPXV) gene target - this specific measure and gene target are proprietary to GT Molecular Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Methicillin-resistant Staphylococcus aureus (MRSA)** (mrsa). Methicillin-resistant Staphylococcus aureus (MRSA) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**ms2 coliphage** (ms2Col). Measure of the amount of ms2 coliphage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Mycobacterium tuberculosis** (mTuberculosis). Mycobacterium tuberculosis Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mu** (mu). B.1.621 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**murine coronavirus** (muCo). Measure of the amount of murine coronavirus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Mumps** (mumps). Mumps Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Measures

**N sars-cov-2 gene target** (n). N sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Combined N1 and N2 sars-cov-2 gene target** (n1n2). Combined N1 and N2 sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron Variant n211i mutation** (n211i). Omicron Variant n211i mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**N50** (n50). The length of the shortest read that, together with other reads, represents at least 50% of the nucleotides in a set of sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Omicron Variant n679k mutation** (n679k). Omicron Variant n679k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Omicron Variant n856k mutation** (n856k). Omicron Variant n856k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Omicron Variant n969k mutation** (n969k). Omicron Variant n969k mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**NB.1.8.1 variant (Nimbus)** (nb181V). The Nimbus variant of SARS-CoV-2 (NB.1.8.1), descendant of the recombinant variant XDV.1.5.1. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**number of base-pairs sequenced** (nBPSeq). The number of total base pairs generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**number of contigs** (nContig). The number of contigs (contiguous sequences) in a sequence assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Neisseria gonorrhoeae** (nGonorrhoeae). Neisseria gonorrhoeae Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Ammonia and Ammonium as Nitrogen** (nh3nh4). Ammonia and Ammonium combined concentration, as Nitrogen Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Ammonium Nitrogen** (nH4N). Ammonium nitrogen concentration, as N. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**niid\_2019-ncov\_n sars-cov-2 gene target** (niid19). niid\_2019-ncov\_n sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Norovirus** (noro). Norovirus. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Norovirus G1** (noroG1). Norovirus genogroup 1 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Norovirus G2** (noroG2). Norovirus genogroup 2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sarbecovirus-specific N sars-cov-2 gene target** (nSarbec). Sarbecovirus-specific N sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2 nsp1 Gene target** (nsp1). SARS-CoV-2 nsp1 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp10 Gene target** (nsp10). SARS-CoV-2 nsp10 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp11 Gene target** (nsp11). SARS-CoV-2 nsp11 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp15 Gene target** (nsp15). SARS-CoV-2 nsp15 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**SARS-CoV-2 nsp16 Gene target** (nsp16). SARS-CoV-2 nsp16 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp2 Gene target** (nsp2 ). SARS-CoV-2 nsp2 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp3 Gene target** (nsp3 ). SARS-CoV-2 nsp3 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp4 Gene target** (nsp4 ). SARS-CoV-2 nsp4 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp5 Gene target** (nsp5 ). SARS-CoV-2 nsp5 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp6 Gene target** (nsp6 ). SARS-CoV-2 nsp6 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp7 Gene target** (nsp7 ). SARS-CoV-2 nsp7 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp8 Gene target** (nsp8 ). SARS-CoV-2 nsp8 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 nsp9 Gene target** (nsp9 ). SARS-CoV-2 nsp9 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**number of total reads** (nTotRead). The total number of non-unique reads generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Number of NTCs per Run** (numNTC). The number of no-template controls included in each PCR instrument run. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**number of unique reads** (nUniRead). The number of unique reads generated by the sequencing process. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**coronavirus OC43** (oc43). Measure of the amount of coronavirus OC43. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron BA.1** (omicr1). Omicron B.1.1.529 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron BA.2** (omicr2). Omicron BA.2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron BA.2.75** (omicr275). Omicron BA.2.75 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron BA.4** (omicr4). Omicron BA.4 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Omicron BA.5** (omicr5). Omicron BA.5 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Orthophosphates** (ophos). Ortho-phosphate concentration. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**SARS-CoV-2 orf10 Gene target** (orf10). SARS-CoV-2 orf10 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf14 Gene target** (orf14). SARS-CoV-2 orf14 Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ORF1a sars-cov-2 gene target** (orf1a). ORF1a sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ORF1ab sars-cov-2 gene target** (orf1ab). ORF1ab sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ORF1b sars-cov-2 gene target** (orf1b). ORF1b sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**SARS-CoV-2 orf3a Gene target** (orf3a). SARS-CoV-2 orf3a Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**SARS-CoV-2 orf3b Gene target** (orf3b). SARS-CoV-2 orf3b Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf6 (ns6) Gene target** (orf6). SARS-CoV-2 orf6 (ns6) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf7a Gene target** (orf7a). SARS-CoV-2 orf7a Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf7b (ns7b) Gene target** (orf7b). SARS-CoV-2 orf7b (ns7b) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf8 (ns8) Gene target** (orf8). SARS-CoV-2 orf8 (ns8) Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf9b Gene target** (orf9b). SARS-CoV-2 orf9b Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SARS-CoV-2 orf9c Gene target** (orf9c). SARS-CoV-2 orf9c Gene target Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Oxidation reduction potential (ORP)** (orp). Oxidation-reduction potential (ORP) measures the ability of a lake or river to cleanse itself or break down waste products, such as contaminants and dead plants and animals. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Variants Other** (otherV). Used for reporting variants detected for which a specific measureID doesn't already exist. The ODM team will periodically migrate collected responses in this category into set measureIDs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Delta Variant p100l mutation** (p100l). Delta Variant p100l mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Omicron Variant p13l mutation** (p13L). Omicron Variant p13l mutation Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Delta Variant p2046l mutation** (p2046l). Delta Variant p2046l mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Delta Variant p2287s mutation** (p2287s). Delta Variant p2287s mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Omicron Variant p3395h mutation** (p3395h). Omicron Variant p3395h mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Delta Variant p681r** (p681r). Delta Variant p681r mutation & gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Paraxanthine (PARA)** (para). A metabolite of the common central nervous system stimulant caffeine, measured levels of paraxanthine have been found to be less affected by the genetic heterogeneity and population structure than caffeine is, and it may serve as a useful population biomarker in wastewater. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**percent read contamination** (percContam). The percent of the total number of reads identified as contamination (not belonging to the target organism) in a sequence dataset. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**percent Ns across total genome length** (percNLength). The percentage of the assembly that consists of ambiguous bases (Ns). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**pH** (ph). pH measurement Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Phagotyping Results** (phagetype). The phagotyping results from an organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Pseudomonas virus phi6** (phi6). Measure of the amount of pseudomonas virus phi6. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Total phosphorous** (phos). Total phosphorous Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Total Phosphates** (phostot). Total phosphates Status: active. First released: 1.1.0. Last updated: 2.0.0.

**PHRED quality score** (phred). PHRED Quality Score For Sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Plasmodium** (plasmadium). Plasmodium Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Polygon Population** (polyPop). An attribute of a polygon, which specifies the population of that polygon. A rough estimate of the number of human residents. Status: active. First released: 2.0.0. Last updated: 2.3.0.

**Populated area type** (popAreaType). Type of populated area being sample (ie. urban, rural) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population density** (popDensity). Measure of population density of a site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population Served** (popServ). An measure of a site, which specifies the population of/population served by a given site. Status: active. First released: 2.0.0. Last updated: 2.3.0.

**Population Served - Interval** (popServRange). Population served by a site, when reported as an interval. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PMMoV-CP** (ppmv). Pepper mild mottle virus capsid protein gene region Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Precipitation - general** (precip). General measure of precipitation, type not specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Storage temperature prior to concentration** (preConcTemp). The temperature at which a sample was stored between collection and concentration. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Storage time prior to concentration** (preConcTime). Length of time for which a sample is stored between collection and concentration. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Storage temperature prior to extraction** (preExtractTemp). The temperature at which a sample was stored between concentration and extraction. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Storage time prior to extraction** (preExtractTime). Length of time for which a sample is stored between concentration and extraction. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**presampling activity** (presampAct). A measure for recording any relevant activities that occur upstream of the sampling source. For example, recording that the river one is sampling from flows through farmland, or that filtration and/or sedimentation occurred at the wastewater treatment plant before the sample was collected. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Pre-sampling weather** (preSampWeath). Weather leading up to, but not including, the day of sampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Pretreatment** (pretreat). Was the sample chemically treated in anyway with the addition of stabilizers or other Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Pseudomonas** (pseudomonas). Pseudomonas Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Puro virus** (puro). Measure of the amount of puro virus. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Poliovirus type 2** (pv2). Poliovirus type 2 Status: active. First released: 2.2.0. Last updated: 2.2.0.

**q19e omicron-variant gene target** (q19e). q19e omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**q493r omicron-variant gene target** (q493r). q493r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**q498r omicron-variant gene target** (q498r). q498r omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**q954h omicron-variant gene target** (q954h). q954h omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**r203m delta-variant gene target** (r203m). r203m delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**R346T Mutation** (r346t). The FLiRT/SLip variant mutation R346T. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**dPCR Rain Percentage** (rainPerc). The percentage of droplets tha fall between the major positive and negative population in digital droplet PCR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**IP2 rdrp sars-cov-2 gene target** (rdrpIP2). IP2 rdrp sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**IP4 rdrp sars-cov-2 gene target** (rdrpIP4). IP4 rdrp sars-cov-2 gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Recombinant Lineage Variant** (recomb). A catch-all measure for viruses of non-specified and recombinant lineages, defined as those virsues wherein viruses of two different parent strains coinfect the same host cell

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and interact during replication to generate virus progeny that have some genes from both parents. Recombination generally occurs between members of the same virus type (e.g., between two influenza viruses or between two herpes simplex viruses). This is particularly common in the evolution of coronaviruses and sarbecoviruses. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Relative humidity** (relHum). The unit of relative humidity, or the air-water mixture. The ratio of the partial pressure of water vapor in the mixture to the equilibrium vapor pressure of water over a flat surface of pure water at a given temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**replicate number** (repNum). The replicate number for a Ct or Cq value - used for specifying out a protocol standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Rickettsia** (rickettsia). Rickettsia Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Ribonuclease P (RNase P)** (rnaseP). Ribonuclease P (RNase P) (usually measured as a human fecal indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rotavirus** (rotavirus). Rotavirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Respiratory syncytial virus A and B combined** (rsvAB). Human Respiratory Syncytial Virus Type A (RSV A) and Type B (RSV B). Status: active. First released: 2.1.0. Last updated: 2.1.3.

**Respiratory syncytial virus A** (rsvAMe). Human Respiratory Syncytial Virus Type A (RSV A). Status: active. First released: 2.1.0. Last updated: 2.1.3.

**Respiratory syncytial virus B** (rsvB). Human Respiratory Syncytial Virus Type B (RSV B). Status: active. First released: 2.1.0. Last updated: 2.1.3.

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**Respiratory syncytial virus** (rsvMe). Human Respiratory Syncytial virus (RSV), generic measure. Status: active. First released: 2.0.0. Last updated: 2.1.2.

**RSV N-gene** (rsvN). Human Respiratory syncytial Virus, N-gene region. Status: active. First released: 2.1.3. Last updated: 2.1.3.

**Rubella** (rubella). Rubella Status: active. First released: 2.2.0. Last updated: 2.2.0.

**s2083i omicron-variant gene target** (s2083i). s2083i omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**s371l omicron-variant gene target** (s371l). s371l omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**s373p omicron-variant gene target** (s373p). s373p omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**s375f omicron-variant gene target** (s375f). s375f omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**s477n omicron-variant gene target** (s477n). s477n omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Salinity** (salinity). Measurement of salinity/salt content Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Salmonella** (salmonella). Salmonella Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sample volume** (samVol). The volume of a given sample. Status: active. First released: 2.2.0. Last updated: 3.0.0.

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**Sapovirus** (sapovirus). Sapovirus Status: active. First released: 2.2.0. Last updated: 2.2.0.

**sequence assembly length** (seqAssLen). The length of the genome generated by assembling reads using a scaffold or by reference-based mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Serological Variant (Serovar)** (serovar). The serovar of the organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Settled solids** (settsol). Amount of settled solids from a wastewater sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sewage equivalent** (sewEq). Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sewage travel time** (sewTrTi). A measure of sewage travel time, often approximate, from sewage source to the sampling site. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Shaker agitation speed** (shaker). The speed/agitation level for a shaker plate/shaker platform. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Shigella** (shigella). Shigella Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sample Limit of Detection (LOD)** (slod). The minimum level of a target within a sample that would be consistently detectable considering all sample processing steps, from sample concentration leading up to and including amplification and quantification steps of RT-qPCR. In this Protocol, the SLOD is the concentration factor-adjusted ALOD, which provides a theoretical estimate of the minimum concentration in the original sample that would yield consistent detection of the target, assuming no method losses. Status: active. First released: 2.2.0. Last updated: 3.0.0.

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**Specific humidity** (specHum). Measure for specific humidity, the unit is the ratio of the mass of water vapour and the mass of total air. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Spike Concentration** (spikeConc). Concentration of the recovery efficiency target in a spike matrix and recovery assay. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SARS-CoV-2 Spike gene (orf2)** (spikeGene). SARS-CoV-2 Spike gene (orf2) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Shiga-toxin-producing Escherichia coli (STEC)** (stec). Shiga-toxin-producing Escherichia coli (STEC). Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Storage temp** (sTemp). Temperature that the sample is stored at in Celsius. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Stercobilin** (sterobilin). Stercobilin is a tetrapyrrolic bile pigment and is one end-product of heme catabolism. It is the chemical responsible for the brown color of human feces and was originally isolated from feces in 1932. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Storage time** (stoTim). Length of time that a sample was in storage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Strain ID** (strainID). The strain identifier for a given organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Streptococcus pneumoniae** (strepPneu). Streptococcus pneumoniae Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sub-variant or lineage** (subVar). A unit used to report a specific genetic lineage, or to specify that a reported variant is a sub-variant of another. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sucralose** (suc). Sucralose (usually measured as a human fecal chemical indicator) Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Surveillance Level** (survLevel). The scale or level of surveillance being done at a site. Ie. Is it institutional, is it only for a single building, or is it for a whol municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**t19r delta-variant gene target** (t19r). t19r delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**t3646a delta-variant gene target** (t3646a). t3646a delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**t547k omicron-variant gene target** (t547k). t547k omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**t9i omicron-variant gene target** (t9i). t9i omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**TaqPath N sars-cov-2 gene target** (taqpatN). TaqPath N sars-cov-2 mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**TaqPath S sars-cov-2 gene target** (taqpatS). TaqPath N sars-cov-2 mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Total Dissolved Solids (TDS)** (tds). Total dissolved solids Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sample temperature** (temp). Temperature of the sample measured in degrees Celcius Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Nucleic acid template volume** (tempVol). The volume of DNA or RNA template used for PCR. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Measures

**TetW Tetracycline-resistance gene target** (tetW). The tetW tetracycline anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Total Kjeldahl Nitrogen** (tkn). A measure of Total Kjeldahl Nitrogen; ie. the sum of nitrogen bound in organic substances, nitrogen in ammonia (NH<sub>3</sub>-N) and in ammonium (NH<sub>4</sub><sup>+</sup>-N) in the chemical analysis of soil, water, or waste water. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Total Nitrogen** (tn). Total nitrogen concentration, as N. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Treponema pallidum** (tPallidum). Treponema pallidum Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Total solids concentration** (ts). Total solids concentration Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Total suspended solids** (tss). Total suspended solids Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Concentration of total suspended solids** (tssConc). Total suspended solids concentration of the wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Turbidity** (turb). A measure for the turbidity of water, or a liquid sample, quantifying the relative clarity or opacity of a liquid. Highly indicative of water quality. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Trichomonas vaginalis** (tVaginalis). Trichomonas vaginalis Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Tube weight empty** (tWeighE). The weight of the tube used for analysis while empty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Tube weight full** (tWeighF). The weight of the tube used for analysis while full of analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

**Ureaplasma** (ureaplasma). Ureaplasma Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Urobilin or urochrome** (urobilin). Urobilin or urochrome is the chemical primarily responsible for the yellow color of urine. It is a linear tetrapyrrole compound that, along with the related colorless compound urobilinogen, are degradation products of the cyclic tetrapyrrole heme. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**V1104L Mutation** (v1104l). The FLiRT/SLip variant mutation V1104L Status: active. First released: 2.2.0. Last updated: 2.2.0.

**v2930l delta-variant gene target** (v2930l). v2930l delta-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

**VanA-A Vancomycin-resistance gene target** (vanAA). The VanA-A vancomycin anti-microbial resistance gene target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Vancomycin resistance** (vanc). Vancomycin resistant bacteria. Status: active. First released: 2.1.0. Last updated: 2.1.0.

**Varicella** (varicella). Varicella Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Vibrio** (vibrio). Vibrio Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Size in volume** (vol). Total volume of water or sludge sampled. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Volatile suspended solids** (vss). Volatile suspended solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Volatile suspended solids - ignition** (vssIg). A water quality measure, captured by via the loss on ignition of the mass of measured total suspended solids. This ignition generally takes place in an oven at a temperature of 550 °C to 600 °C. It represents the amount of volatile matter present in

## *Measures*

the solid fraction of the measured solution. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Verotoxin-producing Escherichia coli (VTEC)** (vtec). Verotoxin-producing Escherichia coli (VTEC) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Wastewater temperature** (watTemp). Temperature of the wastewater. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Weather (time of sampling)** (weath). A measure for weather captured through qualitative categories; part of a larger suite of weather measures that may be useful when collecting samples from outdoor sources. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**West Nile** (westNile). West Nile Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Wind Speed** (wind). A measure for wind speed; part of a larger suite of weather measures that may be useful when collecting samples from outdoor sources. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Delta Variant wt214 gene target** (wt214). Delta Variant wt214 gene target Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Wastewater treatment plant designed capacity** (wwtpCap). A measure for the designed capacity of a wastewater treatment plant, in terms of how much water it was designed to be able to hold and process. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**XEC Variant** (xecV). The XEC variant of SARS-CoV-2, a subvariant of the Omicron strain. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**y505h omicron-variant gene target** (y505h). y505h omicron-variant mutation gene target Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

**Yersinia enterocolitica** (yEnterocolitica). Yersinia enterocolitica Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Zika** (zika). Zika Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Methods

(methods). Procedures or steps for collecting samples or performing measures. For example, `methodExtract` is a method that describes the how a sample was extracted. `met`

**AMR Analysis Software** (amrSoft). Software use to analyse bacterial genomes and genes for anti-microbial resistance (AMR). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bacterial testing method** (bactMeth). Description of the bacterial testing/detection method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lineage- or Clade-analysis Software** (cladeAn). Software tool or pipeline for determining the clade or lineage of an organism. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Consensus Sequence Software** (conSeqSoft). Software use to run consensus sequence on sequencing analyses. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Deduplication Method** (dedup). Sequencing and PCR deduplication method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Dehosting Method** (dehost). Sequencing and PCR dehosting method. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## *Methods*

**Extraction Blank - Control** (extBlank). Binary Y/N indicator for if extraction blank was used as a control for the nucleic acid extraction process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Nucleic acid extraction method** (extraction). Description of the nucleic acid extraction method. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Genomic Target Enrichment** (gte). The molecular technique used to selectively capture and amplify specific regions of interest from a genome. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Inhibition method** (inhibMeth). Description of the method used to evaluate molecular inhibition. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Library Preparation Kit** (libraryKit). The name of the DNA/RNA library preparation kit used to generate the library being sequenced. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Concentration method** (methodConc). Description of the method to concentrate a wastewater sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Pasteurized sample** (pasteur). Binary indicator for whether a sample was pasteurized as part of its processing. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**PCR Action/Activity** (pcrAct). Describes a given PCR cycle for delineating more method information. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**PCR method** (pcrmeth). Description of the PCR method. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Population assessment method** (popAs). Method for assessing the population count for a site/polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Genetic primer** (primer). Method ID used for indicating the primer used for a PCR or sequencing assay. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality assurance method** (qaqc). Quality assurance and quality control method. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Quality Control Method** (qcMethod). Method for quality control or assessment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Raw Sequence Data Processing Method** (rawSeqProc). The software/library/pipeline used to process the raw sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sequencing read mapping software name** (readMapper). The name of the bioinformatics software tool used to align short DNA or RNA sequence reads (obtained from high-throughput sequencing technologies like Illumina, PacBio, or Oxford Nanopore) to a reference genome or transcriptome. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Resuspension method** (resuspension). Describes the method used for resuspending material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Retained Element** (retainedElement). The element retained after centrifugation, filtration, solid separation, etc. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Collection other depreciated** (sampleTypeOther). Description for other type of method not listed in collection. depreciated. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Standard curve frequency** (scf). A method for specifying the frequency over which a standard curve (or ‘Master Curve’) is used. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Methods*

**Genetic sequencing script version** (scriptVersion). Used to specify the script or script version used to extract summary information (i.e. coverage and mutation frequency statistics, etc.) from the sequencing output. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sequence Assembly Software** (seqAss). The name of the software/toolkit/pipeline used for assembling sequences from reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sequencing Layout** (seqLay). The layout of genetic material used in sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sequencing QC Pipeline** (seqQC). The quality control pipeline for sequencing or PCR data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sequencing selection method** (seqSel). The primer sequence selection method used in sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sequencing Strategy** (seqStrat). The sequencing strategy used for an analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Serotyping Method** (seroMeth). The method used to determine the serovar. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Shipped on ice** (shipOnIce). Was the sample kept cool while being shipped to the lab Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Solid separation** (solidSep). Process used to separate solid and liquid phases of the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Spike material** (spikeMat). Material into which the recovery efficiency control target is spiked. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Sets

**Recovery efficiency spike target** (spikeTarget). Method specifying the recovery efficiency control target. This matches on to the the spike material method ID. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Standard Curve Calculation Method** (stdCurveMet). Describes the specific approach used for calculating a standard curve. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sample Storage Medium** (stoMed). The medium used to store a sample before final analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nucelic Acid Template Type** (tempType). Specifies whether a PCR or sequencing used RNA or DNA as the template for the reaction. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Type other deprecate** (tyOtDep). Description for other type of sample not listed in Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

## Missingness

(missingness). The part type for missingness values. Only used for the dictionary entries of parts.

**Data Not Collected** (dnc). A missingness value for when when data was not measured or collected; an analysis not run, etc. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Missing data** (miss). A general missingness value for missing data, used when data is not included for an unknown reason. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## *Missingness sets*

**Not applicable** (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Not a number** (nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, ...) Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Not reported** (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Null** (null). A logical representation of a statement that is neither TRUE nor FALSE. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Restricted data** (restrict). Missing data is withheld because it is restricted access. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Undisclosed or Not Provided** (undisc). A value has been recorded, however it was not included in the dataset. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Missingness sets**

(missingnessSets). Set of missingness values. Examples of missingness sets may include NR or NA esclusive sets, or general all-purpose sets.

### **General missingness set**

(genMissingnessSet)The general set for missingness values. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Data Not Collected** (dnc). A missingness value for when when data was not measured or collected; an analysis not run, etc. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Missing data** (miss). A general missingness value for missing data, used when data is not included for an unknown reason. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Not applicable** (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Not a number** (nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, ...) Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Not reported** (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Null** (null). A logical representation of a statement that is neither TRUE nor FALSE. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Restricted data** (restrict). Missing data is withheld because it is restricted access. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Undisclosed or Not Provided** (undisc). A value has been recorded, however it was not included in the dataset. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Not reported, Not applicable missing set

(nrNAMissingnessSet)Not reported, Not applicable missing set. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Not applicable** (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Not reported** (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Measure, method, or attribute sets**

(mmaSets). A set of categories. For example, site type has a list of different sites, such as a wastewater treatment plant, a septic tank, or a pumping station. Only used for the dictionary entries of parts.

### **Public Health Action Type Value Set**

(actionTypeSet)A set of valid categories for the public health action type field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Antimicrobial resistance (AMR) classification** (amrClass). A public health action type wherein threat level classification has been done on a strain of antimicrobial resistant (AMR) microbes, and communicated to the public. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Control measure implementation** (contMeasImp). A public health action type wherein authorities have begun implementing infection control measures. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Outbreak declaration** (outb). Public health action type used to indicate outbreak status. Given that when outbreaks occur, full data on case counts may not be available or completely accurate, using this measure indicates that case counts may be approximate. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Public health advisory** (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.

