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

Dictionary v2.0.0. Documentation v2.0.1.

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Table of contents

Table of contents

Table of contents

Tables   785

Introduction

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

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

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

How to use the documentation

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

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 develop. 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.

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.

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

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

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 interoperablity.

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

> 💡 What are ODM parts and how to find them?
>
> In the ODM, tables are an example of an 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

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.

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.

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

Background

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

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

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

While the ODM is a complex dictionary, it includes tools to support its use, such as data validation, input templates, and SQL database definitions for data storage. Additionally, it supports collaborations among different organizations seeking to share and combine samples and measurements. As an open model, third parties can extend the model, such as

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[2] FAIR Priniciples.

Background

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

What are "Parts" and "Part Types"?

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

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

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

See the parts reference document for more details.

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, 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

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

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 any 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 to 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 with 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

Fo 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 dat can input in both fields. The idea is to have the reporting tables for measures be as robust as possible to allow for various kinds of timelines.

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

Dates within the ODM

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

Date fields that are more related to data processing and labratory 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 recieved 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.

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

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 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 only need to compete these tables once and then update them as needed. `Protocol steps` and `Protocol relationships` tables are used alongside the `Protocols` table. 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.

- **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.

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**

- `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.

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 ID
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**

	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
Group	Class	Measure	Value	Unit	Aggregation

i) Columns N and O

- `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		
3			BRSV-N	
4			SARS-CoV-2-E	
5			SARS-CoV-2-N1	
6			SARS-CoV-2-N2	
7			SARS-CoV-2-N3	
8			SARS-CoV-2-RdRp	
9			crAssphage-N	
10			PMMoV-CP	
11				

iii) Column Q

- `Value` is where you enter the value of your measure. For instance, if you recorded an `Environmental temperature` of 20 ºC, 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

27

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 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.

28

`Measure set report` **template**

1. **Columns A to G**

	A	B	C	D	E	F	G
1	Report set ID	Protocol ID	Name	Organization ID	Contact ID	Last edited	Notes
2							
3							

i) Columns A, B, D and E

- These are identifier fields.

- `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 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` (or `sampleRelationships`) template represents an interaction (or relationship) between two samples in the form "subject - relationship - object". So, to specify that Sample A is a field sample replicate of Sample B, you would enter `Sample ID` of A - `Field sample replicate` - `Sample ID` of B.

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

Quick Start

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

Samples Template

1. **Mandatory fields**

- **`Sample ID`**: Unique identifier for the `Sample report` template. Each value represents a sample.

- **`Site ID`**: Identifier for the location where a sample was taken.

- **`Sample material`**: Type of material that the sample is made of.

- **`Sample collection type`**: Method used to collect the sample.

- **`Collection period`**: The time period over which the sample was collected, in hours.

- **`Collection number`**: The number of subsamples that were combined to create the sample. Use NA for continuous, proportional or passive sampling.

- **`Collection date time`**: The date, time and time zone the sample was taken.

2. **Examples**

   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
Sample ID	Protocol ID	Organization ID	Contact ID	Site ID	Purpose	Sample material

   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.

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 recieved	Reportable	Last edited	Notes
2								
3								

i) Columns P to T, V:

- 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**

i) Columns A and C:

- These are identifier fields.

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

- 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 report protocols, protocol steps and protocol relationships:

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 `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.

- `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.

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

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

   - `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.
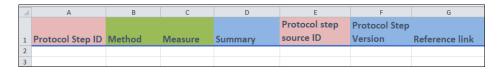
2. **Examples**

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.
- `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
Organization ID	Contact ID	Instrument ID	Value	Unit	Aggregation	Last Edited	Notes

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.

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**

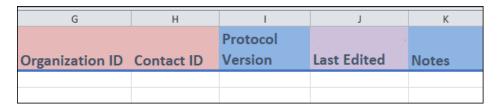|	A	B	C	D	E	F
1	Source Protocol ID	Protocol ID	Dataset ID	Name	Summary	Reference link
2						
3						

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 indi-
cated 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.

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**

i) Columns A to C, E and F:

- These are identifier fields.

	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								

- 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 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:

43

- 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 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.

44

`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.