**Surveillance alert** (survAlert). A public health action type wherein authorities have made a decision about surveillance and communicated the alert. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Threat designation** (threatDes). A public health action type wherein a threat level is determined and communicated by authorities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## All Public Health Actions Set

(allActionsSet)A set of all valid categories for public health action, regardless of action type. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Border closure** (borderClos). A measure shutting entry points to limit cross-border movement and disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Critical priority pathogen** (cpp). A microorganism with resistance to multiple drugs and a high threat to human health. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Decreased surveillance** (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**De-escalated variant** (dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Hand hygiene advisory** (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Stay-at-home order** (homeOrder). A directive requiring people to remain at home except for essential activities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

*Measure, method, or attribute sets*

**High priority pathogen** (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Increased surveillance** (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lockdown** (lockdown). Broad restrictions on movement and activities within a region to control disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mask mandate** (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mask recommendation** (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Medium priority pathogen** (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**End of Outbreak** (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Outbreak - on-going** (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Declared outbreak or Outbreak start** (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Public health emergency (outbreak)** (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

*Sets*

**Quarantine recommendation** (quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Routine surveillance** (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Resistant strain identified** (rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**School closure** (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Social distancing measures** (socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Targetted surveillance initiated** (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Travel ban** (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Travel warning** (travWa). A notice advising against travel to certain areas due to health risks. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Change to Vaccine Schedule** (vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Variant of concern** (voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for

*Measure, method, or attribute sets*

assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Variant of interest** (voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**variant under monitoring** (vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Data Adjustment Standard Value Set**

(allStandardSet)Set of valid input values for the standard field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Bayesian Smoothing applied** (bayesSmooth). This data treatment smooths the measurement value using bayesian smoothing techniques. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Central average smoothing applied** (caSmooth). This data treatment smooths the measurement value using central average smoothing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Crassphage Standarized** (crassStand). This data treatment standardizes the measurement value to concentration levels of crassphage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**7-day smoothing of values** (day7Smooth). This data treatment smooths the measurement value across 7-days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Flow Standardized** (flowStand). This data treatment standardizes the measurement value to flow rates. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gaussian distribution stanrdized/Normalized** (gauss). Standardize the data to a gaussian/normal distribution, such that the data have a mean of zero and a standard deviation of one. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PMMoV Standardized** (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.

**Time standardized** (timeStand). This data treatment standardizes the measurement value against time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Antimicrobial Resistance (AMR) Classification Value Set

(amrClassSet)A set of valid categories for the public health action field, where the action type is ‘antimicrobial resistance (AMR) classification’. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Critical priority pathogen** (cpp). A microorganism with resistance to multiple drugs and a high threat to human health. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**High priority pathogen** (hpp). A resistant organism of serious concern, requiring urgent attention. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Medium priority pathogen** (mpp). A resistant organism of moderate concern, needing ongoing monitoring. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Resistant strain identified** (rsi). Confirmation that a specific microorganism is resistant to one or more antimicrobial agents. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **AMR Software Set**

(amrSoftSet)The valid set of AMR analysis software categories. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**ABRicate Software** (abricate). Software tool for screening bacterial genomes against multiple resistance databases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**AMRFinderPlus Software** (amrFinderPlus). Software tool that was developed by NCBI to detect AMR genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ARG-ANNOT Annotation Tool** (argAnnotSoft). Software annotation tool for antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CARD Resistance Gene Identifier (RGI)** (cardRGI). Software tool that is a part of the Comprehensive Antibiotic Resistance Database (CARD) used for annotation and prediction of AMR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DeepARG Software** (deepARG). Software tool that predicts AMR genes using deep learning on metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MetaPhlAn Software** (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.

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**ResFinder Tool** (resFinderSoft). Software tool that identifies acquired antimicrobial resistance genes in bacterial genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ShortBRED Software** (shortBRED). Software tool that screens for known AMR genes in shotgun metagenomic sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SRST2 Software** (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**StarAMR Software** (starAMR). Software tool that is used to detect AMR genes in genome assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Bacterial testing method set

(bactMethSet)The set capturing containing all of the valid methods for the bacterial testing method. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Antimicrobial gradient test** (agt). A gradient strip test is performed according to the manufacturer's instructions: a short plastic or paper strip impregnated with antibiotic is placed on inoculated agar. On the standardised 100 mm Petri dish, two strips may be placed, while on the larger 150 mm Petri dish, up to six antibiotics may be tested simultaneously. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bacterial culture** (bacCul). Growing a bacterial culture to test for bacterial presence. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gram stain** (gramSt). After the sample is taken, the Gram stain is colored purple. Then, a solvent is added to the stain. When the solvent combines with bacteria in a sample, the bacteria will either stay purple or

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turn pink or red. If the bacteria remain purple, they are Gram-positive. If the bacteria turn pink or red, they are Gram-negative. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Growth in enrichment broth** (growBroth). The selective cultivation of microorganisms in a nutrient-rich liquid medium to increase their concentration before analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Boolean value set**

(booleanSet)Set that contains the valid possible values for a boolean measure (TRUE or FALSE). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**FALSE** (FALSE). Boolean data type = FALSE Status: active. First released: 1.0.0. Last updated: 2.3.0.

**TRUE** (TRUE). Boolean data type = TRUE Status: active. First released: 1.0.0. Last updated: 2.3.0.

## **Calculation type set**

(calcTypeSet)The set of valid inputs for the calculation type field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Normalization Calculation Type** (normalization). A transformation of data to have a mean of zero and a standard deviation of one, commonly used to compare values across different datasets or units. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Predictive Modeling Calculation Type** (predictiveModels). A statistical or machine learning approach used to estimate future values or outcomes based on historical data patterns. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Smoothing Calculation Type** (smoothing). A technique used to reduce short-term fluctuations in data to better reveal underlying trends or patterns, such as using moving averages or splines. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Standardization Calculation Type** (standardization). A method used to scale data to a common range or distribution, often to enable fair comparisons across different variables, time periods, or locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Lineage- or Clade-analysis Software Set

(cladeAnSet)Valid category set for lineage or clade analysis software types. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Bayesian Evolutionary Analysis by Sampling Trees (BEAST) Software** (beast). A lineage or clade analysis software tool for estimating evolutionary relationships and divergence times in a Bayesian framework. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ClonalFrameML Software** (clonalFrameML). A lineage or clade analysis software tool for reconstructing phylogenetic relationships considering recombination, used in bacterial lineage analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**IQ-TREE Software** (iqTree). A lineage or clade analysis software tool for constructing phylogenetic trees with clade support. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**LINEAGE Software** (lineage). LINEAGE - Tool for bacterial lineage analysis, often applied to genome sequences in epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**mash Software** (mash). A lineage or clade analysis software tool for the clustering-based method of lineage and clade analysis, comparing large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**MrBayes Software** (mrBayes). A lineage or clade analysis software tool for bayesian inference of phylogeny, used for inferring clade relationships with high accuracy. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nextstrain Software** (nextstrain). A lineage or clade analysis software tool for real-time tracking of pathogen evolution, with tools for clade and lineage analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**OrthoFinder Software** (orthoFinder). OrthoFinder - For orthogroup identification and phylogenetic tree building, often useful in evolutionary clade studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Pangolin Software** (pangolinSoft). A lineage or clade analysis software tool used for lineage assignment in SARS-CoV-2 and other viral genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PhyloPhlAn Software** (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.

**PhyloSuite Software** (phyloSuite). An integrated platform for sequence alignment, phylogenetic reconstruction, and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PhyML Software** (phyML). A lineage or clade analysis software tool that builds phylogenetic trees using maximum likelihood methods, with clade confidence assessments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**RaxML Software** (raxML). A lineage or clade analysis software tool, popular for rapid maximum likelihood-based phylogenetic tree building with clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**SNAPP Software** (snapp). A lineage or clade analysis software tool in BEAST for species delimitation and clade analysis in population genomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Statistical Analysis of Metagenomic Profiles (STAMP) Software** (stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**StrainPhlAn Software** (strainPhlAb). A lineage or clade analysis software tool within MetaPhlAn for strain-level lineage analysis from metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Taxonium Software** (taxonium). Taxon - 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.

**TreeTime Software** (treeTime). A lineage or clade analysis software tool for phylodynamic analysis, often for molecular clock dating and clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Ultrafast Sample placement on Existing tRees (UShER) Software** (usher). A lineage or clade analysis software tool that adds new genomes to an existing phylogenetic tree, widely used for SARS-CoV-2 clade assignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Collection Approximate Time Period Set

(collAppxSet)The category set of valid inputs for the collGenT attribute field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Afternoon** (aft). Sample was collected in the afternoon, sometime after lunch. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Evening** (eve). Sample was collected in the evening, late in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Morning** (morn). Sample was collected at some point in the morning, early in the day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Night** (night). Sample was collected at night, between sunset and sunrise. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Sample collection set**

(collectSet)Methods for collection samples. Sample collection methods include water, air, and surface. See the attribute **Compartment set** of the sample collection method. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Area proportional sample** (areaPr). An area proportional sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Automatic composite sampling** (autoComp). A composite sampler which is automated to collect and store multiple wastewater samples across multiple time points. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Automatic sequential sampling** (autoSeq). A composite sampler which is automated to collect and combine multiple samples of equal volume taken at a set time interval. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bag Mediated Filtration** (bagFilt). Sample was collected using bag-mediated filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Composite sample - archival** (comp). A composite sample, usually generated by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

Sets

**Cone-shaped sampling** (cone). Instrument 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.

**Core sampling** (core). Instrument 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.

**COSCa ball** (cosca). COSCa passive sampling device. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Flow proportional sample** (flowPr). A flow proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Grab sample** (grb). A single large representative grab sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Horizontal grab sampling** (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.

**Manual Composite Sample** (manComp). Specifies a composite sample where the sub-samples were collected manually. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Moore swab passive sample** (moorSw). Moore swab passive sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Passive Sample - General** (passiveGen). Used to specify a passive sampling method not otherwise specified was used to collect the sample. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Surface swab** (surfSw). Surface swab. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Time proportional sample** (timePr). A time proportional composite sample generally collected by an autosampler. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Passive (trap) sampling** (trap). A composite sampler that passively collects a sample without use of electricity or a battery. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Vacuum sludge sampling** (vac). Instrument 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.

**Vertical grab sampling** (vertGrb). 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 waste from a tank. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Volume proportional sample** (volPr). A volume proportional sample generally collected by an autosampler. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Consensus Sequence Software Set**

(conSeqSoftSet)The valid set of consensus sequencing software categories. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**AliView** (aliView). Sequencing software that is a user-friendly alignment editor with consensus sequence options. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bcftools** (bcfTools). Sequencing software that works with SAMtools to call variants and produce consensus sequences from alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**BioEdit** (bioEdit). Sequencing software that offers sequence alignment and visualization, used to manually generate consensus sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BWA (Burrows-Wheeler Aligner)** (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Clustal Omega** (clustalO). Sequencing software that is widely used for multiple sequence alignment and producing consensus sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Emboss Cons** (embossCons). Sequencing software that is part of the EMBOSS suite, generates consensus sequences from multiple alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Geneious** (geneious). Sequencing software that is popular for sequence assembly, alignment, and consensus sequence generation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MAFFT** (mafft). Sequencing software that performs multiple sequence alignment, commonly used in consensus sequence generation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Molecular Evolutionary Genetics Analysis (MEGA)** (mega). Sequencing software that provides tools for sequence alignment and consensus sequence extraction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SAMtools** (samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**SeqMan Pro (Lasergene)** (seqManPro). Sequencing software that is for de novo sequence assembly and consensus calling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SPAdes** (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Ugene** (uGene). Sequencing software that offers alignment and consensus sequence generation features. Status: active. First released: 3.0.0. Last updated: 3.0.0.

### **Control Measure Implementation Value Set**

(contMeasImpSet)A set of valid categories for the public health action field, where the action type is ‘control measure implementation’. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Border closure** (borderClos). A measure shutting entry points to limit cross-border movement and disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Stay-at-home order** (homeOrder). A directive requiring people to remain at home except for essential activities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lockdown** (lockdown). Broad restrictions on movement and activities within a region to control disease spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mask mandate** (maskMand). A legal requirement for individuals to wear masks in specified settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**School closure** (schoolClos). Temporary shutdown of educational institutions to prevent disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Social distancing measures** (socialDist). Policies encouraging or enforcing physical space between individuals in public or private settings. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Data Repository Set

(dataRepoSet)The mma set for all valid input categories for the dataRepo field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Antibiotic Resistance Genes Database (ARDB)** (ardb). An archive for antibiotic resistance genes and associated information. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BacMet Database** (bacMet). Database of antibacterial biocide and metal resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Comprehensive Antibiotic Resistance Database (CARD)** (card-Dtbase). Database that provides high-quality reference sequences for resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DNA Data Bank of Japan (DDBJ)** (ddbj). DNA Data Bank of Japan (DDBJ) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DDBJ sequence Read Archive (DRA)** (dra). The DNA Data Bank of Japan (DDBJ) sequence read archive (DRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**European Nucleotide Archive (ENA)** (ena). European Nucleotide Archive (ENA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Enterobase archives** (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**GenBank Archives** (genBank). GenBank Archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Global Initiative on Sharing All Influenza Data (GISAID) archives** (gisaid). Global Initiative on Sharing All Influenza Data (GISAID) archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**GitHub** (github). GitHub external data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Genome Sequence Archive (GSA)** (gsa). Genome Sequence Archive (GSA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**International Nucleotide Sequence Database Collaboration (INSDC) Archives** (insdc). International Nucleotide Sequence Database Collaboration (INSDC) Archives - often includes ENA, NCBI, or DDBJ inputs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Internal reference** (internalRef). Reference an internal (i.e. private) database within the user's own organization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MEGARes database** (megares). A comprehensive database of antimicrobial resistance genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**NCBI's Pathogen Detection Isolates Browser** (ncbiPDIB). Database that tracks AMR in pathogens and provides resistance profiles for pathogens worldwide. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**National Database of Antibiotic Resistant Organisms (NDARO)** (ndaro). A database maintained by the USCDC with genomic data on AMR organisms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Open Science Foundation (OSF)** (osf). Open Science Foundation project/data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PATRIC/RAST Database** (patricRast). Database that hosts resistance gene annotations within their microbial genome data resources. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ResFinder Database** (resFinderDbase). nomenclature from the National Center for Biotechnology Information Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sequence Read Archive (SRA)** (sra). Sequence Read Archive (SRA). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Zenodo** (zenodo). Zenodo open data storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Deduplication Method Set

(dedupSet)The valid set of deduplication method categorical inputs. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**bamUtil Dedup** (bamUtil). A deduplication method that removes duplicate reads directly from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BWA-MEM with Duplicate Marking** (bwaMEM). A deduplication method that is used with SAMtools or Picard to mark duplicates during read mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BBMap's Clumpify** (clumpify). A deduplication method that groups identical sequences, often used to deduplicate reads efficiently. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**FastUniq** (fastUniq). A deduplication method that is specifically designed to remove duplicates in paired-end sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MitoZ Deduplication** (mitoZ). A deduplication method that is used primarily for mitochondrial genomes but can handle deduplication by read clustering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Picard MarkDuplicates** (picard). A deduplication method within the Picard suite that marks duplicate reads in BAM files based on mapped location. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SAMtools rmdup** (samRmdup). A deduplication method that identifies and removes PCR duplicates based on alignment data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SeqKit rmdup** (seqKitRmdup). A deduplication method that works within SeqKit for duplicate removal in FASTA/FASTQ files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Unique Molecular Identifier (UMI) Tagging** (umiTag). A deduplication method that adds unique tags to individual DNA fragments, allowing identification and removal of duplicate reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**UMI-tools** (umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Dehosting Method Set**

(dehostSet)The valid set of dehosting method categorical inputs. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

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**BBMap Reformat** (bbmapReform). A dehosting software that filters out host sequences by aligning to reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BMTagger** (bmtagger). A dehosting software developed by NCBI for identifying and removing host sequences based on local alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bowtie2** (bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that maps reads against a host reference genome to remove aligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Host Subtraction with Bowtie2 & SAMtools** (bowtie2XSam). A combined workflow for dehosting where reads mapped to the host are removed from downstream analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BWA for Host Filtering** (bwaHost). A dehosting software that maps reads to a host genome, filtering mapped reads from analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CLARK** (clark). A dehosting software that classifies reads taxonomically, which helps filter out host reads in metagenomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DeconSeq** (deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**FASTQ Screen** (fastqScreen). A dehosting software that checks reads against multiple reference genomes, including host genomes, to remove contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Kraken2** (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**MetaPhlAn Software** (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.

## **Nucleic Acid Extraction set**

(extractSet)set used for storing all the valid category values for the nucleic acid extraction method. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Amicon filter, extract with MP96** (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.

**Bead beating, extract with MP96** (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.

**Chemagic viral dna/rna 300 kit** (chemVir). Nucleic acid extraction performed using the chemagic viral dna/rna 300 kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**exclusions based sample preparation (ESP)** (esp). exclusions based sample preparation (ESP) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**4s method** (extract4s). Nucleic acid extraction performed using the 4s method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**luminultra wastewater extraction kit** (luminWWExtract). luminultra wastewater extraction kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo)** (monarchRNA). monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Nuclisens automated magnetic bead extraction kit** (nucAuto). Nucleic acid extraction performed using the nuclisens automated magnetic bead extraction kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**nucleomag (ref. 744220.4) using kingfisher automated instrument** (nucKingfish). nucleomag (ref. 744220.4) using kingfisher automated instrument Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Nuclisens manual magnetic bead extraction kit** (nucManu). Nucleic acid extraction performed using the nuclisens manual magnetic bead extraction kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Phenol chloroform** (phenCl). Nucleic acid extraction performed using phenol chloroform. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**promega automated tna kit** (promAuto). Nucleic acid extraction performed using the promega automated tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**promega ht tna kit** (promHt). Nucleic acid extraction performed using the promega ht tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**promega manual tna kit** (promManu). Nucleic acid extraction performed using the promega manual tna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**promega wastewater large volume tna capture kit** (promWW). Nucleic acid extraction performed using the promega wastewater large volume tna capture kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**qiagen allprep dna/rna kit** (qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen ez1 virus mini kit v2.0** (qgEz1). Nucleic acid extraction performed using the qiagen ez1 virus mini kit v2.0. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen allprep powerfecal dna/rna kit** (qgPwrFecal). Nucleic acid extraction performed using the qiagen allprep powerfecal dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen allprep powerviral dna/rna kit** (qgPwrViral). Nucleic acid extraction performed using the qiagen allprep powerviral dna/rna kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen powerwater kit** (qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen qiaamp buffers with epoch columns** (qgQiAmp). Nucleic acid extraction performed using the qiagen qiaamp buffers with epoch columns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen rneasy kit** (qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen rneasy powermicrobiome kit** (qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen allprep dna/rna kit** (qiAllprep). qiagen allprep dna/rna kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

**qiagen qiaamp dsp viral rna mini kit** (qiampDSP). qiagen qiaamp dsp viral rna mini kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Resuspend COSCa filter collection** (resCosca). Nucleic acid extraction via resuspension of a sample collected using the COSCa ball method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**sciencell viral rna isolation kit** (sciencellRNA). sciencell viral rna isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

**thermo magmax microbiome ultra nucleic acid isolation kit** (thermMag). Nucleic acid extraction performed using the thermo magmax microbiome ultra nucleic acid isolation kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**thermo magmax viral/pathogen nucleic acid isolation kit** (thermMagmax). thermo magmax viral/pathogen nucleic acid isolation kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

**trizol, zymo mag beads w/ zymo clean and concentrator** (trizol). Nucleic acid extraction performed using the trizol, zymo mag beads w/ zymo clean and concentrator method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**trizol, garnet bead beating, alcohol precipitation** (trizolEtOH). trizol, garnet bead beating, alcohol precipitation Status: active. First released: 2.2.0. Last updated: 2.2.0.

**trizol and RNA purification kit** (trizolRNA). trizol and RNA purification kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

**zymo quick-rna viral kit #r1035** (zymo1035). zymo quick-rna viral kit #r1035 Status: active. First released: 2.2.0. Last updated: 2.2.0.

**zymo quick-rna viral 96 kit #r1041** (zymo1041). zymo quick-rna viral 96 kit #r1041 Status: active. First released: 2.2.0. Last updated: 2.2.0.

**zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)** (zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit/ zymo environ water rna kit (cat. r2042). Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**zymo quick-rna fungal/bacterial miniprep #r2014** (zymoQuick). Nucleic acid extraction performed using the zymo quick-rna fungal/bacterial miniprep #r2014 kit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Sample fraction set**

(fractionSet)set for the fraction of the sample (solid, liquid, etc.). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Liquid fraction** (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Mixed/homogenized sample** (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Multiple fraction** (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Not applicable** (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Solid fraction (general)** (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Solid Fraction (Dry)** (solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Solid fraction (Wet)** (solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. Status: active. First released: 2.3.0. Last updated: 2.3.0.

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### **Geographic set**

(geoTypeSet)set for different type of geographic components. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Sewer Network Health Region** (hlthReg). Health region served by the sewer network Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sewer catchment area** (swrSet). Sewer catchment area. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Genomic Target Enrichment Methods Set**

(gteSet)The set for valid inputs for the Genomic Target Enrichment method. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Hybrid Selection Method** (hySel). Selection by hybridization in array or solution for genomic target enrichment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**rRNA Depletion Method** (rnaDepl). Removal of background RNA for the purposes of enriching the genomic target. Status: active. First released: 3.0.0. Last updated: 3.0.0.

### **Inhibition set**

(inhibitionSet)Category set for inhibition methods. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Serial dilution** (serialDilution). The serial dilution method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Spike matrix and recovery** (spike). The spike matrix and recovery method for assessing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Instrument set**

(insTypeSet)List of instruments that are used for measures and methods  
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Atline Analyzer** (aas). Atline analyzer with sampler. Status: active.  
First released: 1.0.0. Last updated: 2.0.0.

**Autosamplers** (autoInst). Autosampler instruments, used to automatically collect flow- or time-proportional samples over a period (e.g., ISCO autosamplers). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Fragment analyzers or bioanalyzers** (bioanalys). Fragment analyzer or bioanalyzer instruments, used to assess fragment size distribution in libraries. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Centrifuges** (centriInst). Centrifuge instruments; separate solids from liquids or concentrate particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Digital PCR (dPCR) instruments** (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.

**Temperature and pH probes** (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.

**Filtration units** (filtInst). Filtration instruments; remove large particulates or concentrate targets (e.g., tangential flow filtration). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Flow meters** (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.

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**Grab samplers** (grabInst). Grab sampler instruments; manually collect a single sample at a point in time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Hand Measurement** (hma). Handheld measurement analyzer. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Other instrument** (instrumentTypeOther). Type of instrument other than those included in the PHES-ODM. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Library preparation instruments** (libPrepInst). Instruments for the preparation of sequencing libraries, e.g., automation platforms like the Illumina NeoPrep. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Magnetic separation racks** (magInst). Magnetic separation rack instrument; may be used with magnetic beads for nucleic acid extraction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Next-Generation Sequencing (NGS) platforms or intruments** (ngsInst). Next generation sequencer instruments and platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lab Analysis** (ola). Offline laboratory analysis. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Online Sensor** (onse). Online sensor Status: active. First released: 1.0.0. Last updated: 2.0.0.

**qPCR instruments (quantitative PCR)** (qPCRinst). A quantitative PCR instrument, to detect and quantify specific DNA/RNA targets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**RT-qPCR instruments** (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.

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**Spectrophotometers or fluorometers** (spectroFluoro). Spetrometer and fluorometer instruments; may be used to assess concentration and purity (e.g., NanoDrop™, Qubit™). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Thermal cyclers** (thermCyc). A thermal cycler instrument, used to perform temperature-controlled reactions for PCR. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Ultracentrifuges** (ultraCentInst). Ultracentrifuge instruments; used for fine-scale separation of particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Library Preparation Kit Set**

(libraryKitSet)The valid set of categorical values for sequencing library preparation kits. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Accel-NGS 2S Plus DNA Library Kit** (accelNGS2Splus). Accel-NGS 2S Plus DNA Library Kit by Swift Biosciences. A library prep kit designed for efficient library prep from fragmented or damaged DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Apollo PrepX Library Preparation Kits** (apolloPrepX). Apollo PrepX Library Preparation Kit by Takara Bio. An automated library preparation kit for Illumina sequencing on Apollo systems. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bioo Scientific NEXTflex Rapid DNA-Seq Kit** (biooSci). Bioo Scientific NEXTflex Rapid DNA-Seq Kit by PerkinElmer. A rapid and flexible library prep kit for DNA sequencing on Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CleanPlex DNA Library Prep Kit** (cleanPlex). CleanPlex DNA Library Prep Kit by Paragon Genomics. A library target enrichment kit

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optimized for high sensitivity and low input. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Covaris truXTRAC FFPE DNA Library Kit** (covarisTruXTRAC). Covaris truXTRAC FFPE DNA Library Kit. A specialized library prep kit for extracting and preparing DNA from FFPE tissue. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nextera DNA Flex/DNA Prep Library Prep Kit** (dnaPrep). Nextera DNA Flex Library Prep Kit, now called DNA Prep, by Illumina. A flexible, transposase-based library prep kit for a wide range of DNA input amounts, suitable for microbial and human DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**EasySeq NGS Targeted Capture Kit** (easySeqNGS). EasySeq NGS Targeted Capture Kit by Nimagen. A library preparation kit and targeted capture in one, ideal for small panels. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Illumina DNA Prep with Enrichment** (illuminaDNAprep). Illumina DNA Prep with Enrichment by Illumina. A library prep kit that integrates DNA library prep with enrichment for target regions, ideal for targeted sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**KAPA HyperPrep Kit** (kapaHyperPrep). KAPA HyperPrep Kit by Roche. An optimized library prep kit for high-quality libraries from low-input or degraded DNA, commonly used for Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Ligase-Dependent Library Prep Kits** (ligaseDep). Ligase-Dependent Library Prep Kits by Lucigen/Epicentre. A library prep kit suitable for long-read applications and used with Illumina platforms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MGIEasy DNA Library Prep Kit** (mgiEasy). MGIEasy DNA Library Prep Kit by MGI/BGI. A library prep kit designed for MGI sequencing

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platforms, offering flexibility in sample input. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**NEBNext Ultra II DNA Library Prep Kit** (nebnextUltraII). NEB-Next 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.

**Nextera XT DNA Library Preparation Kit** (nexteraXT). Nextera XT DNA Library Preparation Kit by Illumina. A fast and efficient library prep kit for small genomes and amplicons, uses transposase-based fragmentation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**QIAseq FX DNA Library Kit** (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.

**SMARTer ThruPLEX Plasma-seq Kit** (smarterThruPLEX). SMARTer ThruPLEX Plasma-seq Kit by Takara Bio. A library prep kit optimized for low-input DNA, including cell-free DNA for liquid biopsy studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SureSelect XT HS2 DNA Library Preparation Kit** (sureSelectXThs2). SureSelect XT HS2 DNA Library Preparation Kit by Agilent. A high-sensitivity library prep kit with target capture capabilities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Swift 2S Turbo DNA Library Kit** (swift2STurbo). Swift 2S Turbo DNA Library Kit by Swift Biosciences. A fast library prep kit workflow with robust performance for low-input DNA. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ThruPLEX DNA-seq Kit** (thruPLEX). ThruPLEX DNA-seq Kit by Takara Bio. A low-input library prep kit with fast, three-step protocol. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**TruSeq DNA PCR-Free Library Prep Kit** (truseqDNA). TruSeq DNA PCR-Free Library Prep Kit by Illumina. A high-quality library prep kit without PCR amplification, reducing bias. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Data license set

(licSet)The set to describe valid categorical values for the licensing fields for measures or datasets. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**Academic Free License v3.0** (afl30). The licensing for the measure or data set is managed under the Academic Free License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**GNU Affero General Public License v3.0** (agpl30). The licensing for the measure or data set is managed under the GNU Affero General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Apache license 2.0** (apache20). The licensing for the measure or data set is managed under the Apache license 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Artistic license 2.0** (artistic20). The licensing for the measure or data set is managed under the Artistic license 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**BSD Zero-Clause license** (bsd0). The licensing for the measure or data set is managed under the BSD Zero-Clause license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**BSD 2-clause “Simplified” license** (bsd2Clause). The licensing for the measure or data set is managed under the BSD 2-clause “Simplified” license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**BSD 3-clause “New” or “Revised” license** (bsd3Clause). The licensing for the measure or data set is managed under the BSD 3-clause “New” or “Revised” license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**BSD 3-clause Clear license** (bsd3ClauseClear). The licensing for the measure or data set is managed under the BSD 3-clause Clear license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**BSD 4-clause “Original” or “Old” license** (bsd4Clause). The licensing for the measure or data set is managed under the BSD 4-clause “Original” or “Old” license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Boost Software License 1.0** (bsl10). The licensing for the measure or data set is managed under the Boost Software License 1.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Creative Commons Zero v1.0 Universal** (cc010). The licensing for the measure or data set is managed under the Creative Commons Zero v1.0 Universal. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Creative Commons Attribution 4.0** (ccby40). The licensing for the measure or data set is managed under the Creative Commons Attribution 4.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**CC BY-NC 4.0 license** (ccbync40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial international license. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**CC BY-NC-SA 4.0 license** (ccbyncsa40). The licensing for the measure or data set is managed under the Creative Commons 4.0 by-attribution, non-commercial, and sharealike international license. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Creative Commons Attribution ShareAlike 4.0** (ccbysa40). The licensing for the measure or data set is managed under the Creative

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Commons Attribution ShareAlike 4.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**CeCILL Free Software License Agreement v2.1** (cecill21). The licensing for the measure or data set is managed under the CeCILL Free Software License Agreement v2.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Educational Community License v2.0** (ecl20). The licensing for the measure or data set is managed under the Educational Community License v2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Eclipse Public License 1.0** (epl10). The licensing for the measure or data set is managed under the Eclipse Public License 1.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Eclipse Public License 2.0** (epl20). The licensing for the measure or data set is managed under the Eclipse Public License 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**European Union Public License 1.1** (eupl11). The licensing for the measure or data set is managed under the European Union Public License 1.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**European Union Public License 1.2** (eupl12). The licensing for the measure or data set is managed under the European Union Public License 1.2. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**GNU Free Documentation License v1.3** (gfdl13). The licensing for the measure or data set is managed under the GNU Free Documentation License v1.3. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**GNU General Public License v2.0** (gpl20). The licensing for the measure or data set is managed under the GNU General Public License v2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**GNU General Public License v3.0** (gpl30). The licensing for the measure or data set is managed under the GNU General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**ISC** (isc). The licensing for the measure or data set is managed under the ISC license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**GNU Lesser General Public License v2.1** (lgpl21). The licensing for the measure or data set is managed under the GNU Lesser General Public License v2.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**GNU Lesser General Public License v3.0** (lgpl30). The licensing for the measure or data set is managed under the GNU Lesser General Public License v3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**LaTeX Project Public License v1.3c** (lppl13c). The licensing for the measure or data set is managed under the LaTeX Project Public License v1.3c. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**MIT** (mit). The licensing for the measure or data set is managed under the MIT license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**MIT No Attribution** (mit0). The licensing for the measure or data set is managed under the MIT no attribution license. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mozilla Public License 2.0** (mpl20). The licensing for the measure or data set is managed under the Mozilla Public License 2.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Microsoft Public License** (mspl). The licensing for the measure or data set is managed under the Microsoft Public License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mulan Permissive Software License, Version 2** (mulanPSL20). The licensing for the measure or data set is managed under version 2 of the Mulan Permissive Software License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**University of Illinois/NCSA Open Source License** (ncsa). The licensing for the measure or data set is managed under the University of Illinois/NCSA Open Source License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**SIL Open Font License 1.1** (ofl11). The licensing for the measure or data set is managed under the SIL Open Font License 1.1. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Open license not otherwise described** (open). The licensing for the measure or data set is managed under an open license not otherwise described. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Open Software License 3.0** (osl30). The licensing for the measure or data set is managed under the Open Software License 3.0. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**PostgreSQL License** (postgreSQL). The licensing for the measure or data set is managed under the PostgreSQL License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Private data - not for dissemination** (private). The measure or data set is private data - not for dissemination. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**The Unlicense** (unlicense). The licensing for the measure or data set is managed under The Unlicense. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**\*\*Do What The F\*ck You Want To Public License\*\*** (wtfpl). The licensing for the measure or data set is managed under the Do What The F\*ck You Want To Public License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**zLib License** (zlib). The licensing for the measure or data set is managed under the zLib License. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## **Sample Material Characteristics Set**

(matCharSet)The set for recording the possible valid values for describing the sample material characteristics. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Contamination** (contam). The presence of a constituent, impurity, or some other undesirable element that spoils, corrupts, infects, makes unfit, or makes inferior a material, physical body, natural environment, place of human occupancy, or other material entity. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Fast-flowing** (faFlow). A quality of a body of water wherein there is a fast flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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

**Liquid** (liquidMat). Material is liquid, ie. is a state of matter with a definite volume but no fixed shape, adapting to the shape of their container. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Semi-solid** (semSol). A state of matter consisting of molecules in a non-rigid structure that can retain its shape and volume but that is not resistant to such change. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Slow-flowing** (slFlow). A quality of a body of water wherein there is a slow flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Slurry** (slur). An quality in which the fluid like material is more viscous due to the suspension of insoluble solid particles. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Solid** (solidMat). The state in which a substance has no tendency to flow under moderate stress; resists forces (such as compression) that tend to

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deform it; and retains a definite size and shape. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Stagnant** (stag). A quality of a body of water wherein it has no current or flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Treated** (treat). A quality which denotes an altered state of an item resulting from purposeful interventions or processes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Untreated** (untreat). A quality which denotes an absence of purposeful intervention or processes on an item. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Concentration method set

(methodConcSet)A set a concentration methods. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Aloh3 precipitation** (aloh3). Aloh3 precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Amicon ultrafiltration** (amiconUf). Amicon ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Beef extract flocculation** (beeExtractFloc). Beef extract flocculation. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Centricon ultrafiltration** (centriconUf). Centricon ultrafiltration. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Ceres nanotrap** (ceres). Ceres nanotrap. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Flocculation** (floc). The process of aggregating suspended particles into larger clusters (flocs) using coagulants to aid in sedimentation or filtration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Hollow fiber dead end ultrafiltration** (hollowFiberUF). Hollow fiber dead end ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Innovaprep ultrafiltration** (innovaprepUF). Innovaprep ultrafiltration Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Magnetic nanobead binding** (magBead). The use of tiny, magnetized beads to selectively capture and isolate biological molecules (e.g., DNA, proteins) in a magnetic field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**membrane filtration with addition of mgcl3** (memMgCl3). membrane filtration with addition of mgcl3 Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Membrane filtration with acidification and mgcl2** (mfAcidmgcl2). Membrane filtration with acidification and mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Membrane filtration with acidification and mgcl2, membrane recombined with separated solids** (mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Membrane filtration with addition of mgcl2** (mfMgcl2). Membrane filtration with addition of mgcl2 Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Membrane filtration with mgcl2 and separated solids** (mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Membrane filtration with no amendment** (mfNoAmend). Membrane filtration with no amendment Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Membrane filtration with no amendment, membrane recombined with separated solids** (mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Membrane filtration with sample acidification** (mfSampleAcid). Membrane filtration with sample acidification Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Membrane filtration with sample acidification, membrane recombined with separated solids** (mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No liquid concentration, liquid recombined with separated solids** (noliquid). No liquid concentration, liquid recombined with separated solids Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No Separation or Concentration** (noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Polyethyleneglycol (PEG) precipitation** (peg). Peg precipitation Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Precipitation (from solution)** (prec). The formation of a solid from a dissolved substance in a solution, typically induced by chemical reactions or changes in temperature/pH. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**promega wastewater large volume tna capture kit** (promegaLVTNA). promega wastewater large volume tna capture kit Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Skimmed milk flocculation** (skimMilkFloc). Skimmed milk flocculation Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Ultracentrifugation** (untracent). Ultracentrifugation Status: active. First released: 2.0.0. Last updated: 2.0.0.

**water concentrating buffer (R2042-1)** (watConcBuff). water concentrating buffer (R2042-1) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)** (zymoWatRNA). zymo environ water rna kit (cat. r2042) Status: active. First released: 2.2.0. Last updated: 2.2.0.

## **Original Data Format Set**

(ogFormSet)The category set for recording the possible original data formats to be recorded in the originalFormat field in the datasets table. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**ENA Format** (enaForm). Dataset was originally recorded and/or stored in ENA format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**NCBI Format** (ncbiForm). Dataset was originally recorded and/or stored in NCBI format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Norman Format** (normanForm). Dataset was originally recorded and/or stored in Norman format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**US-CDC NWSS Format** (nwssForm). Dataset was originally recorded and/or stored in the US-CDC's NWSS format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Other (or proprietary) Format** (otherForm). Dataset was originally recorded and/or stored in a format not otherwise described. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**PHA4GE Format** (pha4geForm). Dataset was originally recorded and/or stored in PHA4GE format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PHES-ODM Version 1 Format** (phesODMFormV1). Dataset was originally recorded and/or stored in PHES-ODM version 1 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PHES-ODM Version 2 Format** (phesODMFormV2). Dataset was originally recorded and/or stored in PHES-ODM version 2 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PHES-ODM Version 3 Format** (phesODMFormV3). Dataset was originally recorded and/or stored in PHES-ODM version 3 format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**wSphere Format** (wSphereForm). Dataset was originally recorded and/or stored in wSphere format. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Organization level set

(orgLevelSet)Categories of organization levels. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Administrative regions** (admRegLevel). Administrative regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Countries or sovereign states** (countryLevel). Countries or sovereign states Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Districts, counties, regions** (countyLevel). Districts, counties, regions Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Municipalities or communes** (municipalLevel). Municipalities or communes Status: active. First released: 2.0.0. Last updated: 3.0.0.

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**Local administrative units or neighborhoods** (neighborLevel). Local administrative units or neighborhoods Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Departments, states, or provinces** (stateProvLevel). Departments, states, or provinces Status: active. First released: 2.0.0. Last updated: 3.0.0.

## **Organization sector set**

(orgSectorSet) Categories of organization sectors. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Data collection sector or organization** (dataColl). Describes organization who collect, compile, analyze, and/or manage data as their central focus. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**First Nation** (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.

**Health administration or planning agency** (healthAdm). Health administrative or planning organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory** (lab). Laboratory for environmental testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Policy and political sector or organization** (policy). Describes organizations whose core focus is on policy or political activity. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Public Administration** (pubAdm). An organization type that describes governmental organizations that manage or administer programs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Public Authority** (pubAuth). An organization type describing a public agency with authority over a given domain. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Public health agency** (pubHealth). Public health agency. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Research sector or organization** (research). Describes organizations whose focus is on research generation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Utilities sector or organization** (utilities). Describes organization that manage or provide utilities services, whether water, gas, heat, etc. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Wastewater Treatment Agency** (wta). An organization type that includes those organizations who manage wastewater treatment programs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater Treatment Plant Operator** (wtwo). 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.

## Organization type set

(orgTypeSet)The set for storing organization types. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Academic institution** (academ). The category of organization type used for academic institutions or research groups. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Government agency** (govt). The category of organization type used for government agencies, programs, or crown-owned bodies. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Private sector** (priv). The category of organization type used for private sector or non-profit groups that are not otherwise captured by the academic category. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Sample Origin set**

(originSet)The set for storing the valid categorical values of sample origin. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Derived data** (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.

**Field sample** (field). Specifies a sample taken from the field; directly collected from an area for testing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Synthetic sample** (synthetic). A synthetic or artificially generated sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Outbreak declaration Value Set**

(outbreakSet)set for the valid values of the outbreak measure. Status: active. First Released: 2.0.0. Last updated: 3.0.0.

**End of Outbreak** (outbEnd). Indicates an outbreak has ended. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Outbreak - on-going** (outbOngoing). Indicates an outbreak is on-going. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Declared outbreak or Outbreak start** (outbStart). Indicates an outbreak began. Status: active. First released: 2.0.0. Last updated: 3.0.0.

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**Public health emergency (outbreak)** (phEmerg). Indicates a public health emergency from an outbreak. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## PCR action/activity set

(pcrActSet)The set capturing containing all of the valid methods for the PCR activity cycles. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**annealing/extension** (anneal). Describes the annealing and/or extension cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**denaturation** (denat). Describes the denaturation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**polymerase activation** (pAct). Describes the polymerase activation cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**reverse transcription** (rt). Describes the reverse transcription cycle in a PCR process. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## PCR Method set

(pcrSet)The set capturing containing all of the valid methods for the PCR method. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Digital droplet emulsification PCR** (bioRadDdpcr). Describes a PCR analysis done using BioRad's digital droplet emulsification PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Digital Droplet PCR (ddPCR)** (ddpcr). Describes a PCR analysis done using digital droplet PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Digital PCR (dPCR)** (dpcr). Describes a PCR analysis done using digital PCR technology (general). Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Fluidigm digital PCR** (fluiDpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Life technologies digital PCR** (ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**qiagen digital PCR** (qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quantitative Real-Time PCR** (qpcr). Real-time PCR, also called 'quantAggScale' PCR Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Raindance digital PCR** (rainDpcr). Describes a PCR analysis done using Raindance's digital PCR technology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Singleplex, probe-based, one-step RT-qPCR** (sinProbeOne). Describes a PCR method that is singleplex, probe-based, and one-step RT-qPCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## **Public Health Advisory Value Set**

(phAdviseSet)A set of valid categories for the public health action field, where the action type is 'publi health advisory'. Status: active. First

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Released: 3.0.0. Last updated: 3.0.0.

**Hand hygiene advisory** (handHygAdv). Public guidance promoting handwashing or sanitizing to reduce infection risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mask recommendation** (maskRec). Guidance encouraging the public to wear masks to reduce disease transmission. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Quarantine recommendation** (quarRec). Advice that individuals exposed to a disease should isolate to prevent spread. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Travel ban** (travBa). A restriction prohibiting travel to or from specific locations. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Travel warning** (travWa). A notice advising against travel to certain areas due to health risks. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Change to Vaccine Schedule** (vaxSched). A public health advisory has been issued to change the vaccination schedule or roll-out a vaccination campaign in response to a threat. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Polygon Relationship Set

(polyRelSet)Value set for polygon relationships. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Child relationship** (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Co-located relationship** (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected

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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.

**Neighbouring relationship** (neighbour). Locations/polygon are neighbouring each other. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Overlapping relationship** (overlap). Locations/polygon have overlapping portions. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Populated area type set**

(popAreaSet)Set of valid values used to describe the type of a populated area. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Rural** (rural). Rural populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Suburban** (suburban). Suburban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Urban** (urban). Urban populated area type Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Population Interval Set**

(popIntSet)The collection of categorical inputs for population interval measures. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**<10 people** (less10). Fewer than 10 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**10 - 100 people** (less100). Between 10 and 100 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**10,000 - 100,000 people** (less100k). Between 10,000 and 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**1,000 - 10,000 people** (less10k). Between 1,000 and 10,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**100 - 1,000 people** (less1k). Between 100 and 1,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**100,000 - 1,000,000 people** (less1mil). Between 100,000 and 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**1,000,000+ people** (more1mil). More than 1,000,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Population assessment method set

(popMetSet)The set for valid inputs for the population assessment method. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Population census** (census). Government or other agency census for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population count** (count). A count of residents for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Review of records** (rev). A review of records for determining site/polygon population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

### **Presampling activity category set**

(presampSet)The set of valid input values for reporting pre-sampling activity. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Agricultural activity** (agri). Agricultural activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Healthcare activity** (hcAct). Healthcare activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Animal husbandry** (husb). Animal husbandry occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Industrial activity** (indus). Industrial activity occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater aerobic digestion** (wwAerDigest). Wastewater aerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater anaerobic digestion** (wwAnaerDigest). Wastewater anaerobic digestion occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**wastewater comminution process** (wwCominuated). wastewater comminution process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater sludge removal** (wwDesludge). Wastewater sludge removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater sludge dewatering** (wwDewater). Wastewater sludge dewatering occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Wastewater sludge drying** (wwDry). Wastewater sludge drying occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater filtration** (wwFilt). Wastewater filtration occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater grit removal** (wwGrit). Wastewater grit removal occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater microbial treatment** (wwMic). Wastewater microbial treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewtaer primary sedimentation** (wwPriSed). Wastewtaer primary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater screening process** (wwScreen). Wastewater screening process occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater secondary sedimentation** (wwSecSed). Wastewater secondary sedimentation occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater treatment** (wwTrt). Wastewater treatment occurred upstream of the sampling site. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Genetic primer set

(primerSet)The set for genetic primers used in sequencing or PCR assays. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

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**Artic V1 Primer Set** (articV1). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 1.0.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Artic V2 Primer Set** (articV2). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 2.0.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Use of the articV3 primer** (articV3). Initial implementation of an ARTIC bioinformatics platform for nanopore sequencing of nCoV2019 novel coronavirus; Artic Foundation v3 primer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Use of the articV4 primer** (articV4). Artic V4 sequencing primer for VOCs and VOIs. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Artic V4.1 Primer Set** (articV41). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 4.1.0. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Artic V5 Primer Set** (articV500). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.0.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Artic V5.1 Primer Set** (articV510). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-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.

**Artic V5.2 Primer Set, 1200bp** (articV520bp1200). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately

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1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Artic V5.2 Primer Set, 400bp** (articV520bp400). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.2.0 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Artic V5.3.2 Primer Set** (articV532). An amplicon strategy which was developed by the ARTIC consortium for SARS-CoV-2 with the attributes of version 5.3.2 which produces amplicons approximately 400bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bacteroides 16S forward primer (HF183) (ABI)** (bact16sABIFor). Bacteroides 16S forward primer (HF183) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Bacteroides 16S probe (BacP234) (ABI)** (bact16sABIProbe). Bacteroides 16S probe (BacP234) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Bacteroides 16S reverse primer (BacR287) (ABI)** (bact16sABIRRev). Bacteroides 16S reverse primer (BacR287) (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sarbeco\_E forward primer (IDT)** (cdcCovEIDTFor). Sarbeco\_E forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sarbeco\_E probe (IDT)** (cdcCovEIDTProbe). Sarbeco\_E probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Sarbeco\_E reverse primer (IDT)** (cdcCovEIDTRRev). Sarbeco\_E reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**2019-nCoV\_N1 forward primer (IDT)** (cdcCovN1IDTFor). 2019-nCoV\_N1 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N1 probe (IDT)** (cdcCovN1IDTProbe). 2019-nCoV\_N1 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N1 reverse primer (IDT)** (cdcCovN1IDTRev). 2019-nCoV\_N1 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N2 forward primer (IDT)** (cdcCovN2IDTFor). 2019-nCoV\_N2 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N2 probe (IDT)** (cdcCovN2IDTProbe). 2019-nCoV\_N2 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N2 reverse primer (IDT)** (cdcCovN2IDTRev). 2019-nCoV\_N2 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N3 forward primer (IDT)** (cdcCovN3IDTFor). 2019-nCoV\_N3 forward primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N3 probe (IDT)** (cdcCovN3IDTProbe). 2019-nCoV\_N3 probe (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**2019-nCoV\_N3 reverse primer (IDT)** (cdcCovN3IDTRev). 2019-nCoV\_N3 reverse primer (IDT) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Eden V1 Primer Set** (edenV1). An amplicon strategy which was developed by John-Sebastian Eden with primers for SARS-CoV-2 and attributes of version 1.0.0 which produces amplicons approximately 2500bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Midnight and BC-CDC V1 Primer Set** (midnightBCCDCv1). An amplicon strategy which is for SARS-CoV-2 and based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Midnight and BC-CDC V2 Primer Set** (midnightBCCDCv2). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Midnight and BC-CDC V3 Primer Set** (midnightBCCDCv3). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 3.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Midnight and BC-CDC V4 Primer Set** (midnightBCCDCv4). An amplicon strategy which targets SARS-CoV-2 and is based on the original Midnight scheme developed by Oxford Nanopore Technologies, and adapted by the BCCDC Public Health Lab with the attributes of version 4.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Midnight scheme V1 Primer Set** (midnightV1). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 1.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Midnight scheme V2 Primer Set** (midnightV2). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore

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Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Midnight scheme V3 Primer Set** (midnightV3). An amplicon strategy which targets SARS-CoV-2 and was developed by Oxford Nanopore Technologies with the attributes of version 2.0.0 which produces amplicons approximately 1200bp in length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**New England Biolabs VarSKip V1a Long Primer Set** (nebVarSkipV1aLong). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a long. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**New England Biolabs VarSKip V1a short Primer Set** (nebVarSkipV1aShort). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 1a short. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**New England Biolabs VarSKip V2a Primer Set** (nebVarSkipV2a). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2a. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**New England Biolabs VarSKip V2b Primer Set** (nebVarSkipV2b). An amplicon strategy which targets SARS-CoV-2 and was developed by New England BioLabs using PrimalSeq to reduce effects of variants with the attributes of version 2b. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PMMV forward primer (ABI)** (pmmvABIFor). PMMV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**PMMV probe (ABI)** (pmmvABIProbe). PMMV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**PMMV reverse primer (ABI)** (pmmvABIRev). PMMV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**VSV forward primer (ABI)** (vsvABIFor). VSV forward primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**VSV probe (ABI)** (vsvABIProbe). VSV probe (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

**VSV reverse primer (ABI)** (vsvABIRev). VSV reverse primer (ABI) Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Protocol Relationships set

(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.

**Is Before** (before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Is concurrent to** (concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Specifies** (specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Purpose set

(purposeSet) Purpose set for a sample or measure. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Chemical contaminant surveillance** (chemSurv). Purpose of sampling/measure is to test for the presence of certain chemicals or chemical contaminants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Domestic travel hub surveillance** (domSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to domestic travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Drug surveillance** (drugSurv). Purpose of sampling/measure is to surveil drug use in a population. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Education** (education). A measure or sample taken for education or training. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Emergency targetted surveillance program** (emergSurv). A targeted surveillance strategy which is considered important and/or urgent. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**International travel hub surveillance** (internatSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored, related to international travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Longitudinal, repeat sampling surveillance program** (longSurv). A surveillance strategy in which an individual or site is selected to undergo repeat sampling over a defined period of time. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Multiple Purpose** (multiple). A measure or sample taken for multiple purposes, not easily captured by the other purpose categories. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Purpose is normalization** (norm). The purpose of a measure or sample is for normalization. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Environmental survey or profiling** (profil). Purpose of sampling/measure is to record characteristics and profile a given environment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Provisional report** (provisional). A provisional or interim report. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality control** (qualityControl). A measure or sample taken for the purpose of quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Random sampling surveillance program** (randomSurv). A surveillance sampling strategy in which baseline is established at the beginning of a study or project by the selection of sample units via random sampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Regular Pathogen Surveillance** (regular). A measure or sample taken for surveillance or epidemiology. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Research purposes** (researchPurp). Purpose of sampling/measure is for research. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Targeted surveillance program** (targetSurv). A surveillance sampling strategy in which an aspired outcome is explicitly stated. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Protocol testing** (testing). A measure or sample taken to test a new method. These measures are typically used for internal lab uses and not

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reported to external partners. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Travel hub surveillance - general** (travelSurv). A surveillance strategy in which wastewater produced within travel hubs or travel vehicles are monitored. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Validation study** (validationStudy). A measure or sample taken for a validation study. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Viral passage experiment** (viralPass). A research sampling strategy in which samples are selected in order to perform a viral passage experiment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater treatment efficiency assessment** (wwtpAssess). Purpose of sampling/measure is to assess wastewater treatment efficiency. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Raw Sequence Data Processing Method Set**

(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.