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**

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.
   - `Latitude`: 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**

	A	B	C	D	E
1	Address ID	Dataset ID	Address Line 1	Address Line 2	City
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	State, Province, or Region	Postal or Zip Code	Country	Last Edited	Notes
2					
3					

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.

- 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**

   i) Columns F to J:

- Most of these fields are free form in which you can enter various information regarding the contact.

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

- `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.

`Dataset` **template**

1. **Columns A to G**

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

	H	I	J	K	L	M	N
1	Language ID	Funder Contact ID	Custody Contact ID	Funding agency ID	Data custodian ID	Last edited	Notes
2							
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.
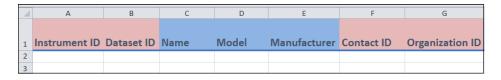
ii) Columns M and N:

- 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**

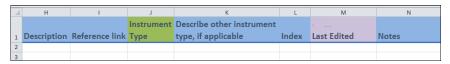|	A	B	C	D	E	F	G
1	Instrument ID	Dataset ID	Name	Model	Manufacturer	Contact ID	Organization ID
2							
3							

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**

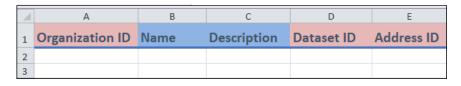| H	I	J	K	L	M	N
Description	Reference link	Instrument Type	Describe other instrument type, if applicable	Index	Last Edited	Notes

i) Columns H, I, L to N:

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

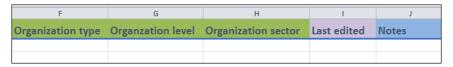| A	B	C	D	E
Organization ID	Name	Description	Dataset ID	Address ID

    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.
- 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	Organzation 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.
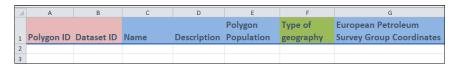
    ii) Columns I and J:

- 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**

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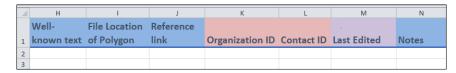
   ii) Columns C to E, G:
   - These are free form fields in which you can enter additional information regarding the Polygon.
   - `Name` (column C) is the name of the polygon.
   - `European Petroleum Survey Group Coordinates` (column G) is a coordinate system that can be used to identify where a polygon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

	H	I	J	K	L	M	N
1	Well-known text	File Location of Polygon	Reference link	Organization ID	Contact ID	Last Edited	Notes
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
1	Quality Report ID	Report ID	Sample ID	Report Set ID	Quality Flag	Severity indicator	Last Edited	Notes
2								
3								

58

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 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 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**

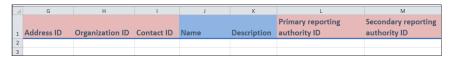|	A	B	C	D	E	F
1	Parent Site ID	Site ID	Dataset ID	Polygon ID	Site Type	Sample shed
2						
3						

   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:

- 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!

Notes regarding templates

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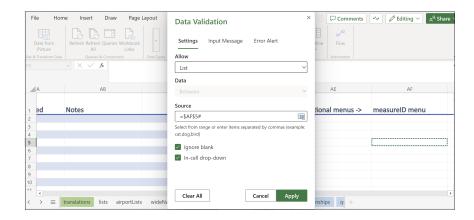
Adding more conditional menus

- 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).

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

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

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

Troubleshooting conditional menus

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

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

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

Part IDs

- In the main parts of each of the templates, labels are used in the menus.

- If you wish to have the part IDs of these values, they are located to the right of the main template and, if applicable, the code for the conditional menus. Unlike the main template, the rows containing the part IDs will not be alternating in colour.

- The part IDs are present in the first 100 rows of each of the templates.

Troubleshooting menus (not including conditional menus)

- The menus are based on what is found in the `lists` tab that is included with the templates.

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

Part I.

Reference guide

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

- `parts` – Parts are the smallest way of describing anything in the ODM. An analogy to parts of a car can be used to illustrate this point. If you own a car, your garage can access a parts list that contains every part of your car, right down to every nut and bolt. There are over 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 pernament 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

Warning in get_latest_dictionary(): Multiple dictionaries found only one
dictionary should be stored.

Dictionary 2.0.0.