**AdapterRemoval** (adapterRemoval). A sequencing data processing application that removes adapters and filters reads based on quality and length. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BayesHammer (from SPAdes)** (bayesHammer). A sequencing data processing application that does error correction tool specifically for Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BBMap Suite** (bbmapSuite). A sequencing data processing application library that includes tools like BBduk for quality trimming, adapter

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removal, and quality filtering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BWA (Burrows-Wheeler Aligner)** (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CD-HIT** (cdHIT). A sequencing data processing application that clusters and removes duplicate sequences, useful for dereplication. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cutadapt** (cutadapt). A sequencing data processing application that does adapter removal and trimming tool for high-throughput sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DADA2** (dada2). A sequencing data processing application that is primarily used in amplicon sequencing for error correction and generating amplicon sequence variants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DeconSeq** (deconSeq). A dehosting software that is used for dehosting by filtering reads against host reference genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**FASTP** (fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**FastQC** (fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**FASTX Toolkit** (fastXTools). A sequencing data processing application that provides various functions for FASTQ processing, including quality filtering. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Fqtrim** (fqtrim). A sequencing data processing fast tool for adapter removal, quality trimming, and quality control. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**iVar** (iVar). A sequencing data processing application that is designed for viral amplicon data, removes primers and can trim low-quality bases. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**KneadData** (kneadData). A sequencing data processing pipeline for quality control, including trimming and host decontamination (uses Trimmomatic and Bowtie2). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Minimap2** (minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Porechop** (porechop). A sequencing data processing application that is specifically designed for adapter trimming in Oxford Nanopore Technologies data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Prinseq-lite** (prinseqLite). A sequencing data processing application that filters sequences based on complexity and removes low-quality reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SAMtools** (samTools). Sequencing software that is used with aligned sequence data to generate consensus sequences from BAM files. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**seqtk** (seqtk). A lightweight sequencing data toolkit for FASTQ and FASTA manipulation, including trimming and subsampling. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sickle** (sickle). A sequencing data processing application that is a quality-based trimming tool for Illumina data with single-end and paired-end support. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Skewer** (skewer). A sequencing data processing application that is a fast tool for adapter trimming and quality trimming in Illumina data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SortMeRNA** (sortMeRNA). A sequencing data processing application that is used for ribosomal RNA filtering in metatranscriptomic data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SPAdes** (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Trimmomatic** (trimmomatic). A sequencing data processing application that trims adapters and low-quality bases from Illumina sequencing reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**UMI-tools** (umiTools). A deduplication method that is dedicated to deduplicating reads using unique molecular identifiers, especially effective in RNA-seq and single-cell workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sequencing read mapping software set

(readMapperSet)The set of valid input values for the sequence read mapping software. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

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

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from platforms like Nanopore or PacBio. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BLASR (Basic Local Alignment with Successive Refinement)** (blasr). BLASR (Basic Local Alignment with Successive Refinement). A long-read specific mapper. Optimized for PacBio data. Best for: High-quality long-read alignment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bowtie2** (bowtie2). Bowtie2. A general-purpose read mapper. Fast and memory-efficient, commonly used for aligning short reads. Best for: Small genomes, RNA-seq preprocessing. Can also be used as a dehosting software that maps reads against a host reference genome to remove aligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BWA (Burrows-Wheeler Aligner)** (bwa). BWA (Burrows-Wheeler Aligner). A general-purpose read mapper. A sequencing software that is often used in workflows where generating consensus sequences from mapped reads is required. Includes algorithms like BWA-MEM, optimized for high-quality read mapping. Best for: Whole-genome sequencing (WGS), high-quality alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cufflinks (with TopHat integration)** (cufflinks). Cufflinks (with TopHat integration). A specialized read mapper. Combines mapping with transcriptome assembly and quantification. Best for: RNA-seq studies with integrated analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**GEM Mapper** (gemMapper). GEM Mapper. A specialized read mapper. High-speed and accurate alignment tool for short reads. Best for: Genomic applications with short reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**GMAP** (gmap). GMAP. A specialized read mapper. A long-read aligner for genomic mapping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**GraphMap** (graphmap). GraphMap. A long-read specific mapper. Long-read aligner optimized for highly error-prone reads. Best for: De novo assemblies using long-read data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**GSNAP** (gsnap). GSNAP. A specialized read mapper. A splice-aware aligner for RNA-seq reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**HISAT2** (hisat2). HISAT2. A general-purpose read mapper. Successor to TopHat, optimized for RNA-seq data with splicing awareness. Best for: Large-scale RNA-seq experiments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**LAST (Large-Scale Alignment and Search Tool)** (last). LAST (Large-Scale Alignment and Search Tool). A long-read specific mapper. Flexible tool for aligning long and error-prone reads. Best for: Comparative genomics with long reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MapSplice** (mapSplice). MapSplice. A specialized read mapper. Designed specifically for spliced alignment of RNA-seq reads. Best for: Transcriptomics with a focus on detecting splice junctions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Minimap2** (minimap2). Minimap2. A general-purpose read mapper, and a sequencing data processing application that is a Fast aligner often used in quality control for host decontamination. A versatile tool for mapping long reads (e.g., PacBio, Nanopore) and short reads. Best for: Large-scale genome or transcriptome assembly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**NGMLR (Next-Generation Mapping and Long-Read Alignment)** (ngmlr). NGMLR (Next-Generation Mapping and Long-Read Alignment). A long-read specific mapper. Specialized for long-read platforms like PacBio and Nanopore. Best for: Structural variant analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Novoalign** (novoalign). Novoalign. A specialized read mapper. Commercial aligner known for high accuracy. Best for: Applications requiring precise alignments. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SMALT** (smalt). SMALT. A highly parallelized mapper. High-speed aligner for genomic DNA reads. Best for: Applications requiring flexibility with non-standard parameters. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Snap** (snap). Snap. A highly parallelized mapper. Ultrafast, designed for genomic and RNA-seq applications. Best for: Large-scale sequencing projects. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Soap2** (soap2). Soap2. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Soap3** (soap3). Soap3. A specialized read mapper. High-throughput short-read mapper. Best for: Alignment of short Illumina reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**STAR (Spliced Transcripts Alignment to a Reference)** (star). STAR (Spliced Transcripts Alignment to a Reference). A general-purpose read mapper. Fast aligner designed for RNA-seq, supports spliced alignment. Best for: Transcriptome data analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Subread** (subread). Subread. A general-purpose read mapper. Includes the subread-align algorithm for mapping DNA and RNA reads. Best for: High-throughput data with a balance of speed and accuracy. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**TopHat** (tophat). TopHat. A general-purpose read mapper. An older RNA-seq aligner, splicing-aware. Replaced by HISAT2 in most workflows. Best for: Historical RNA-seq studies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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## **General Relationship Set**

(relSet)set for valid values of relationshipID across all fields and tables.  
Status: active. First Released: 2.2.3. Last updated: 2.2.3.

**Is Before** (before). Specifies that the object step or protocol occurs before the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Child relationship** (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Co-located relationship** (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Is concurrent to** (concurrent). Specifies that the object step or protocol occurs at the same time as the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Field sample replicate** (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory duplicate** (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory control sample duplicate** (lcsd). Known amounts of an analyte or representative compounds are added to a second “clean” matrix

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(lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Matrix spike duplicate** (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Relationship Not Reported** (relNR). A relationship ID used in relationship tables across the ODM when two entities are related or connected in some way, but the actual nature of that relationship is not clear or reported. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Specifies** (specifies). Specifies that the object step or protocol occurs specifies details for the subject step or protocol in the overall protocol container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Replicate Type set**

(replicateSet)The set for storing valid categorical values of replicate type. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Biological replicate** (bioRep). A biological replicate not otherwise specified - these are parallel measurements of biologically distinct samples that capture random biological variation, which can be a subject of study or a source of noise itself. Biological replicates are important because they address how widely your experimental results can be generalized. They indicate if an experimental effect is sustainable under a different set of biological variables. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Co-located relationship** (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but

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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.

**Derived sample** (derivedSamp). A sample that is derived or made from another sample or material. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Field sample replicate** (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory duplicate** (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory control sample duplicate** (lcSD). Known amounts of an analyte or representative compounds are added to a second “clean” matrix (lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Matrix spike duplicate** (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No amplification control** (nac). Denotes a no amplification control replicate sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Negative experimental control** (negCon). A sample or experimental condition where the expected outcome should not occur, intended to check the original sample matrix for contamination, false positives, or unintended effects. An example would be testing for viral RNA or DNA in a sample known to be free of that virus. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**MinusRT** (nrt). Denotes a replicate/control sample prepared without reverse transcriptase (RT). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Non-template control** (ntc). Denotes a non-template control sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**No target present** (ntp). Denotes a sample replicate/control with no target present. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Optical calibrator sample** (opt). Denotes a sample control or replicate used for optical calibration. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Positive experimental control** (posCon). A sample or experimental condition where the expected outcome is known to occur, intended to confirm that the experimental setup is working properly. An example would be a wastewater sample spiked with a known quantity of SARS-CoV-2 virus. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sampling Event** (sampleEvent). In settings where a person goes out and collects multiple samples, but more accurate location data is not recorded, this is used to group samples from that outing, or ‘sampling event’. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Standard sample** (std). Denotes a standard sample replicate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Subsample (General)** (subSamp). A general replicate type for a sub-sample not otherwise defined. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Technical replicate** (techRep). A sample that comes from the same biological or environmental source (e.g., the same extracted DNA, the same RNA aliquot, or the same water sample). Helps detect inconsistencies due to pipetting errors, instrument fluctuations, or reagent inconsistencies, rather than biological variation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Unique sample** (unique). A unique sample, not duplicated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Unknown sample** (unkn). Denotes an unknown sample replicate type. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Resuspension method set

(resusSet)The set to describe valid categorical values for the resuspension method. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**Elution buffer** (elutionBuff). Elution buffer is used to resuspend material. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Retained Element Set

(retElSet)The set for enumerating the valid possible values of the retained element method. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**Eluate/Resuspended filter material retained** (eluate). The eluate fraction, or material resuspended from filtration, is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Liquid/Supernatant retained** (liquid). The liquid or supernatant is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Solids/Pellet retained** (solid). The solids or pellet is retained after solid separation/centrifugation. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## **Sample material set**

(sampleMatSet)set for the types of material that can be found in a sample.  
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Air filter** (afu). Air filter as part of filtration or circulating unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Desk or counter** (desk). Desk, table, countertop or other flat working surface. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wastewater Effluent - non-specified** (effluNS). Sample material is wastewater effluent - whether primary, secondary or other is unspecified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Fecal matter** (faeces). Fecal matter. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Floor** (floor). Floor of a building or room. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Holding tank wastewater** (htSam). Wastewater sampled from a holding tank, such as from an airplane or ship Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Water** (nww). Non-wastewater, coming from any kind of water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Primary clarifier effluent** (pEfflu). Effluent obtained after primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Primary clarifier sludge** (pSludge). Sludge produced by primary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Post-grit** (pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large solids at a treatment plant but prior to a primary clarifier) Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Sets

**Raw sewage at site** (rawWW). Wastewater without any form of treatment  
Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Raw sewage downstream from a site** (rawWWdown). Downstream from a site. See partType = rawWWup. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Raw sewage upstream from a site** (rawWWup). Upstream from a site. Used when there is not direct access to a site's wastewater inconjuctiion with downstream sample. For example, if the site is a long-term care home, but ther is not access to the building or property cleanout. Use two sameple, one sample upstream and one sample downstream. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Secondary clarifier effluent** (sEfflu). Effluent obtained after secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Septic tank wastewater** (septage). Wastewater from within a septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Wastewater Sludge - non-specified** (sludgeNS). Sample material is wastewater sludge - whether primary, secondary or other is unspecified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Secondary clarifier sludge** (sSludge). Sludge produced by secondary clarifiers Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Other surface** (surface). Surface other than floor or desk. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sewer sediment** (swrSed). Sediments obtained in sewer Status: active. First released: 1.0.0. Last updated: 2.0.0.

## **Sample relationships set**

(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.

**Child relationship** (child). Indicated that this is a sample generated from (an)other sample(s) either because of pooling or sub-sampling. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Co-located relationship** (colocated). Second or multiples samples collected at or near (one-half to three feet away) from the same selected sample location to determine local variability of a given analyte. Analytical results from co-located samples can be used to assess site variation, but only in the immediate sampling area. Samples at the same location but using different media (i.e. water and air samples, soil and sediment samples) are also classified as co-located samples. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Control sample** (control). Denotes a relationship to a primary sample where the object sample serves as a control to the subject sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Field sample replicate** (fieldReplicate). A sample divided into two or more homogeneous parts. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory duplicate** (labDuplicate). Second (time or more) processing and analysis of sample. Usually for general chemistry or metals analyses. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Laboratory control sample duplicate** (lcsd). Known amounts of an analyte or representative compounds are added to a second “clean” matrix (lab water or clean sand) in laboratory. Duplicate of LCS Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sets

**Matrix spike duplicate** (msd). A known amounts of an analyte or representative compounds are added in the laboratory to a second aliquot of the sample used for matrix spike. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sequencing script version set

(scriptSet)The set for script versions Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Freyja Script** (freyja). Freyja Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Gromstole 1.0 Script** (gromstole). Gromstole 1.0 Script for sequencing. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sequence Assembly Software Set

(seqAssSet)The valid set of categorical values for sequence assembly software methods. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**ABySS** (abyss). A sequencing software that is a scalable de novo assembler for large genomes, designed for distributed computing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**AllPaths-LG** (allpathsLG). A sequencing software that was designed for high-quality assemblies using large, paired-end Illumina data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ARACHNE** (arachne). A sequencing software that is an early assembler optimized for large, complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Canu** (canu). A sequencing software that is a de novo assembler specifically optimized for long-read data from PacBio and Oxford Nanopore. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Celera Assembler** (celera). A sequencing software that was initially developed for the Human Genome Project, still used in some workflows for large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DISCOVAR de novo** (discovar). A sequencing software that is an assembler optimized for Illumina data in whole-genome sequencing. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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

**IDBA-UD** (idbaUD). A sequencing software that is an iIterative assembler optimized for metagenomics and complex genomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Maryland Super Read Celera Assembler (MaSuRCA)** (masurca). A sequencing software that is a hybrid assembler that can integrate both short and long reads for high-quality assemblies, and large, complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MEGAHIT** (megahit). A sequencing software that is a fast and memory-efficient assembler for large metagenomic datasets. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MetAMOS** (metAMOS). A sequencing software that is an automated pipeline for metagenomic assembly and annotation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Miniasm** (miniasm). A sequencing software that is a lightweight assembler for long reads, typically followed by polishing steps. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**NovoPlasty** (novoPlasty). A sequencing software that is an assembler tailored for organellar genomes (mitochondrial and chloroplast). Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PEHaplo** (pehaplo). A sequencing software that is an assembler that considers heterozygosity in diploid genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Platanus** (platanus). A sequencing software that is an assembler, optimized for large, diploid genome assemblies, particularly plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Redundans** (redundans). A sequencing software that is a genome assembler that reduces redundancy, useful for fragmented assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Shasta** (shasta). A sequencing software that is a fast assembler optimized for nanopore long-read data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SOAPdenovo** (soapDenovo). A sequencing software that is an assembler for short-read data, suited to large and complex genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SPAdes** (spades). Sequencing software that is primarily an assembler, but it can produce contigs that can be used to infer consensus sequences in assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SSAKE** (ssake). A sequencing software that is a simple de novo assembler for highly overlapping short reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Trinity** (trinity). A sequencing software that is an assembler designed specifically for RNA-seq data, creating transcriptome assemblies. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Unicycler** (unicycler). A sequencing software that is a hybrid assembler for bacterial genomes, combining short and long reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Velvet** (velvet). A sequencing software that is a de novo assembler optimized for short-read data, often used in microbial genomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**WTDBG (aka wtdbg2)** (wtdbg2). A sequencing software that is an assembler for long-read data that generates contigs rapidly. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Sequencing Layout set**

(seqLaySet)The set for the layout of genetic material used in sequencing Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Mate pair layout** (mateLay). Specifies the mate pair layout for a sequencing method. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Paired Layout** (pairLay). Specifies the paired layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Single Layout** (sinLay). Specifies the single layout for a sequencing method Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Sequencing QC Pipeline Set**

(seqQCSet)The category set of valid input 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.

## Sets

**AfterQC** (afterQC). An automated QC pipeline tool for FASTQ data, combining quality assessment and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Atropos** (atropos). A QC pipeline tool for sequencing data that performs adapter trimming and quality filtering with built-in QC reporting. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BamQC (from Qualimap)** (bamQC). A QC pipeline tool for sequencing data that focuses on quality control for mapped data in BAM format, reporting alignment quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BBDuk (from BBTools)** (bbduk). A QC pipeline tool for sequencing data that is a part of the BBMap suite, performs filtering and trimming, and generates QC statistics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bracken** (bracken). A QC pipeline tool for sequencing data and taxonomic profiling that can also be used to identify contamination and assess data quality in metagenomics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DecontaMiner** (decontaMiner). A QC pipeline tool for sequencing data for contamination detection and removal in NGS datasets, especially useful in clinical samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**EAGER** (eager). A QC pipeline tool for sequencing data for ancient DNA, providing quality filtering, contamination estimates, and other QC metrics. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**FASTP** (fastp). A sequencing data processing application that combines quality control, adapter trimming, filtering, and error correction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**FastQC** (fastQC). A sequencing data processing quality control tool that provides visual metrics on raw read quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**FRCbam** (frcBam). A QC pipeline tool for sequencing data that assesses read quality and genome assembly quality metrics for high-throughput data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Kraken2** (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MultiQC** (multiQC). A QC pipeline tool for sequencing data that aggregates QC results from multiple sources (e.g., FastQC, SAMtools) into a single report, useful in large pipelines. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**NanoPlot** (nanoPlot). A QC pipeline tool for sequencing data that does visualizations for quality assessment of long-read data, particularly from Oxford Nanopore. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ncov-tools** (ncovtools). Tools and plots for performing QC on coronavirus sequencing results. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PIQMIE** (piqmie). A comprehensive QC and contamination assessment pipeline for metagenomic datasets and sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PiSeqQC** (piSeqQC). A QC pipeline tool for sequencing data for microbiome and metagenomic sequencing data, including quality filtering and contaminant removal. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**preQC (from Meraculous)** (preQC). A QC pipeline tool for sequencing data that evaluates data quality before assembly, particularly for large genomes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**PRINSEQ** (prinseq). A QC pipeline tool for sequencing data for assessing and filtering sequences based on complexity, quality scores, and GC content. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**QC3** (qc3). A comprehensive QC pipeline for NGS sequencing data that provides summary statistics on sequence quality and contamination. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**qProfiler2** (qProfiler2). A QC pipeline tool for sequencing data that produces reports with detailed QC metrics for aligned and unaligned reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SeqKit stats** (seqKitStats). Part of SeqKit, a QC pipeline tool for sequencing data that providing a summary of sequence metrics like length, GC content, and quality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**TrimGalore!** (trimGalore). A QC pipeline tool for sequencing data that integrates Cutadapt and FastQC to assess sequence quality and remove adapters in one step. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sequencing selection method set

(seqSelSet)The set for the selection method used in sequencing Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**PCR Sequencing Selection Method** (pcrSeq). Specifies the PCR selection method for sequencing, ie. that a pre-determined primer was used. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Random sequencing selection method** (ranSeq). Specifies the random selection method for sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

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## **Sequencing Strategy set**

(seqStratSet)The set for the sequencing strategy used for an analysis Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**16S Ribosomal Gene Sequencing** (16rgs). An amplicon sequencing assay in which the amplicon is derived from universal primers used to amplify the 16S ribosomal RNA gene from isolate bacterial genomic DNA or metagenomic DNA from a 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.

**Amplicon sequencing** (amp). Specifies the amplicon strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Whole genome sequencing** (wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Whole Metagenome Sequencing** (wms). A DNA sequencing assay that intends to provide information on the DNA sequences of multiple genomes (a metagenome) from different organisms present in the same input sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Whole Virome Sequencing** (wvs). A whole metagenome sequencing assay that intends to provide information on multiple genome sequences from different viruses present in the same input sample. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Serotyping Method Set**

(seroMethSet)The set of categorical inputs for populating the serotyping method field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

## Sets

**ARIBA** (ariba). ARIBA. Focus: Genotyping, MLST, and serotyping from raw sequencing reads. Applications: *Salmonella*, *Escherichia coli*, *Klebsiella pneumoniae*, and more. Features: Works with custom databases for serotyping and resistance gene identification. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**BIGSdb (Bacterial Isolate Genome Sequence Database)** (bigsdb). BIGSdb (Bacterial Isolate Genome Sequence Database). A flexible platform that supports serotyping alongside sequence typing and other typing schemes. Can be customized for various bacterial species, including *Neisseria meningitidis*. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CapsuleFinder** (capFin). CapsuleFinder Used for typing capsular polysaccharides in a variety of bacteria, especially *Escherichia coli* and *Klebsiella* species. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ChewBBACA** (chewBBACA). ChewBBACA. Focus: Core genome MLST (cgMLST) with optional serotyping analysis. Applications: Broad-spectrum bacterial pathogens. Features: Efficient with large datasets and highly customizable. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**ClermontTyping** (clermonTyp). ClermontTyping. 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.

**CTFinder** (ctFinder). CTFinder. Designed for *Clostridioides difficile* serotyping and subtyping. Identifies capsular polysaccharide synthesis gene clusters to assign serogroups. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Enterobase archives** (enterobase). Enterobase archives. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**FastMLST** (fastMLST). FastMLST. Focus: Lightweight MLST and serotyping from assembled genomes or raw reads. Applications: Broad

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bacterial species. Features: Quick and simple, designed for routine use. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**GenoTyphi** (genoTyphi). GenoTyphi. Focus: Specific MLST and serotyping for *Salmonella Typhi*. Applications: Outbreak investigations and epidemiology. Features: Highly specialized for typhoidal *Salmonella*. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Kaptive** (kaptive). Kaptive. Identifies capsular (K) serotypes in *Klebsiella pneumoniae* and related species using whole-genome sequence data. Useful for studying capsule diversity and epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Kraken2** (kraken2). A dehosting software that classifies reads against reference databases, used to filter out host reads. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MLST (Center for Genomic Epidemiology)** (mlst). MLST (Center for Genomic Epidemiology). Focus: Classical MLST and optional serotype determination. Applications: Compatible with curated schemes for various pathogens. Features: Web-based and command-line versions available. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Mykrobe** (mykrobe). Mykrobe. Focus: Rapid detection of resistance, MLST, and serotyping. Applications: *Mycobacterium tuberculosis* and other pathogens. Features: Fast processing and species-specific database compatibility. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Pathogenwatch** (pathogenwatch). Pathogenwatch. Focus: Integrates MLST, serotyping, and resistance typing with a user-friendly interface. Applications: Primarily used for *Salmonella* and *Escherichia coli*. Features: Combines typing results with interactive visualization. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PBPfinder** (pbpfinder). PBPfinder. Used for typing and serotyping of *Streptococcus pneumoniae* through analysis of penicillin-binding proteins

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and capsular genes. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PGAP (Prokaryotic Genome Annotation Pipeline)** (pgap). PGAP (Prokaryotic Genome Annotation Pipeline). Focus: Annotation pipeline that integrates MLST and antigen typing. Applications: Broad bacterial pathogens. Features: Provided by NCBI, designed for high-throughput workflows. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Phandango** (phandango). Phandango. A visualization tool that integrates serotype predictions with phylogenetic analyses for population studies. Often used alongside other serotyping tools. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Prokka (with serotyping integration)** (prokka). Prokka (with serotyping integration) While primarily an annotation tool, Prokka outputs can be paired with databases for identifying serotypes of certain bacterial pathogens. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Prokka + Roary Pipeline (Nextflow)** (prokkaRoary). Prokka + Roary Pipeline. Focus: Genome annotation (Prokka) with MLST and serotyping integration via Roary. Applications: Broad compatibility with bacterial pathogens. Features: Facilitates core-genome MLST and accessory gene analysis. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**PubMLST** (pubMLST). PubMLST. Focus: Web-based platform for MLST and serotyping analyses. Applications: Neisseria, Campylobacter, Salmonella, and more. Features: Combines curated databases with user-uploaded sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SalmonellaTypeFinder** (salTypeFin). SalmonellaTypeFinder A specialized tool for predicting Salmonella serotypes based on genomic data, similar to SeqSero. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**SeqSero2** (seqSero2). SeqSero2. Specifically designed for *Salmonella* serotyping using raw sequence reads, assemblies, or even complete genomes. Provides results based on antigenic formulas or serotype names. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SeqTyping** (seqTyping). SeqTyping. Focus: Simultaneous MLST and serotyping for *Escherichia coli* and *Salmonella*. Applications: Integrated with bacterial genome typing databases. Features: Compatible with short-read sequencing data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SerotypeFinder** (serotypeFin). SerotypeFinder. A web-based tool that predicts serotypes for *Escherichia coli* and other bacteria by detecting genes encoding O-antigens and H-antigens. Developed by the Center for Genomic Epidemiology. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Salmonella In Silico Typing Resource (SISTR)** (sistr). Salmonella In Silico Typing Resource (SISTR). Used for in silico serotyping of *Salmonella enterica* based on whole-genome sequencing. Combines genomic data with the traditional White-Kauffmann-Le Minor serotyping scheme. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**SRST2 Software** (srst2). Software tool for analyzing antimicrobial resistance using short read sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Streptococcus Serotyping Tool (SSI)** (SSI). Streptococcus Serotyping Tool (SSI) A web-based platform for serotyping *Streptococcus pneumoniae* based on capsular polysaccharide synthesis loci. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Statistical Analysis of Metagenomic Profiles (STAMP) Software** (stamp). A lineage or clade analysis software tool for analyzing taxonomic profiles and differentiating clades. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Traditional Serotyping methods** (tradSero). Traditional Serotyping methods used for serotyping. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Severity set

(sevSet)A set for severity indicators. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**High severity** (high). Indicates a very sever quality issue, likely meaning the data should not be reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low severity** (low). A marker for low severity Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Mid-level severity** (mid). A marker for med-level severity, where there are some concerns. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sampleshed set

(shedSet)The set for all valid values of sampleshed. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Airplane** (airpln). Airplane sample shed category type Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Airport** (airport). Airport sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Bus** (bus). A large motor vehicle carrying passengers by road, typically one serving the public on a fixed route and for a fare. Status: active. First released: 2.2.3. Last updated: 2.2.3.