Parts are the smallest way of describing anything in the ODM. An analogy to parts of a car c

::: {.callout-tip collapse="true"}
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 hav

The unique construction of part IDs serves several purposes in addition to generating valid
:::

::: {.cell}

:::

Parts

```
### a1306s delta-variant gene target { #a1306s }
(a1306s). a1306s delta-variant gene target  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### a1918v delta-variant gene target { #a1918v }
(a1918v). a1918v delta-variant gene target  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
```

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

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

a63t omicron-variant gene target { #a63t }
(a63t). a63t omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

a67v omicron-variant gene target { #a67v }
(a67v). a67v omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

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

Atline Analyzer { #aas }
(aas). Atline analyzer with sampler. An atline analyzer with sampler. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Absolute humidity { #absHum }
(absHum). A measure of the total mass of water vapour present in the air per
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: siteFeat </br>
Class: humid </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: absHumidUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Absolute humidity unit set { #absHumidUnitSet }
(absHumidUnitSet). Unit set for absolute humidity measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: absHumidUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Academic institution { #academ }
(academ). The category of organization type used for academic institutions or research group
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

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

Active { #active }
(active). Indicator that a part is in current use. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>

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

Analysis date { #aDate }
(aDate). Date the measurement was performed in the lab. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Analysis date end { #aDateEnd }
(aDateEnd). Date the measurement or analysis was completed. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Analysis date start { #aDateStart }
(aDateStart). Date the measurement or analysis was started. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Address Line 1 { #addL1 }
(addL1). Line 1 (the street name, number and direction) for a given address. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Address Line 2 { #addL2 }
(addL2). Line 2 (the unit number) for a given address. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Address table { #addresses }
(addresses). The table that contains information about addresses. Addresses
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

80

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

Addresses table column order { #addressesOrder }
(addressesOrder). Specifies the order of the columns in the Addresses table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>

Parts

Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

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

Address ID { #addressID }
(addressID). A unique identifier for an address. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

82

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

Administrative regions { #admRegLevel }
(admRegLevel). Administrative regions </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: ISCU </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: <a href="/sets.html#nrNAMissingnessSet">nrNAMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Air filter { #afu }
(afu). Air filter as part of filtration or circulating unit. Typically the u
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#airCompartmentSet">airCompartmentSet<
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Aggregation scale { #aggragationScale }
(aggragationScale). A scale used for an aggregation. Only applicable for meas
Part Type: attributes </br>
Domain: naDomain </br>

Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Aggregation { #aggregation }
(aggregation). Statistical measures used to report a measure. Each aggregation has a corresp
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Aggregations { #aggregations }
(aggregations). Statistical measures used to report a measure. Each measure
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Aggregation scales { #aggregationScales }
(aggregationScales). The scale of an aggregation set. Aggregation scales incl
Part Type: partType </br>

86

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

Aggregation set { #aggregationSet }
(aggregationSet). The aggregation set for a unit. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

Parts

Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Aggregation sets { #aggregationSets }
(aggregationSets). Sets of aggregations. Examples of aggregation sets include
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Air compartment { #air }
(air). A measure or observation made from a substance in the air. </br>

Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: airCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Air compartment set { #airCompartmentSet }
(airCompartmentSet). A compartment set for measures and methods in the air compartment. </b
Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: airCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Airplane { #airpln }
(airpln). Airplane sample shed category type </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Airport { #airport }

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

Airport lists worksheet { #airportLists }
(airportLists). Parts lists used to generate airport and airplane data entry templates. </b
Part Type: dictionarySupport </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

91

Parts

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Air and surface compartment set { #airSurfaceCompartmentSet }
(airSurfaceCompartmentSet). A compartment set for measures and methods in the
Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#airSurfaceCompartmentSet">airSurfaceCo
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

92

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

Air and water compartment set { #airWaterCompartmentSet }
(airWaterCompartmentSet). A compartment set for measures and methods in the air or water com
Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: airWaterCompartmentSet </
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Alias depreciated { #aliasDep }
(aliasDep). ID of an assay that is the same or similar. A comma separated lis
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

94

Alias ID depreciated { #aliasIDDep }
(aliasIDDep). Alias id ID of an assay that is the same or similar. a comma separated list. <
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