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**Bus Station** (busStat). A terminal where buses arrive and depart. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Long-term acute care hospital** (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.

**Child day care** (cdc). Child day care facility. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Clinic** (clinic). A medical clinic, may be used to provide treatment, remedial work, and/or instruction. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Commercial facility - not specified** (commFacOth). Specifies a site type which is a commercial facility/worksite that is not otherwise captured or described in the geotype set. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Correctional facility** (corFcil). Correctional facility Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Higher education dormitory or residential building** (dorm). Higher education dormitory or residential building Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Educational facility** (edFac). A school or other educational facility not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Farm** (farm). An agricultural 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.

**First Nation** (fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Healthcare facility** (hcf). A building for the provision of healthcare, not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Hospital** (hosptl). Hospital Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Industrial plant** (indPl). A factory not otherwise specified - A building or collection of buildings used for manufacturing, building, producing or storing goods, and occasionally services, and making them into products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Land-based Transit Hub** (landTH). A transport hub is a place where passengers and cargo are exchanged between land-based vehicles and/or between land-based transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Long-term care facility** (ltcf). A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Long-term care - assisted living or retirement home** (ltcfAl). A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Other long-term care** (ltcfO). Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or assisted living facilities. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Shopping mall** (mall). A large commercial complex with multiple retail stores, services, and restaurants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Meat processing plant** (meatPl). A processing plant for slaughtering, processing, packaging, labelling, handling, and storing of food animal

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carcasses, parts of carcasses, and meat products. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Municipality** (municip). A complete municipality, this specifies an entire metropolitan area, either a city, town, etc. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Neighbourhood** (neigh). A municipal neighbourhood, this specifies a sub-section of a larger municipality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Office** (office). A workplace where administrative, managerial, or clerical tasks are performed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Other residential building** (orb). Individual residential buildings or institutions not captured in other categories Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Pharmaceutical manufacturing plant** (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.

**Port or Harbour** (port). A harbor is any sheltered body of water where boats or ships may moor or anchor. A port is an installation that has been built around a harbor with facilities for loading and unloading such vessels. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Refugee camp** (refCamp). A temporary, often makeshift shelter for persons displaced by war, political oppression, or for religious beliefs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Restaurant** (restaurant). A commercial establishment that prepares and serves food and beverages to customers. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Road** (road). A paved or unpaved pathway designed for vehicular and pedestrian travel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Roadside** (roadside). The area adjacent to a road, including sidewalks, shoulders, or drainage ditches. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**School** (school). A school serving students in the kindergarten to 12th grade range Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Ship** (ship). A cruise ship or other ship. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Social services shelter** (sss). Other type of social services shelter Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Airport terminal** (terminal). Airport terminal sample shed category type Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Transport hub - General** (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.

**Train** (train). A series of railroad cars moved as a unit by a locomotive or by integral motors. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Transportation vehicle - general** (transp). A vehicle, i.e. a mobile machine, transporting people or cargo, of a type not otherwise specified. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Train Station** (trStat). A place on a railroad line where trains regularly stop so that passengers can get on or off. Status: active. First released: 2.2.3. Last updated: 2.2.3.

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**University campus** (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.

**Water-based Transit Hub** (waterTH). A transport hub is a place where passengers and cargo are exchanged between water-based vehicles and/or between water-based transport modes. Status: active. First released: 2.2.3. Last updated: 2.2.3.

## **Site Level Category Set**

(siteLevelSet)The category set containing all valid entries for the siteLevel field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**A-Tier Region-level Aggregation at Site** (aRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an “A-Tier” region and refers to large, dense urban areas made up of multiple overlapping cities/boroughs. This would be a greater metropolitan area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**B-Tier Region-level Aggregation at Site** (bRegLevel). Specifies that a sewershed/site represents an entire region - where region here is an “B-Tier” region, and thus a region within a greater metropolitan area and larger than a single municipality, but smaller than the entire metropolitan area. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Country-level Aggregation at Site** (countLevel). Specifies that a sewershed/site represents an entire nation or country. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**First Nation Territory/Métis Settlement-level Aggregation at Site** (fnmiLevel). Specifies that a sewershed/site represents the entirety of a First Nations territory or reservation, or a Métis settlement. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Municipality-level Aggregation at Site** (muniLevel). Specifies that a sewershed/site represents an entire municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Neighbourhood-level Aggregation at Site** (neighLevel). Specifies that a sewershed/site represents an entire neighbourhood, or a zone within a municipality. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Province-level Aggregation at Site** (provLevel). Specifies that a sewershed/site represents a sub-national state, province, or region. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Site set

(siteTypeSet)set for the type of sampling site. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Aeration tank** (aerTank). A chamber in wastewater treatment where air is introduced to promote microbial breakdown of organic pollutants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Bar screen** (barScreen). A bar screen is a mechanical device used to remove large solid debris from wastewater or sewage as it enters a treatment plant. It consists of a series of parallel bars or rods, spaced at specific intervals, that allow water to pass through while capturing larger objects. This process prevents damage to downstream equipment and ensures efficient treatment. Bar screens are typically installed at the inlet of wastewater treatment facilities and can be cleaned manually or mechanically, depending on the design and operational requirements. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Body of water** (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.

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**Branch sewer pipeline** (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.

**Building cleanout** (buildCO). Specifies a site type that is a capped pipe that connects to a building's main sewer line. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Canal** (canal). Artificial watercourse with no flow or a controlled flow used for navigation, drainage or irrigation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cesspit** (cesspit). Cesspit, cesspool and soak pit in some contexts are terms with various meanings: they are used to describe either an underground holding tank (sealed at the bottom) or a soak pit (not sealed at the bottom). A cesspit can be used for the temporary collection and storage of feces, excreta, or fecal sludge as part of an on-site sanitation system and has some similarities with septic tanks or with soak pits. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Communitor** (communitor). A mechanical device that grinds large solid waste in wastewater into smaller particles to prevent clogging. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Composting toilet** (compToi). A self-contained toilet system wherein human waste is designed to be composted. Usually with the addition of secondary materials, like sawdust. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Sewer (drain)** (drain). A pipe that carries water or sewage away from a place, or an opening in a surface that leads to said pipe. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Estuary, natural water body** (estuary). Estuary, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

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**Grit chamber** (gritCham). A sedimentation basin in wastewater treatment that removes heavy, inorganic particles (e.g., sand, gravel) before biological treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Ground water** (grWa). Underground water which is located in pore spaces found in rock or unconsolidated deposits such as soil, clay, or gravel. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Holding tank** (htSite). Holding tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Influent pump station** (infPump). A facility that lifts and transports raw wastewater from collection systems to treatment plants. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lagoon system** (lagoon). Lagoon system for extensive wastewater treatment Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Lake, natural water body** (lake). Lake, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Latrine** (latrine). A toilet or outhouse, especially a communal one in a camp or barracks. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Major sewer pipeline** (mSwrPpl). Major sewer pipeline Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Ocean, natural water body** (ocean). Ocean, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Odour Control Unit** (ocu). Odour Control Unit ventilation extends the life of a sewer by reducing the amount of maintenance the pipeline needs, making management of the network much more efficient. The filters used in the Odour Control Unit and ventilation stacks absorb gases such as hydrogen sulphide, which is a common source of odours from sewerage systems. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Surface water** (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.

**Plumbing drain** (pluDra). An artificial channel which transports unwanted water or waste liquids away from their source, either to a more useful area, a receptacle, or into sewers or stormwater mains as waste discharge to be released or processed. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Primary clarifier** (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.

**Pumping station** (pStat). Pumping station Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Reservoir** (res). An artificial body of water, often contained by a dam, constructed for the purpose of water storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Retention pond** (retPond). Retention pond Status: active. First released: 1.0.0. Last updated: 2.0.0.

**River, natural water body** (river). River, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sludge dryer** (sDryer). A facility or equipment used to reduce moisture content in wastewater sludge for easier handling and disposal. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sea, natural water body** (sea). Sea, natural water body Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Secondary clarifier** (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.

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**Septic tank** (septTnk). Septic tank Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Spring** (spr). A surface landform which provides an egress for groundwater or steam to flow out of the ground. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Stabilization pond** (stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment to reduce the organic content and remove pathogens from wastewater. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Stream** (str). A watercourse which is linear and flows across the solid portion of a planetary surface. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sewage truck** (swgTrck). Sewage truck Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Wastewater Triturator** (triturator). The location where wastewater transportation vehicles unload wastewater. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Upstream sites** (upstream). A general site type for upstream wastewater sampling sites. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Well** (well). A cylindrical hole, pit, or tunnel drilled or dug down to a depth from which water, oil, or gas can be pumped or brought to the surface. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Wastewater treatment plant** (wwtp). A general site type for wastewater treatment plants. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Back-up wastewater treatment site** (wwtpBack). Indicates a wastewater treatment plant where multiple labs are or were sampling, and where secondary samples are being taken. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Industrial wastewater treatment plant** (wwtpInd). Industrial wastewater treatment plant Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Municipal wastewater treatment plant for combined sewage** (wwtp-MuC). Municipal wastewater treatment plant for combined sewage Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Municipal wastewater treatment plant for sanitary sewage only** (wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Solid separation set**

(solidSeparationSet)set for the separation of solids. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Centrifugation** (cent). Describes solid separation from a wastewater sample via centrifugation. Likely connected to other method steps prior to analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Filtration** (filt). Describes solid separation from a wastewater sample via filtration. Proceeds further concentration or analysis of the liquid filtrate. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Gravity settling** (graSet). Describes solid separation from a wastewater sample where the sample material is allowed to settle by gravity, and then separated. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No Separation or Concentration** (noSep). Denoted that a sample did not undergo a solids separation protocol, or did not undergo a sample concentration protocol. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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### **Spike material set**

(spikeMatSet)set for spikeMat (aterial into which the recovery efficiency control target is spiked). Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Clarified sample** (clari). Clarified sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Dewatered solids** (deso). Dewatered solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Lysis buffer** (lysi). Lysis buffer. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Raw wastewater** (raws). Raw wastes water sample Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Raw post-pasteurized wastewater** (rppw). Raw wastewater sample post-pasteurization Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample concentrate** (samConc). Sample concentrate. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Recovery efficiency spike target set**

(spikeTargetSet)The set capturing containing all of the valid categories for the recovery efficiency control (or spike) target. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**bcov culture spike target** (bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**bcov spike target (unspecified)** (bcovGen). The bovine coronavirus (unspecified) is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**bcov vaccine spike target** (bcovVac). The bovine coronavirus vaccine is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**brsv culture spike target** (brsvCul). Cultured bovine respiratory syncytial virus (BRSV) is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**brsv vaccine spike target** (brsvVac). The bovine respiratory syncytial virus (BRSV) vaccine is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Heat inactivated sars-cov-2 virus spike target** (heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**hep g armored rna spike target** (hepGRnaMat). Hepatitis G armored RNA is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**murine hepatitis virus (MHV) spike target** (mhvSpike). Murine hepatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**ms2 coliphage spike target** (ms2ColMat). ms2 coliphage is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**murine coronavirus spike target** (muCoMat). Murine coronavirus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**oc43 spike target** (oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Parapoxvirus Orf Virus Spike Target** (parapoxSpike). parapoxvirus // Orf virus is used as the recovery efficiency control target. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**phi6 spike target** (phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Puro virus spike target** (puroMat). Puro Virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Vesicular stomatitis virus (VSV) target** (vsv). Vesicular stomatitis virus is used as the recovery efficiency control target. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Status set

(statusSet)A set for partID = Status to indicate whether a part is in current use or not. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Active** (active). Indicator that a part is in current use. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Deprecated** (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.

**Development** (development). Indicator that a part is under development use. See partID = status Status: active. First released: 2.0.0. Last updated: 2.0.0.

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## **Standard Curve Calculation Set**

(stdCurveSet)The set capturing containing all of the valid methods for the PCR standard curve calculations. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**serial dillution** (serDil). Describes a serial dilution process for standard curve generation for PCR. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## **Sample Storage Medium Set**

(stoMedSet)The set of valid categorical inputs for the stoMed field. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Amies Transport Medium** (atm). A buffer solution/medium that maintains viability of bacteria in wastewater and environmental samples during transport. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Buffered Peptone Water** (bpw). A buffer solution/medium used for bacterial enrichment, can also serve as a temporary preservative. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cary-Blair Transport Medium** (cbtm). A buffer solution/medium commonly used for bacterial preservation in stool and wastewater samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**DNA/RNA Shield** (dnRNAshield). 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.

**10% Glycerol Solution** (glycerol10). 10% Glycerol Solution - Common cryoprotectant for bacterial and viral storage in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Guanidine Thiocyanate** (gt). A buffer solution/medium that serves as a strong preservative for viral RNA, commonly used in molecular biology for RNA preservation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Hank's Balanced Salt Solution (HBSS)** (hbss). Hank's Balanced Salt Solution (HBSS) - Nutrient-rich buffer that maintains cell and microbial integrity in samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Lactated Ringer's Solution** (lrs). A buffer solution/medium sometimes used in combination with other preservatives to stabilize microbial samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**No sample storage medium used** (none). No sample storage medium used Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Phosphate Buffered Saline (PBS)** (pbs). An isotonic solution for general sample preservation, used when immediate freezing is available. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Peptone Water with Glycerol** (pwWg). A buffer solution/medium used in environmental sampling, especially for preserving microorganisms. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**RNAlater** (rnaLater). A buffer solution/medium that 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.

**Sterile Distilled Water with Sodium Thiosulfate** (sDWwST). Sterile Distilled Water with Sodium Thiosulfate - Used to neutralize chlorine for microbiological analysis in wastewater samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Skim Milk–Glycerol Medium** (smgm). A buffer solution/medium that protects bacteria in environmental samples, preventing freeze-thaw damage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Sucrose Phosphate Glutamate (SPG) Buffer** (spg). A buffer solution/medium that stabilizes viruses, including in wastewater samples, by preventing RNA degradation. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Sodium Thiosulfate Solution** (sts). A buffer solution/medium that neutralizes residual chlorine in wastewater samples, ensuring microbial viability. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**TE Buffer (Tris-EDTA)** (trisEDTA). A buffer solution/medium that preserves DNA stability in environmental samples. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Tryptic Soy Broth (TSB)** (tsb). Tryptic Soy Broth (TSB) - A nutrient-rich medium for bacterial survival, sometimes used for short-term storage. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Universal Transport Medium (UTM)** (utm). Universal Transport Medium (UTM) - Used for microbial preservation in various environmental samples, including wastewater. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Viral Transport Medium (VTM)** (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.

### **Surveillance Alert Value Set**

(survAlertSet)A set of valid categories for the public health action field, where the action type is ‘surveillance alert’. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Decreased surveillance** (decSurv). Scaling back of monitoring activities, often due to reduced risk. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**Increased surveillance** (incSurv). Intensified efforts to monitor disease trends or case counts. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Routine surveillance** (routSurv). Standard, ongoing collection of public health data. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Targetted surveillance initiated** (targSurv). Monitoring focused on a specific population, location, or risk factor. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Surveillance Level Set

(survLevelSet)The list of valid categories for the survLevel measure. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Building-level Surveillance** (builLev). Surveillance is done only at the level of a single building. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Community-level Surveillance** (communitLev). Surveillance is done at the level of an entire community. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Institution-level Surveillance** (instituLev). Surveillance is done at the level of an entire institution. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Multi-Community-level Surveillance** (multiComLev). The scope of the surveillance covers multiple communities. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Table column set**

(tableSet)The set for valid inputs in table columns. These categories are used in the parts list for columns named after tables to indicate the position and function of a given part in the entity relationship diagram of the data model. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Composite Key** (cK). Composite key for a table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Foreign key** (fK). Foreign key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Header** (header). Header for a table. Also known as a table variable or entiy relationship ‘attribute’. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Input** (input). Input for a table. Indicates if a part can be used in a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Primary key** (pK). Primary key for a table. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Template Set**

(tempSet)The organizing set for templates. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**DNA Template** (dna). Deoxyribonucleic Acid (DNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**RNA Template** (rna). Ribonucleic Acid (RNA) template is used for PCR or sequencing work. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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### **Threat designation Value Set**

(threatDesSet)A set of valid categories for the public health action field, where the action type is ‘threat designation’. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**De-escalated variant** (dev). A given microbial threat has been de-escalated; a de-escalated variant - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Variant of concern** (voc). A given microbial threat has been deemed a variant of concern - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Variant of interest** (voi). A given microbial threat has been deemed a variant of interest - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**variant under monitoring** (vum). A given microbial threat has been deemed a variant under monitoring - different institutions may use different criteria for assigning this threat level. Status: active. First released: 3.0.0. Last updated: 3.0.0.

### **Value treatment value set**

(valTreatSet)Valid set of values for the value treatment set. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Derived data** (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.

### *Measure, method, or attribute sets*

**Estimated data** (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.

**Predicted data** (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.

**Raw data** (raw). Raw data, without adjustment or additional treatment. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## **Weather set**

(weathSet)A set of the valid qualitative categories for the qualitative weather measure. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Cloudy** (cloudy). Qualitative category for the weather measure, specifying an overcast day with no rain. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Foggy** (foggy). Qualitative category for the weather measure, specifying a foggy or hazy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No rain** (noRain). Qualitative category for the weather measure, specifying no rainfall for a given day. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Rainy** (rainy). Qualitative category for the weather measure, specifying a rainy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Snowy** (snowy). Qualitative category for the weather measure, specifying a snowy day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Stormy Weather** (stormy). Stormy weather Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Sunny** (sunny). Qualitative category for the weather measure, specifying a clear and sunny day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### Fraction set for wide names

(wideFractionSet)Fraction set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**See Header for Fraction Analyzed** (hFr). An indicator in wide-names to show that information on the fraction analyzed is found under a separate header. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Liquid fraction** (liq). Liquid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Mixed/homogenized sample** (mix). Mixed or homogenized sample or fraction analyzed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Multiple fraction** (mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Not applicable** (NA). The field for which the expected value is not a property of the described object. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Not reported** (nr). A value could have been recorded, however, it was not. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Solid fraction (general)** (sol). Solid fraction of a sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Solid Fraction (Dry)** (solDry). Solid fraction of a sample - dry material is analyzed, by drying, baking, etc. of sludge or other solids. Status: active. First released: 2.3.0. Last updated: 2.3.0.

## *Nomenclatures*

**Solid fraction (Wet)** (solWet). Solid fraction of a sample - wet material is analyzed, and not dried. Ex. Sludge. Status: active. First released: 2.3.0. Last updated: 2.3.0.

## **Nomenclatures**

(nomenclatures). A classification system to report the measure class. See partID = nomenclatureID.

**International Classification of Diseases** (icd). Classification system for diseases in humans. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Nomenclature not applicable** (naNomenclature). Not applicable. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Nomenclaturre from the NCBI** (ncbiNom). Nomenclaturre from the National Center for Biotechnology Information Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NextClade nomenclature** (nextclade). Specifies variant or genetic nomenclature as set out by NextClade. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Pangolin nomenclature** (pangolin). Specifies variant or genetic nomenclature as set out by the Phylogenetic Assignment of Named Global Outbreak Lineages (Pangolin). Status: active. First released: 2.0.0. Last updated: 2.0.0.

**WHO nomenclature** (who). Specifies variant or genetic nomenclature as set out by the World Health Organization. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

## Quality indicators

(qualityIndicators). A measure of the quality of a reported value or sample. Only used for the dictionary entries of parts.

**Sequence Amplification Artifacts** (ampliArtifact). Sequence amplification artifacts detected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Below LOD** (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measured levels below LOQ** (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Delayed Arrival or Prolonged Transit** (delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Experiment Failed** (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**AI - Inhibition present but addressed** (flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**B - Trace levels of contamination** (flagB). Analytical result may be subject to “trace” levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**FI - Inhibition present and unaddressed** (flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed.

## *Quality indicators*

Therefore, no concentration estimate has been reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**J - Weak signal extrapolation** (flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ND - Non-detect** (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**UJ - Trace signal extrapolation** (flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., “trace” signal observed); the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**UQ - Unquantifiable** (flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample frozen** (frozen). Sample was frozen before analysis or processing Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low Average Genome Coverage** (lAGC). Average coverage of the genome is low/poor. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low breadth of coverage** (lBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low depth of coverage** (lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Leaked sample** (leaked). Sample leaked, some volume and material was lost. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low Coverage of Characteristic Mutations** (lowCovMut). Low coverage of characteristic mutations. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low-quality Sequence** (lowQualSeq). Low-quality sequence. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low Signal-to-Noise Ratio** (lowSNRatio). Low signal-to-noise ratio. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low-volume sample** (lowVol). Sample is low-volume, but was run regardless. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low Percent of Genome Captured** (lPGC). Only captured a small/low percentage of the genome. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Multiple issues** (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No quality concerns** (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample not labelled** (noLabel). Sample had no label Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample missing time stamp** (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NTC Amplification Detected** (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

## *Quality indicators*

**Control-plate Flag - NTCs** (ntcFlag). quality indicator for when there is observed amplification in the non-template controls (NTCs) of a PCR reaction. Status: depreciated. First released: 2.0.0. Last updated: 3.0.0.

**Value out of range** (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Value is an outlier** (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality concerns** (qf1). A flag to indicate there is a quality concern, not otherwise specified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sparse coverage** (sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sequence Contaminated** (seqContam). Sequence is contaminated. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Read Lengths Shorter Than Expected** (shortRead). Read lengths are shorter than expected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Sample spilled** (spill). Sample contents spilled from container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wide 95% interval** (wi). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample stored incorrectly** (wrongStorage). Sample was stored inappropriately. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample stored at wrong temperature** (wrongTemp). Sample was stored at an inappropriate temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

*Sets*

## **Quality indicator sets**

(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality measure set.