All domains { #allDo }
(allDo). Domain that specifies that it could apply to al domains; biological, chemical, and
Part Type: domains </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 15 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Alleles class { #allele }
(allele). Measures and methods related to alleles.  </br>
*Part Type:* <a href="#classes">classes</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#allele">allele</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

96

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Allele unit set { #alleleUnitSet }
(alleleUnitSet). Unit set for alleles. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: alleleUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Access to all org { #allOrgs }
(allOrgs). If this is 'no', this data will not be available to any partner organization. If
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Aloh3 precipitation { #aloh3 }
(aloh3). Aloh3 precipitation </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Assay method id default depreciated { #amDefDep }
(amDefDep). Used as default when a new measurement is created for this lab. See ID in AssayM
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Amicon ultrafiltration { #amiconUf }
(amiconUf). Amicon ultrafiltration </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>

Parts

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

Amicon filter, extract with MP96 { #amiMP96 }
(amiMP96). Nucleaic acid extraction, usually used for the liquid fraction of
Part Type: categories </br>
Domain: bio </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Amplicon sequencing { #amp }
(amp). Specifies the amplicon strategy for genetic sequencing </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

AND Boolean aggregation { #andBoo }
(andBoo). "AND" aggreation. If all values in the aggregation is "TRUE" then the AND aggregat
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>

Parts

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Any compartment set { #anyCompartmentSet }
(anyCompartmentSet). A compartment set for measures and methods in any compar
Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

102

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Any specimen set { #anySpecimenSet }
(anySpecimenSet). A specimen set that inculdes any specimen. </br>
Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Area proportional sample { #areaPr }
(areaPr). An area proportional sample. Used for surface testing. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: surfaceCompartmentSet </br>

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

Arrival temperature { #arTemp }
(arTemp). The temperature of a sample upon arrival at the laboratory for anal
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: temperature </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Use of the articV3 primer { #articV3 }
(articV3). Initial implementation of an ARTIC bioinformatics platform for nanopore sequencin
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Use of the articV4 primer { #articV4 }
(articV4). Artic V4 sequencing primer for VOCs and VOIs. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

Parts

Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Assay ID { #asID }
(asID). Links with the AssayMethod used to perform the analysis. Use instrume
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Attributes { #attributes }
(attributes). Attributes describe the who, where, when, and why of environmental surveillanc
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Bacteria Class { #bacteria }
(bacteria). Measures and methods relating to bacteria. </br>
Part Type: classes </br>
Domain: bio </br>