### **Generic quality flag set**

(genQualitySet)A quality set to specify any generic quality concerns about a measure or sample. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

**Multiple issues** (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No quality concerns** (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Quality concerns** (qf1). A flag to indicate there is a quality concern, not otherwise specified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Measures quality set**

(measQualitySet)A quality set for any measure, includes all the quality flag options for any measure. Used as an “any quality set” for measures, but excludes the sample quality flags to avoid confusion and data entry errors. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Below LOD** (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Quality indicator sets*

**Measured levels below LOQ** (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Delayed Arrival or Prolonged Transit** (delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Experiment Failed** (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**AI - Inhibition present but addressed** (flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**B - Trace levels of contamination** (flagB). Analytical result may be subject to “trace” levels of contamination; the target analyte was also detected in negative controls on the same run as the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**FI - Inhibition present and unaddressed** (flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**J - Weak signal extrapolation** (flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ND - Non-detect** (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**UJ - Trace signal extrapolation** (flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., “trace” signal observed);

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the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**UQ - Unquantifiable** (flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low breadth of coverage** (lBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low depth of coverage** (lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Multiple issues** (mI). Multiple issues have arisen in the sequencing process. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No quality concerns** (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample missing time stamp** (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NTC Amplification Detected** (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Value out of range** (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Quality indicator sets*

**Value is an outlier** (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Quality concerns** (qf1). A flag to indicate there is a quality concern, not otherwise specified. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sparse coverage** (sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wide 95% interval** (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **PCR quality set**

(pcrQualitySet) Quality set for PCR measures. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Below LOD** (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measured levels below LOQ** (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Experiment Failed** (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**AI - Inhibition present but addressed** (flagAI). The original sample was inhibited; however, the inhibition has been addressed through dilution. The reported concentration estimate is the updated result after addressing inhibition. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**B - Trace levels of contamination** (flagB). Analytical result may be subject to “trace” levels of contamination; the target analyte was also

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detected in negative controls on the same run as the sample. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**FI - Inhibition present and unaddressed** (flagFI). The original sample was inhibited; however, the inhibition has not been successfully addressed. Therefore, no concentration estimate has been reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**J - Weak signal extrapolation** (flagJ). Analytical result falls below the lowest concentration of the experiment-specific standard curve but above the y-intercept value; the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**ND - Non-detect** (flagND). No amplification occurred in the reaction; non-detect. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**UJ - Trace signal extrapolation** (flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve intercept value but evidence of clear amplification was present (i.e., “trace” signal observed); the reported value is based on the extrapolation of the standard curve in the non-linear region. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**UQ - Unquantifiable** (flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard curve. There was a detect, but we cannot quantify it with certainty. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No quality concerns** (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**NTC Amplification Detected** (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more

## *Quality indicator sets*

positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

**Value out of range** (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Value is an outlier** (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Sample quality set**

(sampleQualitySet)Quality set for a sample. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Delayed Arrival or Prolonged Transit** (delayArriv). A substantial delay (ie. of more than 14 days) between sample collection and the start of analysis. Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Sample frozen** (frozen). Sample was frozen before analysis or processing Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Leaked sample** (leaked). Sample leaked, some volume and material was lost. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low-volume sample** (lowVol). Sample is low-volume, but was run regardless. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**No quality concerns** (noConcern). A flag to indicate there is no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample not labelled** (noLabel). Sample had no label Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Sample missing time stamp** (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample spilled** (spill). Sample contents spilled from container. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample stored incorrectly** (wrongStorage). Sample was stored inappropriately. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample stored at wrong temperature** (wrongTemp). Sample was stored at an inappropriate temperature. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sequencing quality set

(seqQualitySet) Quality set for sequencing measures Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Sequence Amplification Artifacts** (ampliArtifact). Sequence amplification artifacts detected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Below LOD** (beLOD). Measure is below the limit of detection (LOD) for a specific analyte. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measured levels below LOQ** (belowLOQ). Indicates that a measurement detected the analyte, but at levels below the limit of quantification (LOQ). Status: active. First released: 2.2.3. Last updated: 2.2.3.

**Experiment Failed** (expFail). PCR experiment failed. No value reported. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low Average Genome Coverage** (lAGC). Average coverage of the genome is low/poor. Status: active. First released: 2.3.0. Last updated: 2.3.0.

## *Quality indicator sets*

**Low breadth of coverage** (lBC). The percentage of the genome covered by reads (the breadth) is low. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low depth of coverage** (lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing reads that are mapped incorrectly. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Low Coverage of Characteristic Mutations** (lowCovMut). Low coverage of characteristic mutations. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low-quality Sequence** (lowQualSeq). Low-quality sequence. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low Signal-to-Noise Ratio** (lowSNRatio). Low signal-to-noise ratio. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Low Percent of Genome Captured** (lPGC). Only captured a small/low percentage of the genome. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**No quality concerns** (noConcern). A flag to indicate there are no quality concern about the measure or sample. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample missing time stamp** (noTime). Sample is missing the autosampler time; incomplete metadata on collection. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**NTC Amplification Detected** (ntcAmp). Quality flag for when the non-template control (NTC) still sees amplification - ie. The NTCs in qPCR show a Ct value less than 40, or NTCs in a ddPCR have 3 or more positive droplets. Status: active. First released: 2.0.0. Last updated: 3.0.0.

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**Value out of range** (oor). Value is outside of the allowable range for quality control. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Value is an outlier** (out). Value is an outlier and may be of questionable quality. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sparse coverage** (sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate but coverage plots reveal missing genome pieces. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sequence Contaminated** (seqContam). Sequence is contaminated. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Read Lengths Shorter Than Expected** (shortRead). Read lengths are shorter than expected. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Wide 95% interval** (wI). The 95% interval is too wide, low confidence in results. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Shorthand or Short Name Set Type

(shortSets). Sets used to group together short names for tables or part types in ODM.

### Short Name Set

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

*Shorthand or Short Name Set Type*

**Accessions report table Shorthand** (ac). The abbreviated short name used to reference the report table for accessions and accessionIDs. Status: active. First released: 2.2.2. Last updated: 2.2.2.

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

**Calculations Table Short Name** (cl). The abbreviated short name used to reference the table for recording data on data treatments and calculations applied to measurements and reported values. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Contact table Shorthand** (co). The abbreviated short name used to reference the The table that contains information about a contact; a person who is the contact of a site or laboratory. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Countries look-up tables Shorthand** (cu). The abbreviated short name used to reference the Look up table for the possible country inputs. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Dataset table Shorthand** (ds). The abbreviated short name used to reference the report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Instrument table Shorthand** (in). The abbreviated short name used to reference the The table that contains information about instruments. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Language Look-up table Shorthand** (la). The abbreviated short name used to reference the Look up table for all languages, used to give structure to the translation table. Status: active. First released: 2.2.2. Last updated: 2.2.2.

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**Measures Part-type Shorthand** (mes). The abbreviated short name used to reference the The attribute to describe a part type of measures. All measures have `partType` = “measurements”. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Methods part-type Shorthand** (met). The abbreviated short name used to reference the Procedures or steps for collecting samples or performing measures. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Measure report table Shorthand** (mr). The abbreviated short name used to reference the The table that contains information and details about a given measure Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Measure set report table Shorthand** (ms). The abbreviated short name used to reference the The table that identifies sets of measures. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Organization table Shorthand** (or). The abbreviated short name used to reference the The table that contains information about a laboratory. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Parts Look-up table Shorthand** (pa). The abbreviated short name used to reference the Look up table containing all parts in of the data model. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Public Health Actions Report Table Shortname** (pha). The abbreviated short name used to reference the table for recording information on public health actions. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Polygon table Shorthand** (po). The abbreviated short name used to reference the The table that contains information about the geometry of a geographic area. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Polygon Relationships Table Short Name** (por). The abbreviated short name used to reference the table for recording the relationships

*Shorthand or Short Name Set Type*

between polygons. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Protocol relationships table Shorthand** (pr). The abbreviated short name used to reference the The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Protocols table Shorthand** (pro). The abbreviated short name used to reference the the table that contains the summary information and details about a given protocol. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Protocol steps table Shorthand** (ps). The abbreviated short name used to reference the The table for collecting metadata on individual steps in a protocol, methodological process, or assay. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Quality reports table Shorthand** (qr). The abbreviated short name used to reference the The table for recording the various quality metrics and indicators for samples and measures. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Sample relationships table Shorthand** (sar). The abbreviated short name used to reference the Table for recording the relationships between samples. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Sample report table Shorthand** (sas). The abbreviated short name used to reference the The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Sets look-up table Shorthand** (se). The abbreviated short name used to reference the Look up table for all sets, managing how categorical inputs

## Sets

for various methods and attributes are grouped together. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Sites table Shorthand** (si). The abbreviated short name used to reference the The table that contains information about a site; the location where an environmental sample was taken. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Translation look-up table Shorthand** (tr). The abbreviated short name used to reference the Look up table for translations of the description, label, and instruction for all parts. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Wide name table Shorthand** (wn). The abbreviated short name used to reference the The table for wide names. Status: active. First released: 2.2.2. Last updated: 2.2.2.

**Zones look-up table Shorthand** (zo). The abbreviated short name used to reference the Look up table for the possible sub-national region or zone inputs. Status: active. First released: 2.2.2. Last updated: 2.2.2.

## Specimens

(specimens). Measures or observations are taken from three types of substances: populations (humans or geographic areas), samples, sites. See partID = specimenID.

**See Header for Specimen** (hSp). An indicator to show in a wide-name that specimen information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Specimen not applicable** (naSpecimen). Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Specimen sets*

**Polygon** (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population** (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample** (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Site** (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Specimen sets**

(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be recorded for more than one specimen.

### **Any specimen set**

(anySpecimenSet)A specimen set that inculdes any specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Polygon** (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population** (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample** (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Site** (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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### **Specimen set not applicable**

(naSpecimenSet)A specimen set for when specimen/specimen set is not applicable. Use ‘not applicable’ when there is no specimen/set for the part  
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Specimen not applicable** (naSpecimen). Non applicable specimen.  
Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Polygon or site specimen set**

(polySiSpecimenSet)A specimen set that inculdes polygon or site specimen.  
Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Polygon** (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Site** (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Polygon specimen set**

(polySpecimenSet)A specimen set that inculdes only a polygon specimen.  
Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Polygon** (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## *Specimen sets*

### **Population or polygon specimen set**

(poPolySpecimenSet)A specimen set that inculdes population or polygon specimen. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Polygon** (poly). A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population** (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Population or sample set**

(poSaSpecimenSet)A specimen set that inculdes population or sample specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Population** (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample** (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Population or site set**

(poSiSpecimenSet)A specimen set that inculdes population or site specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Population** (pop). An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Site** (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Sets

### **Population specimen set**

(poSpecimenSet)A specimen set that includes only a population specimen.  
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Population** (pop). A measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

### **Sample specimen set**

(saSpecimenSet)A specimen set that includes only a sample specimen.  
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Sample** (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Site or sample specimen set**

(siSaSpecimenSet)A specimen set that includes site or sample specimen.  
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Sample** (sa). A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Site** (sit). A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## *Specimen sets*

### **Site specimen set**

(siSpecimenSet)A specimen set that inculdes only a site specimen. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Site (sit).** A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Speciment set for wide names**

(wideSpecimenSet)Speciment set for wide names. For wide names. Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**See Header for Specimen (hSp).** An indicator to show in a wide-name that specimen information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Specimen not applicable (naSpecimen).** Non applicable specimen. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Polygon (poly).** A measure made on a compartment or property within a polygon. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population (pop).** An measure or observation for a geographic area or population. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sample (sa).** A measure made on a compartment or property from a sample of a substance. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Site (sit).** A measure made on a compartment or property at a site. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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## Tables

(tables). Tables are where measures, methods and attributes are recorded. Tables represent the main entities of the environmental surveillance. An example of a table is **site** a collection of attributes such as site name and address to describe where environment samples are taken. PHES-ODM has report tables, but users can create their own tables as well.

**accessions Table** (accessions). Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Address table** (addresses). The table that contains information about addresses. Addresses can 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.

**Calculations Table** (calculations). Table for recording data on data treatments and calculations applied to measurements and reported values. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Contact table** (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Countries look-up tables** (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

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**Dataset table** (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Instrument table** (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Language Look-up table** (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Measure report table** (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Measure set report table** (measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or varients that are identified in a single sample. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Organization table** (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Parts Look-up table** (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Public Health Actions Report Table** (phActions). Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Polygon Relationships Table** (polygonRelationships). Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.3.0. Last updated: 2.3.0.

**Polygon table** (polygons). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Protocol relationships table** (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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.

**Protocols table** (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Protocol steps table** (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Quality reports table** (qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short

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name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Reporter table depreciated** (reportersDep). The table that contains information about a reporter of a sample, method, measure, or attribute. The short name for the table (partID) can be found in the instructions field. Status: depreciated. First released: 1.0.0. Last updated: 2.0.0.

**Sample relationships table** (sampleRelationships). Table for recording the relationships between samples. Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sample report table** (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site. Samples can be combined, split, stored and reused. The **Sample relationships** (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sets look-up table** (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Sites table** (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an environmental sample. Information in the site table does not regularly change. Consider using the MeasureReport table if the infomation changes often.

## Sets

The short name for the table (partID) can be found in the instructions field. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Translation look-up table** (translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Wide name table** (wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Zones look-up table** (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. Status: active. First released: 2.1.0. Last updated: 2.1.0.

## Units

(units). The unit of the measurement. Every measurement must have a unit. Meaning, **units** are a mandatory field whenever a measurement is recorded.

**Number of active cases** (acti). Number of active cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Number of active cases by Onset date** (actiCaseOn). Number of active cases by onset date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number of active cases by episode date** (actiEp). Number of active cases by episode date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

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**Number of active cases by Report date** (actiRep). Number of active cases by report date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number of active cases by test date** (actiTest). Number of active cases by test date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Breadth of coverage (>=5x depth)** (boc). The percentage of the reference genome covered by the sequenced data, to a prescribed read depth greater or equal to 5. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Base-pairs** (bps). A base pair (bp) is a unit of measurement in molecular biology that represents a pair of complementary nucleotides in DNA or RNA. The length of DNA sequences is often measured in base pairs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Episode date of confirmed cases** (caseEpDate). Episode date is the earliest of onset, test or reported date for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Onset date of confirmed cases** (caseOnDate). Earliest that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Report date of confirmed cases** (caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and this measure is most commonly reported and used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Test date of confirmed cases** (caseTestDate). Date that the covid-19 test was performed for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Degrees Celcius** (cel). Degrees Celsius. Status: active. First released: 1.1.0. Last updated: 2.0.0.

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**Colony Forming Units** (cfu). Colony forming units Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CFU per 100 ml** (cfu100). Colony forming units per 100 ml of filtered sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Colony forming units per grams total solids** (cfgTS). colony forming units per grams total solids (CFU/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Colony forming units per milliliter** (cfumL). colony forming units per milliliter (CFU/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Centimetres** (cm). Unit part for the SI unit of centimetres. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Number of confirmed cases** (conf). Number of confirmed cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Number of confirmed cases by episode date** (confEp). Number of confirmed cases of a given disease, totaled by episode date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Number of confirmed Cases Onset date** (confOn). Number of confirmed cases of a given disease, totaled by onset date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Number of confirmed cases by report date** (confRep). Number of confirmed cases of a given disease, totaled by report date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Number of confirmed cases test date** (confTest). Number of confirmed cases of a given disease, totaled by test date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Gene copies per well** (cpWell). Gene or variant copies per well. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Cycle threshold or quantification cycle (Ct or Cq) (ct).** Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Cycle threshold per quantification cycle (ctcq).** cycle threshold (Ct) / quantification cycle (Cq) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Days** (days). A unit for indicating a length of time in days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Deaths** (death). Units for describing a population measure of patients who have died from a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Detected** (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Depth of coverage** (doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Efficiency** (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Degree Fahrenheit** (fah). Unit for temperature, degrees Fahrenheit. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Formazin nephelometric unit** (fnu). formazin nephelometric unit (FNU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Feet** (foot). foot (ft) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gene copies** (gc). Gene or variant copies Status: active. First released: 1.0.0. Last updated: 2.0.0.

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**Gene copies per copy of crAssphage** (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per day** (gcDay). Unit of measurement of the number of gene copies per day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**gene copies per day per 100,000 people** (gcDay100k). The unit for measures reflecting the gene copies per day per 100,000 people in the population. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Gene copies per gram solids** (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per L** (gcL). Gene or variant copies per litre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per mL** (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per millilitre per 100,000 people** (gcMl100k). Unit of measurement of the number of gene copies per millilitre per 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gene copies per PMMoV copy** (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per Reaction** (gcRx). Gene or variant copies per reaction in PCR Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gram per kilogram** (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gram per liter** (gL). gram per liter (g/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Gram per cubic metre** (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Nitrogen per total solids** (gNgTS). nitrogen per total solids (gN/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Grams per total solids** (gPergTS). Grams per total solids (g/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Orthophosphate per total solids** (gPO43gTS). orthophosphate per total solids (gPO43-/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Orthophosphate as phosphorus per total solids** (gPO4PgTS). orthophosphate as phosphorus per total solids (gPO4-P/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Grams** (grams). A unit of mass or weight. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**General Hospital Admissions** (hosa). Hospital admissions or patients newly admitted to hospital. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Hospital Census** (hosc). Hospital census or the number of people admitted with an ailment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Hours** (hours). A unit for indicating a length of time in hours. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Intensive care unit patients** (icu). Units for describing a population measure of patients who are in intensive care due to a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Inch** (inch). inch (in) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Intercept** (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Kilogram per cubic meter** (kgm3). Kilogram per cubic meter (kg/m<sup>3</sup>) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Kilogram per second** (kgS). Kilograms per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Kilolitres** (kl). Kilolitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Litres** (l). Litres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Litres per day** (lday). Unit of litres per day, usually for measuring flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Liter per hour** (lhour). liter per hour (L/h) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Liter per minute** (lmin). liter per minute (L/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**log10 gene copies per g** (log10cpG). Unit for log10 copies per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

**log10 gene copies per L** (log10cpL). Unit for log10 copies per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

**log10 gene copies per mL** (log10cpml). Unit for log10 copies per mililitre Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Log10 gene copies per 100 milliliter** (log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Log10 gene copies per nanogram total DNA** (log10gcngDNA). log10 gene copies per nanogram total DNA Status: active. First released: 3.0.0. Last updated: 3.0.0.

**log10 micrograms per g** (log10ugG). Unit for log10 micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

**log10 micrograms per L** (log10ugL). Unit for log10 micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Liter per second** (lsec). liter per second (L/s) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cubic metres per day** (m3D). Cubic metres per day. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Cubic metres per hour** (m3H). Cubic metres per hour. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Cubic meter per minute** (m3min). cubic meter per minute ( $m^3/min$ ) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cubic metres per second** (m3S). Cubic metre per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Mega-bases or Mega-base-pairs** (megaB). A mega-base (Mb) or mega-base-pair (Mbp) is equal to one million base pairs (1,000,000 bp). It is commonly used to describe the size of genomes or large DNA sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Milliequivalent per liter** (meqL). Unit for alkalinity, miliequivalents per litre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Meter** (meter). meter (m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Millions of gallons per day (MG/D)** (mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of

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gallons per day. Also can be used to measure flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Milligrams per litre** (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Milligram per liter of calcium carbonate** (mgLCaCO<sub>3</sub>). Unit for alkalinity, milligram per litre of calcium carbonate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Milligrams orthophosphate per liter** (mgPO<sub>4</sub>3L). milligrams orthophosphate per liter (mg PO<sub>4</sub>3-/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Milligrams orthophosphate as phosphorus per liter** (mgPO<sub>4</sub>PL). milligrams orthophosphate as phosphorus per liter (mg PO<sub>4</sub>-P/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Minutes** (minutes). A unit for indicating a length of time in minutes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Millilitres** (ml). Millilitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Megalitres per day (ML/d)** (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Millimetres** (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Millimho per centimeter** (mmhocm). Millimho per centimeter (mmho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Months** (months). A unit for indicating a length of time in months. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Most probable number per 100 milliliters** (mpn100mL). most probable number per 100 milliliter (MPN/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Most probable number per milliliter** (mpnmL). most probable number per milliliter (MPN/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Metres per second** (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**MillSiemen per centimeter** (mScm). MilliSiemens per centimeter (mS/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**MilliVolt** (mvolt). milliVolt (mV) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Unit not applicable** (naUnit). Not applicable for units. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population of newly vaccinated persons** (newVax). Population of newly vaccinated persons Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Nanograms per liter** (ngL). nanograms per liter (ng/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nano-molar** (nM). the unit of nanomolar. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number per 100 kilo-base-pairs** (nPerKbp). This unit expresses the frequency of an event (such as a mutation, binding site, or feature) per 100,000 base pairs (kbp) of DNA or RNA. It normalizes counts across genomic regions of different lengths, making comparisons more meaningful. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nephelometric turbidity unit** (ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see “turbidity” under measureIDs). Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Other Unit deprecated** (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.

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**PCR Quanitification Cycles** (pcrCycles). A count unit of how many Polymerase Chain Reaction (PCR) cycles it took to detect a real signal from a sample. Equivalent to the PCR cycle number at which a sample's reaction curve intersects the threshold line. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Number of people** (peeps). Unit specifying a number of people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Percent** (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Percent recovery** (percRec). Percent of the surrogate recovery for a recovery efficiency control assay (as a unit). Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Persons for square kilometre** (personPerKm). Persons per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Persons per square mile** (personPerMile). Persons per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Population equivalents** (popEq). A unit for measuring of design capacity for wastewater treatment plants, represented as the approximate amount of water a signle person would use. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Percent positive** (pp). Percent positive of sample measures. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**parts per million** (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Percent positivity rate** (pprt). Percent positivity rate of tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Percent primary sludge** (pps). Percentage of total solids, for primary sludge. Status: active. First released: 1.0.0. Last updated: 2.0.0.

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**parts per thousand** (ppt). Parts per thousand. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Proportion of total** (prop). Proportion as a percent of total. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Proportion of variant in sample** (propV). Proportion of a variant as percent of total variants. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Practical salinity unit** (psu). practical salinity unit (PSU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Number of positive tests** (ptot). Number of positive tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**R squared** (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Ratio** (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Recovered patients** (recov). Units for describing a population measure of patients who have recovered from a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Residents per square kilometre** (resPerKm). Residents per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Residents per square mile** (resPerMile). Residents per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Rate per 100,000** (rP100). Units for describing a population measure of a rate of case incidence per 100,000 people of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Revolutions per minute (RPM)** (rpm). RPM stands for “Revolutions per minute.” This is how centrifuge manufacturers generally describe how

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fast the centrifuge is going. The rotor, regardless of its size, is revolving at that rate. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Seconds** (seconds). The unit of time, seconds. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**slope** (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Siemens per meter** (sm). Siemens per meter (S/m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Number of tests performed** (test). Number of tests performed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Micrograms per gram** (ugG). Micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Micrograms per litre** (ugL). Micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Micrograms per milligram** (ugmg). Concentration unit of micrograms per milligram. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Micro-litres** (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Micromho per centimeter** (umhocm). Micromho per centimeter ( mho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Unitless measure** (unitless). A unit for unitless measures, like pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Micro-Siemens per centimetre** (uSCm). Micro-siemens per centimetre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Frequency of variants detected** (varFreq). A description of the frequency of a variants detected. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Population with 1 dose of vaccine** (vax1). The population with exactly 1 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Proportion of population with 1+ vaccine dose(s)** (vax1p). Specifies the portion of the population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 1+ dose(s) of vaccine** (vax1plus). The population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population with 2 or more doses of vaccine** (vax2). The population with exactly 2 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Proportion of population with 2+ vaccine doses** (vax2p). Specifies the portion of the population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 2+ or more doses of vaccine** (vax2plus). The population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population with 3 or more doses of vaccine** (vax3). The population with exactly 3 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.2.0.

**Proportion of population with 3+ vaccine doses** (vax3p). Specifies the portion of the population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 3+ or more doses of vaccine** (vax3plus). The population with 3 or more doses of vaccine, with the vaccine specified in

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the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population with 4 or more doses of vaccine** (vax4). The population with exactly 4 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Proportion of population with 4+ vaccine doses** (vax4p). Specifies the portion of the population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 4+ or more doses of vaccine** (vax4plus). The population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Weeks** (weeks). A unit of measuring time in weeks, or periods of seven days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Weight for weight** (ww). weight for weight (% w/w) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Relative Centrifugal Force (RCF) or x g units** (xg). RCF (Relative Centrifugal Force) denotes the degree of force exerted on a sample. RCF is quantified in multiples of the gravitational acceleration that is standard at the Earth's surface (x g). Thus, the terms RCF and XG are often used interchangeably in centrifugation protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Years** (years). A unit for indicating a length of time in years. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Unit sets**

(unitSets). Sets of units. Contains units that are associated with part types such as measures. Sets are lists of input values. Each input value within a set is a part (has a partID) that can be reused between sets. For example, a set A could contain the values of ‘yes’ and ‘no’; and set B could contain the values of ‘yes’, ‘no’, and ‘maybe.’ partTypes with sets include aggregations, compartments, missingness, quality flags, specimens, and units. Measures with categories and dataTypes have their own specific sets (catSetID) because their input values are unique and are not reused.

### **Absolute humidity unit set**

(absHumidUnitSet)Unit set for absolute humidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Gram per cubic metre** (gm3). Density unit. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

### **Alkalinity unit set**

(alkalinitySet)Unit set for alkalinity measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Milliequivalent per liter** (meqL). Unit for alkalinity, miliequivalents per litre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Milligrams per litre** (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**parts per million** (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Allele unit set

(alleleUnitSet)Unit set for alleles. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Cycle threshold or quantification cycle (Ct or Cq) (ct)**. Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Detected** (det). Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Depth of coverage** (doc). The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Efficiency** (efficient). The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Gene copies per copy of crAssphage** (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per gram solids** (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per mL** (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

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**Gene copies per PMMoV copy** (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Intercept** (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**R squared** (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**slope** (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Bacteria unit set**

(bacteriaUnitSet)Unit set for bacteria-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Colony Forming Units** (cfu). Colony forming units Status: active. First released: 3.0.0. Last updated: 3.0.0.

**CFU per 100 ml** (cfu100). Colony forming units per 100 ml of filtered sample. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Colony forming units per grams total solids** (cfugTS). colony forming units per grams total solids (CFU/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Colony forming units per milliliter** (cfumL). colony forming units per milliliter (CFU/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Most probable number per 100 milliliters** (mpn100mL). most probable number per 100 milliliter (MPN/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Most probable number per milliliter** (mpnmL). most probable number per milliliter (MPN/mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Base-pair unit set

(basePairSet)Unit set for base-pair measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Base-pairs** (bps). A base pair (bp) is a unit of measurement in molecular biology that represents a pair of complementary nucleotides in DNA or RNA. The length of DNA sequences is often measured in base pairs. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Mega-bases or Mega-base-pairs** (megaB). A mega-base (Mb) or mega-base-pair (Mbp) is equal to one million base pairs (1,000,000 bp). It is commonly used to describe the size of genomes or large DNA sequences. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Number per 100 kilo-base-pairs** (nPerKbp). This unit expresses the frequency of an event (such as a mutation, binding site, or feature) per 100,000 base pairs (kbp) of DNA or RNA. It normalizes counts across genomic regions of different lengths, making comparisons more meaningful. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Capacity unit set

(capacityUnitSet)Unit set for capacity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Millions of gallons per day (MG/D)** (mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of gallons per day. Also can be used to measure flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Megalitres per day (ML/d)** (mld). Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population equivalents** (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.

## Conductivity unit set

(conductivityUnitSet)Unit set related to conductivity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Millimho per centimeter** (mmhocm). Millimho per centimeter (mmho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Millisiemen per centimeter** (mScm). Millisiemens per centimeter (mS/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**Micromho per centimeter** (umhocom). Micromho per centimeter ( mho/cm) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Micro-Siemens per centimetre** (uSCm). Micro-siemens per centimetre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Dissolved gas concentration unit set

(dissGasUnitSet)Unit set for carbon dioxide concentrations measurements in water or air. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Milligrams per litre** (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**parts per million** (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

## Electrical potential unit set

(electricPotentSet)Unit set for measurements of electrical potential. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Volume flow rate unit set

(flowUnitSet)Unit set for volume flow measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Kilogram per second** (kgS). Kilograms per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Litres per day** (lday). Unit of litres per day, usually for measuring flow. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Liter per hour** (lhour). liter per hour (L/h) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Liter per minute** (lmin). liter per minute (L/min) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Liter per second** (lsec). liter per second (L/s) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cubic metres per day** (m3D). Cubic metres per day. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Cubic metres per hour** (m3H). Cubic metres per hour. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Cubic meter per minute** (m3min). cubic meter per minute ( $m^3/min$ ) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cubic metres per second** (m3S). Cubic metre per second. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Millions of gallons per day (MG/D)** (mgd). A unit for measuring of design capacity for wastewater treatment plants, represented as millions of

## Sets

gallons per day. Also can be used to measure flow. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Megalitres per day (ML/d) (mld)**. Megalitres per day. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Genetics unit set

(geneticUnitSet)Unit set for genetic-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Breadth of coverage (>=5x depth) (boc)**. The percentage of the reference genome covered by the sequenced data, to a prescribed read depth greater or equal to 5. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Gene copies per well (cpWell)**. Gene or variant copies per well. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Cycle threshold or quantification cycle (Ct or Cq) (ct)**. Cycle thresholds in a PCR assay. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Cycle threshold per quantification cycle (ctcq)**. cycle threshold (Ct) / quantification cycle (Cq) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Detected (det)**. Substance detected or not detected. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Depth of coverage (doc)**. The average number of reads representing a given nucleotide in the reconstructed sequence, provided as a value as a fold of coverage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Efficiency (efficient)**. The efficiency reported for a standard curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Gene copies** (gc). Gene or variant copies Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per copy of crAssphage** (gcCrA). Gene or variant copies per copy of crAssphage. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per day** (gcDay). Unit of measurement of the number of gene copies per day. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gene copies per gram solids** (gCGS). Gene or variant copies per gram solids. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per L** (gcL). Gene or variant copies per litre. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per mL** (gcMl). Gene or variant copies per millilitre of solution. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per millilitre per 100,000 people** (gcMl100k). Unit of measurement of the number of gene copies per millilitre per 100,000 people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gene copies per PMMoV copy** (gcPpmov). Gene or variant copies per copy of PMMoV. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Gene copies per Reaction** (gcRx). Gene or variant copies per reaction in PCR Status: active. First released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Intercept** (inter). Intercept value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

Sets

**log10 gene copies per g** (log10cpG). Unit for log10 copies per gram  
Status: active. First released: 2.2.0. Last updated: 2.2.0.

**log10 gene copies per L** (log10cpL). Unit for log10 copies per litre  
Status: active. First released: 2.2.0. Last updated: 2.2.0.

**log10 gene copies per mL** (log10cpml). Unit for log10 copies per millilitre  
Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Log10 gene copies per 100 milliliter** (log10gc100mL). log10 gene copies per 100 milliliter (log10 GC/100 mL) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Log10 gene copies per nanogram total DNA** (log10gcngDNA). log10 gene copies per nanogram total DNA Status: active. First released: 3.0.0. Last updated: 3.0.0.

**log10 micrograms per g** (log10ugG). Unit for log10 micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

**log10 micrograms per L** (log10ugL). Unit for log10 micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

**PCR Quanitification Cycles** (pcrCycles). A count unit of how many Polymerase Chain Reaction (PCR) cycles it took to detect a real signal from a sample. Equivalent to the PCR cycle number at which a sample's reaction curve intersects the threshold line. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Percent recovery** (percRec). Percent of the surrogate recovery for a recovery efficiency control assay (as a unit). Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Proportion of total** (prop). Proportion as a precent of total. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Proportion of variant in sample** (propV). Proportion of a variant as percent of total variants. Status: active. First released: 1.1.0. Last updated: 2.0.0.

## *Unit sets*

**R squared** (r2). R-squared value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**slope** (slope). Slope value of the calibration curve. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Unit set not applicable**

(naUnitSet)Not applicable for unit sets. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Unit not applicable** (naUnit). Not applicable for units. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Percent unit set**

(percentUnitSet)Unit set for percentages. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Percent** (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Population density unit set**

(popDensUnitSet)Unit set for measures of population density of a site. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Sets

**Persons for square kilometre** (personPerKm). Persons per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Persons per square mile** (personPerMile). Persons per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Residents per square kilometre** (resPerKm). Residents per square kilometre. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Residents per square mile** (resPerMile). Residents per square mile. Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Population unit set

(populationUnitSet)Unit set for hospital-related measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Number of active cases** (acti). Number of active cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Number of active cases by Onset date** (actiCaseOn). Number of active cases by onset date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number of active cases by episode date** (actiEp). Number of active cases by episode date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number of active cases by Report date** (actiRep). Number of active cases by report date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Number of active cases by test date** (actiTest). Number of active cases by test date. Status: active. First released: 2.2.0. Last updated: 2.2.0.

*Unit sets*

**Episode date of confirmed cases** (caseEpDate). Episode date is the earliest of onset, test or reported date for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Onset date of confirmed cases** (caseOnDate). Earliest that symptoms were reported for a confirmed case. This data is often not known and reported. In lieu, episode is used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Report date of confirmed cases** (caseRepDate). Date that the numbers were reported publicly for a confirmed case. Typically, reported data and this measure is most commonly reported and used. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Test date of confirmed cases** (caseTestDate). Date that the covid-19 test was performed for a confirmed case. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Number of confirmed cases** (conf). Number of confirmed cases. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Number of confirmed cases by episode date** (confEp). Number of confirmed cases of a given disease, totaled by episode date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Number of confirmed Cases Onset date** (confOn). Number of confirmed cases of a given disease, totaled by onset date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Number of confirmed cases by report date** (confRep). Number of confirmed cases of a given disease, totaled by report date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

**Number of confirmed cases test date** (confTest). Number of confirmed cases of a given disease, totaled by test date. Status: active. First released: 1.0.0. Last updated: 2.2.0.

## Sets

**Deaths** (death). Units for describing a population measure of patients who have died from a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**General Hospital Admissions** (hosa). Hospital admissions or patients newly admitted to hospital. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Hospital Census** (hosc). Hospital census or the number of people admitted with an ailment. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Intensive care unit patients** (icu). Units for describing a population measure of patients who are in intensive care due to a given cause. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population of newly vaccinated persons** (newVax). Population of newly vaccinated persons Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Number of people** (peeps). Unit specifying a number of people. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Percent positivity rate** (pprt). Percent positivity rate of tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Number of positive tests** (ptot). Number of positive tests conducted within a day in a given region. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Recovered patients** (recov). Units for describing a population measure of patients who have recovered from a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

*Unit sets*

**Rate per 100,000** (rP100). Units for describing a population measure of a rate of case incidence per 100,000 people of a given disease. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Number of tests performed** (test). Number of tests performed. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Population with 1 dose of vaccine** (vax1). The population with exactly 1 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Proportion of population with 1+ vaccine dose(s)** (vax1p). Specifies the portion of the population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 1+ dose(s) of vaccine** (vax1plus). The population with 1 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population with 2 or more doses of vaccine** (vax2). The population with exactly 2 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Proportion of population with 2+ vaccine doses** (vax2p). Specifies the portion of the population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 2+ or more doses of vaccine** (vax2plus). The population with 2 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population with 3 or more doses of vaccine** (vax3). The population with exactly 3 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.2.0.

## Sets

**Proportion of population with 3+ vaccine doses** (vax3p). Specifies the portion of the population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 3+ or more doses of vaccine** (vax3plus). The population with 3 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Population with 4 or more doses of vaccine** (vax4). The population with exactly 4 dose of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Proportion of population with 4+ vaccine doses** (vax4p). Specifies the portion of the population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Population with 4+ or more doses of vaccine** (vax4plus). The population with 4 or more doses of vaccine, with the vaccine specified in the measure field. Status: active. First released: 2.2.0. Last updated: 2.2.0.

## Precipitation unit set

(precipitationUnitSet)Unit set for percipitation measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Centimetres** (cm). Unit part for the SI unit of centimetres. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Feet** (foot). foot (ft) Status: active. First released: 3.0.0. Last updated: 3.0.0.

## *Unit sets*

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Inch** (inch). inch (in) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Meter** (meter). meter (m) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Millimetres** (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

### **Relative humidity unit set**

(relHumidUnitSet)Unit set for relative humidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Percent** (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

### **Salinity unit set**

(salinityUnitSet)Unit set for salinity measurements. Status: active. First Released: 3.0.0. Last updated: 3.0.0.

**Gram per kilogram** (gkg). gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Gram per liter** (gL). gram per liter (g/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Sets

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**parts per thousand** (ppt). Parts per thousand. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Practical salinity unit** (psu). practical salinity unit (PSU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Weight for weight** (ww). weight for weight (% w/w) Status: active. First released: 3.0.0. Last updated: 3.0.0.

## Specific humidity unit set

(specHumidUnitSet)Unit set for specific humidity. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Ratio** (ratio). Ratio (unitless) Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Speed Unit Set

(speedUnitSet)Unit set for reporting speeds (centrifugation speed, etc.) Status: active. First Released: 2.2.0. Last updated: 2.2.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Metres per second** (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**Revolutions per minute (RPM)** (rpm). RPM stands for “Revolutions per minute.” This is how centrifuge manufacturers generally describe how fast the centrifuge is going. The rotor, regardless of its size, is revolving at that rate. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Relative Centrifugal Force (RCF) or x g units (xg).** RCF (Relative Centrifugal Force) denotes the degree of force exerted on a sample. RCF is quantified in multiples of the gravitational acceleration that is standard at the Earth’s surface (x g). Thus, the terms RCF and XG are often used interchangeably in centrifugation protocols. Status: active. First released: 2.2.0. Last updated: 2.2.0.

### **Standard concentration unit set**

(stdConcentrationUnitSet)Unit set for concentration measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Gram per kilogram (gkg).** gram per kilogram (g/kg) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nitrogen per total solids (gNgTS).** nitrogen per total solids (gN/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Grams per total solids (gPergTS).** Grams per total solids (g/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Orthophosphate per total solids (gPO43gTS).** orthophosphate per total solids (gPO43-/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Orthophosphate as phosphorus per total solids (gPO4PgTS).** orthophosphate as phosphorus per total solids (gPO4-P/gTS) Status: active. First released: 3.0.0. Last updated: 3.0.0.

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**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Kilogram per cubic meter** (kgm3). Kilogram per cubic meter (kg/m<sup>3</sup>) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Milligrams per litre** (mgL). Milligrams per litre. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Milligram per liter of calcium carbonate** (mgLCaCO3). Unit for alkalinity, miligram per litre of calcium carbonate. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Milligrams orthophosphate per liter** (mgPO43L). milligrams orthophosphate per liter (mg PO43-/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Milligrams orthophosphate as phosphorus per liter** (mgPO4PL). milligrams orthophosphate as phosphorus per liter (mg PO4-P/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nanograms per liter** (ngL). nanograms per liter (ng/L) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Nano-molar** (nM). the unit of nanomolar. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Percent** (perc). Percentage. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**parts per million** (ppm). Parts per million. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Percent primary sludge** (pps). Percentage of total solids, for primary sludge. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Micrograms per gram** (ugG). Micrograms per gram Status: active. First released: 2.2.0. Last updated: 2.2.0.

## *Unit sets*

**Micrograms per litre** (ugL). Micrograms per litre Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Micrograms per milligram** (ugmg). Concentration unit of micrograms per milligram. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Micro-litres** (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

### **Temperature unit set**

(temperatureUnitSet)Unit set for temperature measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Degrees Celcius** (cel). Degrees Celsius. Status: active. First released: 1.1.0. Last updated: 2.0.0.

**Degree Fahrenheit** (fah). Unit for temperature, degrees Fahrenheit. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

### **Time unit set**

(timeUnitSet)The unit set for measures of time. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Days** (days). A unit for indicating a length of time in days. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Hours** (hours). A unit for indicating a length of time in hours. Status: active. First released: 2.0.0. Last updated: 2.0.0.

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**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Minutes** (minutes). A unit for indicating a length of time in minutes. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Months** (months). A unit for indicating a length of time in months. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Seconds** (seconds). The unit of time, seconds. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Weeks** (weeks). A unit of measuring time in weeks, or periods of seven days. Status: active. First released: 3.0.0. Last updated: 3.0.0.

**Years** (years). A unit for indicating a length of time in years. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Turbidity unit set

(turbidityUnitSet)Unit set for turbidity measurements. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**Formazin nephelometric unit** (fnu). formazin nephelometric unit (FNU) Status: active. First released: 3.0.0. Last updated: 3.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Nephelometric turbidity unit** (ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see “turbidity” under measureIDs). Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Unitless unit set**

(unitlessUnitSet)Unit set for measurements that does not have units. Status: active. First Released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Unitless measure** (unitless). A unit for unitless measures, like pH. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## **Volume unit set**

(volumeUnitSet)Unit set of volume measurements. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

**Grams** (grams). A unit of mass or weight. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Kilolitres** (kl). Kilolitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Litres** (l). Litres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Millilitres** (ml). Millilitres of volume Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Millimetres** (mm). Unit part for the SI unit of millimetres. Status: active. First released: 1.1.0. Last updated: 2.0.0.

## Sets

**Percent positive** (pp). Percent positive of sample measures. Status: active. First released: 1.0.0. Last updated: 2.0.0.

**Sub-variant or lineage** (subVar). A unit used to report a specific genetic lineage, or to specify that a reported variant is a sub-variant of another. Status: active. First released: 2.0.0. Last updated: 2.0.0.

**Micro-litres** (uL). The unit of microlitres. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Frequency of variants detected** (varFreq). A description of the frequency of variants detected. Status: active. First released: 2.0.0. Last updated: 2.0.0.

## Wind speed unit set

(windSpeedUnitSet)Unit set for wind speed measurements. Status: active. First Released: 1.0.0. Last updated: 2.0.0.

**See Header for Unit** (hUn). An indicator to show in a wide-name that unit information is located in a different column. Status: active. First released: 2.2.0. Last updated: 2.2.0.