Parts

Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: bacteria </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: bacteriaUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Bacteria unit set { #bacteriaUnitSet }
(bacteriaUnitSet). Unit set for bacteria-related measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: bacteriaUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Miscellaneous bacteria group { #bactMisc }
(bactMisc). A group of measures/methods related to miscellaneous bacteria. The miscallenous
Part Type: groups </br>
Domain: bio </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: bactMisc </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Bead beating, extract with MP96 { #bbMP96 }
(bbMP96). Nucleaic acid extraction, usually used for solid fraction of a wastewater sample,
Part Type: categories </br>

```
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#waterCompartmentSet">waterCompartmentS
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 10 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### bcov { #bcov }
(bcov). Measure of the amount of bovine coronavirus.  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#virusMisc">virusMisc</a> </br>
*Class:* <a href="#allele">allele</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

110

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

bcov culture spike target { #bcovCul }
(bcovCul). Cultured bovine coronavirus is used as the recovery efficiency control target. <
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

bcov vaccine spike target { #bcovVac }
(bcovVac). The bovine coronavirus vaccine is used as the recovery efficiency control target.

Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Beef extract flocculation { #beeExtractFloc }
(beeExtractFloc). Beef extract flocculation. </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

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

Is Before { #before }
(before). Specifies that the object step or protocol occurs before the subject step or proto
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Beta { #beta }

(beta). B.1.351 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Biologic { #bio }
(bio). A living organism or biological substance. </br>
Part Type: domains </br>
Domain: bio </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Digital droplet emulsification PCR { #bioRadDdpcr }
(bioRadDdpcr). Describes a PCR analysis done using BioRad's digital droplet emulsification P
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Binary Large Object (BLOB) data type { #blob }
(blob). The data type for Binary Large Object (BLOB) data. Only used for the
Part Type: dataTypes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Breadth of coverage (>=5x depth) { #boc }
(boc). Positions with read depth greater or equal to 5. Report as percentage
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

5-Day carbonaceous kiochemical oxygen demand { #bod5c }
(bod5c). The quantity of oxygen utilized for the biochemical degradation of organic matter u
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: https://doi.org/10.1002/wer.1541 </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

5-day total biochemical oxygen demand { #bod5t }
(bod5t). 5 day total biochemical oxygen demand. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUni
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: https://doi.org/10.1002/wer.1541 </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Boolean data type { #boolean }
(boolean). The data type for boolean/binary data. Encoded as 'TRUE' or 'FALSE
Part Type: dataTypes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Boolean aggregation set { #booleanAggrSet }
(booleanAggrSet). Aggreagation set for boolean. </br>
Part Type: aggregationSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Boolean value set { #booleanSet }
(booleanSet). Set that contains the valid possible values for a boolean measu
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: NA </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Bovine respiratory syncytial virus group { #brsv }
(brsv). Bovine respiratory syncytial virus. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>

120

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

brsv culture spike target { #brsvCul }
(brsvCul). Cultured bovine respiratory syncytial virus (BRSV) is used as the recovery effici
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

BRSV-N { #brsvN }
(brsvN). bovine respiratory syncytial virus capsid protein gene region </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

brsv vaccine spike target { #brsvVac }
(brsvVac). The bovine respiratory syncytial virus (BRSV) vaccine is used as t
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: naClass </br>

122

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

Branch sewer pipleline { #bSwrPpl }
(bSwrPpl). Specifies a site type that is collection pipe that run lateral to other municpal
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Building cleanout { #buildCO }
(buildCO). Specifies a site type that is a capped pipe that connects to a bu:
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Capacity class { #capacity }
(capacity). Measures and methods relating to capacity. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>

124

Class: capacity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: capacityUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Capacity unit set { #capacityUnitSet }
(capacityUnitSet). Unit set for capacity measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: capacityUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Case report date { #caRepDate }
(caRepDate). Date that the numbers were reported publicly. Typically, reporte
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Categorical data type { #categorical }
(categorical). The data type for categorical data. Only used for the dictiona
Part Type: dataTypes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</

126

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Categories { #categories }
(categories). A discrete list of values that can be reported for a measure, method or attrib
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Long-term acute care hospital { #ccc }
(ccc). Acute care hospitals, or complex contuing care, that provide care for
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<,
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Child day care { #cdc }
(cdc). Child day care facility. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Degrees Celcius { #cel }
(cel). Degrees Celsius. </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>

Parts

Missingness Set: NA </br>
Minimum Value: -60 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Centrifugation { #cent }
(cent). Describes solid separation from a wastewater sample via centrifugatic
Part Type: categories </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Centricon ultrafiltration { #centriconUf }
(centriconUf). Centricon ultrafiltration. </br>
Part Type: categories </br>
Domain: che </br>

130

Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Ceres nanotrap { #ceres }
(ceres). Ceres nanotrap. </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

CFU per 100 ml { #cfu }
(cfu). Colony forming units per 100 ml of filtered sample. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Changes column { #changes }
(changes). A column for recording the changes from a previous version. Use th
Part Type: tableSupport </br>

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

Chemical { #che }
(che). A chemical compound. </br>
Part Type: domains </br>
Domain: che </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

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

Chemagic viral dna/rna 300 kit { #chemVir }
(chemVir). Nucleic acid extraction performed using the chemagic viral dna/rna
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Child relationship { #child }
(child). Indicated that this is a sample generated from (an)other sample(s)

Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

City { #city }
(city). The city where a site or organization is located; part of the address. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Clarified sample { #clari }
(clari). Clarified sample. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Class { #class }

136

(class). A unique identifier for a class, which is akin to a sub-group; it's a way of groupi
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Classes { #classes }
(classes). A class is a collection of one or more related measures or methods within a group
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Cloudy { #cloudy }
(cloudy). Qualitative category for the weather measure, specifying an overcas
Part Type: categories </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: siteFeat </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

138

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

Carbon Dioxide { #co2 }
(co2). A measure of an amount or concentraion of carbon dioxide. </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: gas </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: dissGasUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Chemical Oxygen Demand { #cod }
(cod). Chemical oxygen demand. </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Collection group { #colGrp }
(colGrp). A group of measurement-like attributes related to sample collection. </br>
Part Type: groups </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Collection date time { #collDT }
(collDT). For grab samples this is the date, time and timezone the sample was taken. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Collection date time end { #collDTEnd }
(collDTEnd). For integrated time average samples this is the date, time and t
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Collection date time start { #collDTStart }
(collDTStart). For integrated time averaged samples this is the date, time and timezone the
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sample collection set { #collectSet }
(collectSet). Methods for collection samples. Sample collection methods include water, air,
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#collectSet">collectSet</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Collection number { #collNum }
(collNum). The number of subsamples that were combined to create the sample.
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#colGrp">colGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* 1 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
```

144

Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Collection number and period { #collNumPer }
(collNumPer). Composite collection number.period. This a composite measure that combines \`c

In case of Composite, Flow-proportional collection, the number of subsamples followed by a d
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

For a COSCA ball or Moore swab collecting for 24 hours, the entry would be 1.24 </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 1:1 </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 6 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Collection period { #collPer }

(collPer). Collection period. The time period over which the sample was colle
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample collection type { #collType }
(collType). The type of collection. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: collectSet </br>
Unit Set: naUnitSet </br>

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Co-located sample { #colocated }
(colocated). Second or multiples samples collected at same location but different time (wate
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Column name depreciiated { #columnNameDep }
(columnNameDep). Name for the column Depreciated in ODM version 2. Look-up ta
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite sample - archival { #comp }
(comp). A composite sample, usually generated by an autosampler. This is inte
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

148

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Composite grab sample of 3 { #comp3 }
(comp3). A grab-composite sample composed of 3 separate grab samples. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Composite grab sample of 3 depreciate { #comp3dep }
(comp3dep). A grab-composite sample composed of 3 separate grab samples. Depr
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Composite 3hr grab sample { #comp3h }
(comp3h). A 3-hour composite with 3 grab samples each taken once per hour, ge
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Composite 3hr grab sample depreciate { #comp3hdep }
(comp3hdep). A 3-hour composite with 3 grab samples each taken once per hour, generally manu
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite 8hr grab sample depreciated { #comp8h }
(comp8h). An 8-hour composite with 8 grab samples each taken once per hour, g
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Composite 8hr grab sample deprecated { #comp8hDep }
(comp8hDep). A 8-hour composite with 8 grab samples each taken once per hour
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

152

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Compartment { #compartment }
(compartment). The attribute identifying the substance from which where a sample was taken.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Compartments { #compartments }
(compartments). The substance from which a sample was taken. For example, was
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Compartment sets { #compartmentSets }
(compartmentSets). Sets of compartments. Compartment sets are used to identi:
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<,
Group: naGroup </br>
Class: naClass </br>

154

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample concentrate { #conc }
(conc). Sample concentrate. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

```
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>


### Confirmed Cases Case report date { #conCase }
(conCase). Date that the numbers were reported publicly for a confirmed case
*Part Type:* <a href="#units">units</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#poSpecimenSet">poSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#dateTime">dateTime</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>


### Is concurrent to { #concurrent }
(concurrent). Specifies that the object step or protocol occurs at the same t
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
```

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

Water conductivity { #cond }
(cond). Measurement of conductivity of sample or site. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: siteFeat </br>
Class: conductivity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: conductivityUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>

Parts

Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Conductivity class { #conductivity }
(conductivity). Measures and methods related to conductivity. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: conductivity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: conductivityUnitSet
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Conductivity unit set { #conductivityUnitSet }
(conductivityUnitSet). Unit set related to conductivity measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<

158

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: conductivityUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Number of confirmed cases { #conf }
(conf). Number of confirmed cases. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>

Parts

Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Confirmed cases episode date { #confEp }
(confEp). Episode date is the earliest of onset, test or reported date for a
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: dateTime </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Confirmed Cases Onset date { #confOn }
(confOn). Earliest that symptoms were reported for a confirmed case. This dat
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>