**Metres per second** (mps). metres per second. Status: active. First released: 2.0.0. Last updated: 2.0.0.

# Tables

New names:

```
* `` -> `...108`  
* `` -> `...109`  
* `` -> `...110`  
* `` -> `...111`  
* `` -> `...112`  
* `` -> `...113`  
* `` -> `...114`  
* `` -> `...115`  
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### Tables

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```

## Dictionary v3.0.0 Documentation v2.1.0

The ODM database model has 21 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. Each table has mandatory and optional headers.

### Data storage

Store all ODM data in the 21 recommended tables to ensure optimal interoperability and support by the [ODM validation toolkit](#) and other ODM libraries.

Users can, however, create custom tables or ‘views’ by merging fields from any table. A common format for data entry format are “wide” table format, with *one day per row* and multiple measures or attributes per row. It is important to note that this guide does not provide instructions on generating wide tables.

## **Table types**

There are five table types:

- 1) **Regular report tables.** The `measures` and `samples` tables are used for daily reporting of new measurements and information on sample collection. There are three tables that support regular reporting:- `measureSets` (optional) is used to link measures, `sampleRelationships` (optional) is used when samples are pooled or split, and `qualityReports` is used for detailed quality assurance and control measures.
- 2) **Contact information tables.** The `sites`, `organizations`, `contacts`, and `addresses` tables store contact information for the testing site and the person who performed the testing.
- 3) **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.
- 4) **Other report tables.** The `polygons` table stores information on the sample area and the `datasets` table includes information on the data custodian and owner.
- 5) **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. 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.

## Tables

### Header roles

Each table in the ODM has column headers, also known as table variables, fields, or entity relationship attributes. The header serves as the top row and contains the variable name.

**Primary key (PK)** - With the exception of the dictionary tables, 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 connects an entry to another table with a primary key. 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 **measurement date**. The ODM validation toolkit can be used to validate data, and will return an error if a table lacks a mandatory header or if there are missing row entries for mandatory fields.

Additionally, there are special headers called **mandatoryIf** headers. These headers are mandatory if certain conditions apply. For example, the **protocol steps** table has row entries that are either **measures** or **methods**. If the row entry is a **measure**, then a **unit** becomes **mandatory** since all measures must have a unit. Therefore, units are **mandatoryIf** in the protocol steps table.

## **Table list**

accessions Table  
Address table  
Calculations Table  
Contact table  
Countries look-up tables  
Dataset table  
Instrument table  
Language Look-up table  
Measure report table  
Measure set report table  
Organization table  
Parts Look-up table  
Public Health Actions Report Table  
Polygon Relationships Table  
Polygon table  
Protocol relationships table  
Protocols table  
Protocol steps table  
Quality reports table  
Sample relationships table  
Sample report table

## Tables

Sets look-up table

Sites table

Translation look-up table

Wide name table

Zones look-up table

### **accessions Table**

partID: accessions. Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field. ac

**Accession Number in Repository** (accessNum). The accession number for the data entry in the given data repository or hosting platform.Role: Header.Requirement: mandatory.Data type: varchar.

**Version of Data Hosting Platform/Repository** (hostVersion). The version of the data repository or hosting platform being used.Role: Header.Requirement: optional.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### **Address table**

partID: addresses. The table that contains information about addresses. Addresses can recorded for sites, organizations or contacts (individuals). The Sites, Organizations, and Contacts tables include a link to the addresses

### *Table list*

table through Address ID. The short name for the table (partID) can be found in the instructions field. ad

**Address Line 1** (addL1). Line 1 (the street name, number and direction) for a given address.Role: Header.Requirement: mandatory.Data type: varchar.

**Address Line 2** (addL2). Line 2 (the unit number) for a given address.Role: Header.Requirement: optional.Data type: varchar.

**City** (city). The city where a site or organization is located; part of the address.Role: Header.Requirement: mandatory.Data type: varchar.

**Postal or Zip Code** (pCode). The zip code or postal code for a given address, specifying a specific geographic area.Role: Header.Requirement: optional.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Calculations Table**

partID: calculations. Table for recording data on data treatments and calculations applied to measurements and reported values. cl

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: optional.Data type: varchar.

**Summary worksheet** (summary). Summary sheet of the dictionary.xlsx file.Role: Header.Requirement: optional.Data type: varchar.

## Tables

**Sequence Order** (order). The order a single calculation/data treatment takes within the full container pipeline/workflow.Role: Header.Requirement: recommended.Data type: integer.

**Equation** (equation). The equation used in the calculation/data treatment.Role: Header.Requirement: recommended.Data type: varchar.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

**Source Code** (sourceCode). The source code for the calculation/data treatment, more applicable for algorithms/more complex steps.Role: Header.Requirement: recommended.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## Contact table

partID: contacts. The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field. co

**First name of contact** (firstName). Specifies the first name of a given contact.Role: Header.Requirement: optional.Data type: varchar.

**Last name of contact** (lastName). Specifies the last name of a given contact.Role: Header.Requirement: optional.Data type: varchar.

**Contact email** (email). Contact e-mail address, for the lab.Role: Header.Requirement: mandatory.Data type: varchar.

## *Table list*

**Contact phone** (coPhone). Contact phone number, for the lab.Role: Header.Requirement: optional.Data type: varchar.

**Role of contact** (role). Specifies the organizational role of a given contact.Role: Header.Requirement: optional.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Countries look-up tables**

partID: countries. Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field. cu

**ISO 3166-1 alpha-3 country code** (isoCodeX). The ISO 3166-1 alpha-3 code, a three-letter country code which may allow a better visual association between the code and the country names than the 3166-1 alpha-2 code.Role: Header.Requirement: mandatory.Data type: varchar.

**ISO 3166-1 numeric country code** (numCode). The ISO 3166-1 numeric code, a three-digit country code which is identical to that developed and maintained by the United Nations Statistics Division, with the advantage of script (writing system) independence, and hence useful for people or systems using non-Latin scripts.Role: Header.Requirement: mandatory.Data type: varchar.

**Country code top-level domain** (tld). The internet top-level domain generally used or reserved for a country, sovereign state, or dependent territory identified with a country code.Role: Header.Requirement: mandatory.Data type: varchar.

## Tables

**English name for countries** (nameEngl). English-language name of a given country.Role: Header.Requirement: mandatory.Data type: varchar.

**Official state name** (nameOfficial). Official english-language name of a given state.Role: Header.Requirement: mandatory.Data type: varchar.

**Sovereign status of a country** (sovereignty). Sovereign status of a country, indicating which state has the highest jurisdiction over a given territory.Role: Header.Requirement: mandatory.Data type: varchar.

**Country exonym** (countryExonym). The English name foreigners use for the country.Role: Header.Requirement: mandatory.Data type: varchar.

**Capital city exonym** (capitalExonym). The English name foreigners use for the country's capital.Role: Header.Requirement: mandatory.Data type: varchar.

**Country endonym** (countryEndonym). The name locals use for their country.Role: Header.Requirement: mandatory.Data type: varchar.

**Capital city endonym** (capitalEndonym). The name locals use for their country's capital.Role: Header.Requirement: mandatory.Data type: varchar.

**National language script** (langScript). The language(s) and script(s) used for the country's capital endonyms.Role: Header.Requirement: mandatory.Data type: varchar.

**Country national phone prefix** (phone). International dialing code for the country.Role: Header.Requirement: mandatory.Data type: varchar.

**Coordinated universal time (UTC) zone** (utc). UTC – Time zone.Role: Header.Requirement: mandatory.Data type: varchar.

**Coordinated universal time (UTC) zone in daylight savings** (utcDST). Time zone during Daylight Saving Time.Role: Header.Requirement: mandatory.Data type: varchar.

*Table list*

## **Dataset table**

partID: datasets. A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field. ds

**Dataset creation date** (datasetDate). Specifies the date a given dataset was created.Role: Header.Requirement: recommended.Data type: datetime.

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: recommended.Data type: varchar.

**Description** (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

**Original Data Format** (originalFormat). The original structure or model used to record and store the data. This helps indicate if data have been transformed or mapped into the ODM structure.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: ogFormSet

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## Tables

### Instrument table

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

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: recommended.Data type: varchar.

**Model** (model). Model number or version of the instrument.Role: Header.Requirement: mandatory.Data type: varchar.

**Manufacturer** (manufacturer). Manufacturer of an instrument.Role: Header.Requirement: optional.Data type: varchar.

**Description** (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

**Describe other instrument type, if applicable** (insTypeOth). Description of the instrument in case it is not listed in instrumentType.Role: Header.Requirement: optional.Data type: varchar.

**Index** (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

*Table list*

## **Language Look-up table**

partID: languages. Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field. la

**Language family** (langFam). Specifies the language family of a given language for translation and language tracking purposes.Role: Header.Requirement: mandatory.Data type: varchar.

**Language name** (langName). Specifies the name of the language in roman alphabet characters for translation and language tracking purposes.Role: Header.Requirement: mandatory.Data type: varchar.

**Native Name** (natName). The native name of the language, i.e. what the language is called by its speakers.Role: Header.Requirement: mandatory.Data type: categorical.

**ISO639-1** (iso6391). The first part of the ISO 639 series of international standards for language codes. Part 1 covers the registration of two-letter codes. There are 183 two-letter codes registered as of June 2021. The registered codes cover the world's major languages.Role: Header.Requirement: mandatory.Data type: categorical.

**ISO639-2T** (iso6392T). A set of international standards that lists short codes for language names. These ISO639-2 are the three-letter codes defined in part two (ISO 639-2) of the standard, including the corresponding two-letter (ISO 639-1) codes where they exist. The 'T' specifies the terminological code (T code).Role: Header.Requirement: mandatory.Data type: categorical.

**First released version** (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

**Last updated version** (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

## Tables

**Changes column** (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## Measure report table

partID: measures. The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field. mr

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: optional.Data type: varchar.

**Analysis date start** (aDateStart). Date the measurement or analysis was started.Role: Header.Requirement: optional.Data type: datetime.

**Analysis date end** (aDateEnd). Date the measurement or analysis was completed.Role: Header.Requirement: mandatory.Data type: datetime.

**EpiWeek Start Date** (epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start date resolves the possible ambiguity.Role: Header.Requirement: optional.Data type: date.

**EpiWeek Number** (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.

**Year of the EpiWeek** (epiYear). The year in which the epi week is occurring.Role: Header.Requirement: optional.Data type: integer.

*Table list*

**Measure relevance start date** (relDateStart). The start date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons.Role: Header.Requirement: mandatoryIf.Data type: datetime.

**Measure relevance end date** (relDateEnd). The end date of the relevancy period of a measure - mostly for time-varying metrics for sites or polygons.Role: Header.Requirement: mandatoryIf.Data type: datetime.

**Report date** (reportDate). The date a measure was reported.Role: Header.Requirement: optional.Data type: datetime.

**Value** (value). Value of a measure, observation or attribute.Role: Header.Requirement: mandatory.Data type: varchar.

**Value Treatment** (valTreat). A field which specifies what kinds of data treatments or the nature of the measurement value.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: valTreatSet

**Index** (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

**Measure license** (measureLic). Specifies the access and use licensing for a given single measurement.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: licSet

**Reportable** (reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied.Role: Header.Requirement: optional.Data type: boolean.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## Tables

### **Measure set report table**

partID: measureSets. The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or 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). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: optional.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### **Organization table**

partID: organizations. The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field. or

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: recommended.Data type: varchar.

**Description** (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

**Organization Type** (orgType). Specifies the type or purpose of a given organization.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: orgTypeSet

## *Table list*

**Organization level** (orgLevel). The geographic level of an organization.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: orgLevelSet

**Organization sector** (orgSector). The sector of an organizationRole: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: orgSectorSet

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Parts Look-up table**

partID: parts. Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short name for the table (partID) can be found in the instructions field. pa

**Label** (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

**Part types** (partType). Part types describe the purpose or use of the part. Envornment 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.Role: Header.Requirement: mandatory.Data type: categorical.

**Short names** (shortName). Shortened names for tables and other important parts for use in wide names.Role: Header.Requirement: optional.Data type: varchar.

**Part description** (partDesc). The description of the part.Role: Header.Requirement: mandatory.Data type: varchar.

## Tables

**Part instruction** (partInstr). Additional notes and instructions on how a part is used and/or defined.Role: Header.Requirement: optional.Data type: varchar.

**Domain** (domain). Domain is the highest level of describing of a measure.Role: Header.Requirement: mandatory.Data type: categorical.

**Group** (group). Unique identifier for a group of measures. Mostly applicable for measures, methods, units, and aggregations.Role: Header.Requirement: mandatory.Data type: categorical.

**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.

**Nomenclature** (nomenclature). A classification system to report the measure class. Only applicable to variants, mutations, and diseases.Role: Header.Requirement: optional.Data type: categorical.

**Ontology reference** (ontologyRef). Ontology reference for a part.Role: Header.Requirement: optional.Data type: varchar.

**LaTeX expression** (latExp). LaTeX expression used to generate formulas, symbols, etc. Mainly relevant for units.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Aggregation scale** (aggregationScale). A scale used for an aggregation. Only applicable for measures and units.Role: Header.Requirement: optional.Data type: categorical.

**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: varchar.

**First released version** (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

*Table list*

**Last updated version** (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

**Changes column** (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

**Protocol steps table** (protocolSteps). The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Protocol steps table required headers** (protocolStepsRequired). Specifies the columns required in a Protocol Steps table.Role: Header.Requirement: optional.Data type: varchar.

**Protocol steps table column order** (protocolStepsOrder). Specifies the order of the columns in a Protocol Steps table.Role: Header.Requirement: optional.Data type: integer.

**Protocol relationships table** (protocolRelationships). The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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.Role: Header.Requirement: optional.Data type: varchar.

**Protocol Relationship table required headers** (protocolRelationshipsRequired). Specifies the columns required in the Protocol Organization table.Role: Header.Requirement: optional.Data type: varchar.

## Tables

**Protocol relationships table column order** (protocolRelationshipsOrder). Specifies the order of the columns in the Protocol Organization table.Role: Header.Requirement: optional.Data type: integer.

**Measure report table** (measures). The table that contains information and details about a given measure. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Measures table required headers** (measuresRequired). Specifies the columns required in a Measures table.Role: Header.Requirement: optional.Data type: varchar.

**Measures table column order** (measuresOrder). Specifies the order of the columns in a Measures table.Role: Header.Requirement: optional.Data type: integer.

**Measure set report table** (measureSets). The table that identifies sets of measures. Examples of measure sets include a set of replicates, dilutions (used to generate a Ct curve) or 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.

**Measure sets table column order** (measureSetsOrder). Specifies the order of the columns in a Measure Sets table.Role: Header.Requirement: optional.Data type: integer.

**Measure Set table required headers** (measureSetsRequired). Specifies the columns required in a Measure Sets table.Role: Header.Requirement: optional.Data type: varchar.

**Dataset table** (datasets). A report table for capturing details about data's parental data set and data custodians. Supplying attribution for data collectors. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

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**Dataset table required headers** (datasetsRequired). Specifies the columns required in a Datasets table.Role: Header.Requirement: optional.Data type: varchar.

**Datasets table column order** (datasetsOrder). Specifies the order of the columns in a Datasets table.Role: Header.Requirement: optional.Data type: integer.

**Sites table** (sites). The table that contains information about a site; the location where an environmental sample was taken. The site of an 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.

**Sites table required headers** (sitesRequired). Specifies the columns required in a Sites table.Role: Header.Requirement: optional.Data type: varchar.

**Sites table column order** (sitesOrder). Specifies the order of the columns in a Sites table.Role: Header.Requirement: optional.Data type: integer.

**Sample report table** (samples). The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site.Samples can be combined, split, stored and reused. The **Sample relationships** (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Sample table required headers** (samplesRequired). Specifies the columns required in a Samples table.Role: Header.Requirement: optional.Data type: varchar.

## Tables

**Samples table column order** (samplesOrder). Specifies the order of the columns in a Samples table.Role: Header.Requirement: optional.Data type: integer.

**Address table** (addresses). The table that contains information about addresses. Addresses can 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.

**Address table required headers** (addressesRequired). Specifies the columns required in a Addresses table.Role: Header.Requirement: optional.Data type: varchar.

**Addresses table column order** (addressesOrder). Specifies the order of the columns in the Addresses table.Role: Header.Requirement: optional.Data type: integer.

**Contact table** (contacts). The table that contains information about a contact; a person who is the contact of a site or laboratory. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Contact table required headers** (contactsRequired). Specifies the columns required in a Contacts table.Role: Header.Requirement: optional.Data type: varchar.

**Contacts table column order** (contactsOrder). Specifies the order of the columns in a Contacts table.Role: Header.Requirement: optional.Data type: integer.

**Organization table** (organizations). The table that contains information about a laboratory. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

*Table list*

**Organziation table required headers** (organizationsRequired). Specifies the columns required in a Organizations table.Role: Header.Requirement: optional.Data type: varchar.

**Organizations table column order** (organizationsOrder). Specifies the order of the columns in a Organizations table.Role: Header.Requirement: optional.Data type: integer.

**Public Health Actions Report Table** (phActions). Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: mandatory.Data type: varchar.

**Public health actions table required headers** (phActionsRequired). Required headers in the public health actions table.Role: Header.Requirement: mandatory.Data type: varchar.

**Public health actions table column order** (phActionsOrder). Specifies the order of the columns in the public health actions table.Role: Header.Requirement: mandatory.Data type: integer.

**Calculations Table** (calculations). Table for recording data on data treatments and calculations applied to measurements and reported values.Role: Header.Requirement: optional.Data type: varchar.

**Calculations table required headers** (calculationsRequired). Required headers in the calculations table.Role: Header.Requirement: mandatory.Data type: varchar.

**Calculations table column order** (calculationsOrder). Specifies the order of the columns in the calculations table.Role: Header.Requirement: mandatory.Data type: integer.

**Instrument table** (instruments). The table that contains information about instruments. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

## Tables

**Instrument table required headers** (`instrumentsRequired`). Specifies the columns required in the Instruments table. Role: Header. Requirement: optional. Data type: varchar.

**Instruments table column order** (`instrumentsOrder`). Specifies the order of the columns in the Instruments table. Role: Header. Requirement: optional. Data type: integer.

**Polygon Relationships Table** (`polygonRelationships`). Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. Role: Header. Requirement: optional. Data type: varchar.

**Polygon relationships table required headers** (`polygonRelationshipsRequired`). Required headers in the polygon relationships table. Role: Header. Requirement: mandatory. Data type: varchar.

**Polygon relationships table column order** (`polygonRelationshipsOrder`). Specifies the order of the columns in the polygon relationships table. Role: Header. Requirement: mandatory. Data type: integer.

**Polygon table** (`polygons`). The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. Role: Header. Requirement: optional. Data type: varchar.

**Polygon table required headers** (`polygonsRequired`). Specifies the columns required in a Polygons table. Role: Header. Requirement: optional. Data type: varchar.

**Polygons table column order** (`polygonsOrder`). Specifies the order of the columns in a Polygons table. Role: Header. Requirement: optional. Data type: integer.

**accessions Table** (`accessions`). Table for recording accession IDs for external data, namely sequences in large sequencing databases and repositories. The short name for the table (partID) can be found in the instructions field. Role: Header. Requirement: optional. Data type: varchar.

*Table list*

**Accessions table required headers** (accessionsRequired). Required headers in the accessions table.Role: Header.Requirement: mandatory.Data type: varchar.

**Accessions table column order** (accessionsOrder). Specifies the order of the columns in the accessions table.Role: Header.Requirement: mandatory.Data type: integer.

**Language Look-up table** (languages). Look up table for all languages, used to give structure to the translation table. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Language table required headers** (languagesRequired). Required headers in the Languages table.Role: Header.Requirement: optional.Data type: varchar.

**Language table column order** (languagesOrder). Specifies the order of the columns in the Languages table.Role: Header.Requirement: optional.Data type: integer.

**Translation look-up table** (translations). Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Translation table required headers** (translationsRequired). Required headers in the Translations table.Role: Header.Requirement: optional.Data type: varchar.

**Translation table column order** (translationsOrder). Specifies the order of the columns in the Translation table.Role: Header.Requirement: optional.Data type: integer.

**Parts Look-up table** (parts). Look up table containing all parts in of the data model. Contains all parts, including self-referential parts. The short

## Tables

name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Parts table required headers** (partsRequired). Required headers in the Parts table.Role: Header.Requirement: optional.Data type: varchar.

**Parts table column order** (partsOrder). Order of headers in the Parts table.Role: Header.Requirement: optional.Data type: integer.

**Sets look-up table** (sets). Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Sets table required headers** (setsRequired). Required headers in the Sets table.Role: Header.Requirement: optional.Data type: varchar.

**Sets table column order** (setsOrder). Specifies the order of the columns in the Sets table.Role: Header.Requirement: optional.Data type: integer.

**Quality reports table** (qualityReports). The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Quality report table required headers** (qualityReportsRequired). Specifies the columns required in the Quality Reports table.Role: Header.Requirement: optional.Data type: varchar.

**Quality reports table column order** (qualityReportsOrder). Specifies the order of the columns in the Quality Reports table.Role: Header.Requirement: optional.Data type: integer.

**Sample relationships table** (sampleRelationships). Table for recording the relationships between samples.Samples can be pooled or split. The sample relationships table holds information on parent-child relationships

*Table list*

between samples, and allow for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Sample relationships table required headers** (sampleRelationshipsRequired). Specifies the columns required in a Sample Relationships table.Role: Header.Requirement: optional.Data type: varchar.

**Sample relationships table column order** (sampleRelationshipsOrder). Specifies the order of the columns in a Sample Relationships table.Role: Header.Requirement: optional.Data type: integer.

**Protocols table** (protocols). The table for protocols. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Protocols table required headers** (protocolsRequired). Specifies the columns required in the Protocols table.Role: Header.Requirement: optional.Data type: varchar.

**Protocols table column order** (protocolsOrder). Specifies the order of the columns in the Protocols table.Role: Header.Requirement: optional.Data type: integer.

**Countries look-up tables** (countries). Look up table for the possible country inputs. The short name for the table (partID) can be found in the instructions field.Role: Header.Requirement: optional.Data type: varchar.

**Countries table required headers** (countriesRequired). Required headers in the countries table.Role: Header.Requirement: optional.Data type: varchar.

**Countries table column order** (countriesOrder). Specifies the order of the columns in the countries table.Role: Header.Requirement: optional.Data type: integer.

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**Zones look-up table** (zones). Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. Role: Header. Requirement: optional. Data type: varchar.

**Zones table required headers** (zonesRequired). Required headers in the zones table. Role: Header. Requirement: optional. Data type: varchar.

**Zones table column order** (zonesOrder). Specifies the order of the columns in the zones table. Role: Header. Requirement: optional. Data type: integer.

**Wide name table** (wideNames). The table for wide names. The short name for the table (partID) can be found in the instructions field. Role: Header. Requirement: optional. Data type: varchar.

**Wide name table required** (wideNamesRequired). Column for indicating which fields in the wide names table are mandatory. Role: Header. Requirement: optional. Data type: varchar.

**Wide name table order** (wideNamesOrder). Column for indicating the order of the fields in the wide names table. Role: Header. Requirement: optional. Data type: integer.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc. Role: Header. Requirement: optional. Data type: varchar.

**Data types** (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. Role: Header. Requirement: mandatory. Data type: categorical.

### *Table list*

**Minimum value part support** (minValue). The minimum value of part.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Maximum value part support** (maxValue). The maximum value of a part.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Minimum length** (minLength). The maximum value of measure.Role: Header.Requirement: mandatoryIf.Data type: integer.

**Maximum length** (maxLength). The maximum length of the value of a part or measure.Role: Header.Requirement: mandatoryIf.Data type: integer.

## **Public Health Actions Report Table**

partID: phActions. Table for recording information on public health actions. The short name for the table (partID) can be found in the instructions field. pha

**Public health action datetime** (actionDT). The date and Time of the public health action.Role: Header.Requirement: optional.Data type: datetime.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Polygon Relationships Table**

partID: polygonRelationships. Table for recording the relationships between polygons. The short name for the table (partID) can be found in the instructions field. por

## Tables

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### Polygon table

partID: polygons. The table that contains information about the geometry of a geographic area. The short name for the table (partID) can be found in the instructions field. po

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: recommended.Data type: varchar.

**Description** (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

**Type of geography** (geoType). Type of geography that is represented by the polygon.Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: geoTypeSet

**European Petroleum Survey Group Coordinates** (geoEPSG). The unique EPSG code specifying a given geospatial area.Role: Header.Requirement: mandatory.Data type: float.

**Well-known text** (geoWKT). Well-known text of the polygonRole: Header.Requirement: mandatory.Data type: varchar.

**File location of polygon** (fileLocation). The location of the file containing the geometry of the polygon.Role: Header.Requirement: optional.Data type: varchar.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

### *Table list*

**Polygon License** (poLic). The license for the availability of the polygon shapefile.Role: Header.Requirement: recommended.Data type: categorical.Measure, method or attribute set: licSet

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Protocol relationships table**

partID: protocolRelationships. The table that contains the organizational information and details (such as order) about a given protocol, recorded as a series of protocol steps (protocolSteps). Protocols are a group of related protocol steps. For example a protocol step can describe a sample concentration, extraction, inhibition or a measurement. Protocols can include both methodID (a 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

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Protocols table**

partID: protocols. The table for protocols. The short name for the table (partID) can be found in the instructions field. pro

## Tables

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: optional.Data type: varchar.

**Summary** (summ). Short description of the assay and how it is different from the other assay methods.Role: Header.Requirement: optional.Data type: varchar.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

**Protocol version** (protocolVersion). Specifies the version of a method set.Role: Header.Requirement: optional.Data type: integer.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## Protocol steps table

partID: protocolSteps. The table for collecting metadata on individual steps in a protocol, methodological process, or assay. The short name for the table (partID) can be found in the instructions field. ps

**Summary** (summ). Short description of the assay and how it is different from the other assay methods.Role: Header.Requirement: optional.Data type: varchar.

**Protocol step version** (stepVer). Specifies the version of a given protocol step.Role: Header.Requirement: optional.Data type: varchar.

**Reference link** (refLink). Link to the reference material for a part. May link to literature on a method, measure, etc.Role: Header.Requirement: optional.Data type: varchar.

## *Table list*

**Value** (value). Value of a measure, observation or attribute.Role: Header.Requirement: mandatoryif.Data type: varchar.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### **Quality reports table**

partID: qualityReports. The table for recording the various quality metrics and indicators for samples and measures. The short name for the table (partID) can be found in the instructions field. qr

**Quality flag** (qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample or measure.Role: Header.Requirement: mandatory.Data type: categorical.

**Severity indicator** (severity). An indicator of the severity or seriousness of a quality flag.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: sevSet

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### **Sample relationships table**

partID: sampleRelationships. Table for recording the relationships between samples.Samples can be pooled or split. The sample relationships table holds information on parent-child relationships between samples, and allow

## Tables

for tracking sample lineage for single and pooled samples. The short name for the table (partID) can be found in the instructions field. sar

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### Sample report table

partID: samples. The table that contains information about a sample. A sample is defined as a representative volume of wastewater (or other forms of water or liquid), air, or surface area taken from a site.Samples can be combined, split, stored and reused. The **Sample relationships** (sampleRelationships) is used to describe the relationships between samples. The short name for the table (partID) can be found in the instructions field. sas

**Organization ID** (organizationID). A unique identifier for the organization to which the reporter is affiliated.Role: Header.Requirement: optional.Data type: varchar.

**Sample origin** (origin). An attribute of a sample specifying the origin.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: originSet

**Sample collection type** (collType). The type of collection.Role: Foreign Key.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: collectSet

**Collection period** (collPer). Collection period. The time period over which the sample was collected, in hours. Alternatively, use collectionStart and collectionEnd.Role: Header.Requirement: mandatory.Data type: float.

*Table list*

**Collection number** (collNum). The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling.Role: Header.Requirement: mandatory.Data type: integer.

**Pooled** (pooled). Is this a pooled sample, and therefore composed of multiple child samples obtained at different sitesRole: Header.Requirement: optional.Data type: boolean.

**Collection date time** (collDT). For grab samples this is the date, time and timezone the sample was taken.Role: Header.Requirement: mandatory.Data type: datetime.

**Collection date time start** (collDTStart). For integrated time averaged samples this is the date, time and timezone the sample was started being taken.Role: Header.Requirement: optional.Data type: datetime.

**Collection date time end** (collDTEnd). For integrated time average samples this is the date, time and timezone the sample was finished being taken.Role: Header.Requirement: optional.Data type: datetime.

**Collection Date (time not included)** (collDate). Sample collection date, where time is reported in a separate field.Role: Header.Requirement: optional.Data type: date.

**Collection Approximate Time Period** (collAppxT). The general time period (ie. Morning, afternoon, evening) of sample collection.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: collAppxSet

**EpiWeek Start Date** (epiWeekStart). Start date of a given epi week. Noted that not all epi weeks use the same start dates, despite being a standard, so including the start dat resolves the possible ambiguity.Role: Header.Requirement: optional.Data type: date.

**EpiWeek Number** (epiWeek). The number of the epi week in which a sample what collected, or to which a measure would apply.Role: Header.Requirement: optional.Data type: integer.

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**Year of the EpiWeek** (epiYear). The year in which the epi week is occurring.Role: Header.Requirement: optional.Data type: integer.

**Date sample was sent** (sentDate). Date that the sample was sent from the collection site to the lab.Role: Header.Requirement: optional.Data type: datetime.

**Date sample received** (recDate). The date the sample was received at the laboratory for analysis.Role: Header.Requirement: optional.Data type: datetime.

**Reportable** (reportable). Flag for whether a measure is reportable or not, based on confidence in the measure and methods applied.Role: Header.Requirement: optional.Data type: boolean.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## Sets look-up table

partID: sets. Look up table for all sets, managing how categorical inputs for various methods and attributes are grouped together. This table manages many-to-many relationships and category recycling within the ODM. The short name for the table (partID) can be found in the instructions field.  
se

**Set type** (setType). The type of set. i.e. quality set, aggregation set, unit setRole: Header.Requirement: mandatory.Data type: categorical.

**Label** (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

## *Table list*

**Enumeration for set values** (enumeration). The numeric value that corresponds to a given value in a set, defined in the sets table.Role: Header.Requirement: mandatory.Data type: integer.

**Status** (status). Whether the part is still active and can be used in the most current ODM version. Values are ‘active’ or ‘inactive’.Role: Header.Requirement: mandatory.Data type: varchar.

**First released version** (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

**Last updated version** (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

**Changes column** (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## **Sites table**

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

**Sample shed** (sampleShed). A geographic area, physical space, or structure. A sample is taken from a sampleshed for a representative measurement of a substance(s).Role: Header.Requirement: mandatory.Data type: categorical.Measure, method or attribute set: shedSet

**Level of Aggregation of a Sampling Site** (siteLevel). Specifies the level of aggregation that occurs at the site - essentially, what size and type

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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 sewersheds together without a correction for size.Role: Header.Requirement: optional.Data type: categorical.Measure, method or attribute set: siteLevelSet

**Name** (name). Name of a domain, specimen, group, class, attribute, unit, nomenclature or other entity.Role: Header.Requirement: recommended.Data type: varchar.

**Description** (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: optional.Data type: varchar.

**Health Region for a Site** (healthRegion). A free-text variable for listing the health region for a given site.Role: Header.Requirement: optional.Data type: varchar.

**Latitude** (geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.424721)Role: Header.Requirement: mandatoryIf.Data type: float.

**Longitude** (geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000)Role: Header.Requirement: mandatoryIf.Data type: float.

**European Petroleum Survey Group Coordinates** (geoEPSG). The unique EPSG code specifying a given geospatial area.Role: Header.Requirement: mandatoryIf.Data type: float.

**Last edited** (lastEdited). The date the entry was last updated.Role: Header.Requirement: optional.Data type: datetime.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

## *Table list*

### **Translation look-up table**

partID: translations. Look up table for translations of the description, label, and instruction for all parts. The default language if a translation is not specified is English. The short name for the table (partID) can be found in the instructions field. tr

**Label** (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

**Part description** (partDesc). The description of the part.Role: Header.Requirement: mandatory.Data type: varchar.

**Part instruction** (partInstr). Additional notes and instructions on how a part is used and/or defined.Role: Header.Requirement: optional.Data type: varchar.

**First released version** (firstReleased). The version in which a part was first releasedRole: Header.Requirement: mandatory.Data type: varchar.

**Last updated version** (lastUpdated). The version in which the part was last updated.Role: Header.Requirement: mandatory.Data type: varchar.

**Changes column** (changes). A column for recording the changes from a previous version.Role: Header.Requirement: optional.Data type: varchar.

**Notes** (notes). A note used to describe details that are not captured in other attributesRole: Header.Requirement: optional.Data type: varchar.

### **Wide name table**

partID: wideNames. The table for wide names. The short name for the table (partID) can be found in the instructions field. wn

**Label** (label). A human readable label of a part.Role: Header.Requirement: mandatory.Data type: varchar.

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**character length** (charLength). The number of characters used for the wide names.Role: Header.Requirement: optional.Data type: varchar.

**Description** (descr). A detailed description of a measure, method, or attribute.Role: Header.Requirement: mandatory.Data type: varchar.

**Wide name source** (source). The database or table sourced for the wide name.Role: Header.Requirement: mandatory.Data type: varchar.

**Measure identification (wide table)** (wideMeasure). Unique identifier for a measure in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Specified protocol (wide table)** (wideProtocol). Unique identifier for a protocol in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Specified attribute (wide table)** (wideAttribute). Unique identifier for an attribute in a wide table only. Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Report table name (wide table)** (reportTableName). The report table that the wide name calls from.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Part type name (wide table)** (partTypeName). The part type being used in a wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Compartment name (wide table)** (compartmentName). The compartment referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Specimen name (wide table)** (specimenName). The specimen referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

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**Fraction name (wide table)** (fractionName). The fraction analyzed referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Measure name (wide table)** (measureName). The measure referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Method name (wide table)** (methodName). The method referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Unit name (wide table)** (unitName). The unit referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Aggregation name (wide table)** (aggregationName). The aggregation referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

**Index** (index). Index number in case the measurement was taken multiple times.Role: Header.Requirement: optional.Data type: varchar.

**Attribute name (wide table)** (attributeName). The attribute referenced for the wide name.Role: Header.Requirement: mandatoryIf.Data type: varchar.

## **Zones look-up table**

partID: zones. Look up table for the possible sub-national region or zone inputs. The short name for the table (partID) can be found in the instructions field. zo

**English name of country sub-domains** (zoneName). The english-language name for a given country sub-domain.Role: Header.Requirement: mandatory.Data type: varchar.

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