160

Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: dateTime </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Contact ID { #contactID }
(contactID). A unique identifier for a given contact person. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Contact name { #contactName }
(contactName). Contact person or group, for the lab. Depreciated in ODM vers:
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Contact table { #contacts }
(contacts). The table that contains information about a contact; a person who
Part Type: tables </br>
Domain: naDomain </br>

162

Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Contacts table column order { #contactsOrder }
(contactsOrder). Specifies the order of the columns in a Contacts table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Contact table required headers { #contactsRequired }
(contactsRequired). Specifies the columns required in a Contacts table. </br
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Contact table set { #contactTableSet }
(contactTableSet). Tables are where measures, methods and attributes are rec
Part Type: dictSets </br>

164

Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Confirmed cases test date { #conTest }
(conTest). Date that the covid-19 test was performed for a confirmed case. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>

Reference Link: NA </br>
Data Type: dateTime </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Cphd ID { #corFcil }
(corFcil). Correctional facility </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

COSCa ball { #cosca }
(cosca). COSCa passive sampling device. Use collectionPeriod to describe how

Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: https://pubs.rsc.org/en/content/articlelanding/2021/ew/d1ew00207d </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Country { #country }
(country). The country where a site or organization is located; part of the address. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Countries or sovereign states { #countryLevel }
(countryLevel). Countries or sovereign states </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: ISCU </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#nrNAMissingnessSet">nrNAMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Districts, counties, regions { #countyLevel }

(countyLevel). Districts, counties, regions </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: ISCU </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: nrNAMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Covid-19 { #cov }
(cov). Covid-19 infection. Any form of Covid-19 human infetion - including testing for Covid
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: humanCompartmentSet </br>
Group: sarsCov2 </br>
Class: disease </br>
Nomenclature: ICD </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: populationUnitSet </br>

Parts

Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

SARS-CoV-2 measure { #cov2Me }
(cov2Me). Measure the amount of SARS-CoV-2 virus. This measure should only be
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

170

SARS-CoV-2-B.1.1.7 { #covB117 }
(covB117). Variant B.1.1.7 of the SARS-CoV-2 virus. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: pangolin </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

SARS-CoV-2-B.1.351 { #covB135 }
(covB135). Variant B.1.351 of the SARS-CoV-2 virus. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: pangolin </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

SARS-CoV-2-E { #covE }
(covE). SARS-CoV-2 E gene. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

SARS-CoV-2-N1 { #covN1 }
(covN1). SARS-CoV-2 nucleocapsid gene, allele 1. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

SARS-CoV-2-N2 { #covN2 }
(covN2). SARS-CoV-2 nucleocapsid gene, allele 2. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>


### SARS-CoV-2-N3 { #covN3 }
(covN3). SARS-CoV-2 nucleocapsid gene, allele 3.  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#allele">allele</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
```

Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

SARS-CoV-2-P.1 { #covP1 }
(covP1). Variant P.1 of the SARS-CoV-2 virus. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: pangolin </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

SARS-CoV-2-RdRp { #covRdrp }
(covRdrp). SARS-CoV-2 RdRp gene. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>

Parts

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Covid-19 population measurement date { #cphDate }
(cphDate). date of reporting for covid-19 measure. Depreciated in ODM versior
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Cphd ID { #cphid }
(cphid). Unique identifier for the table. Depreciated in ODM version 2. The measure identica
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

crAssphage-N { #cra }
(cra). crAssphage virus capsid protein gene region </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Crosswalk table set { #crosswalkTableSet }
(crosswalkTableSet). Tables used to translate to and from other environmental
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Cycle threshold or quantification cycle (Ct or Cq) { #ct }
(ct). Cycle thresholds in a PCR assay. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Cumulative count { #cuCo }
(cuCo). Units for describing a population measure of a cumulative count of cases of a given
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>

Parts

```
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 0 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Custody Contact ID { #custodyCont }
(custodyCont). A unique identifier for data custodians.  </br>
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet 
*Minimum Value:* NA </br>
```

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Data custodian ID { #custodyID }
(custodyID). The data custodian of a database. Use Organization ID to populate this field, a
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

d377y delta-variant gene target { #d377y }
(d377y). d377y delta-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

```
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### d3g omicron-variant gene target { #d3g  }
(d3g ). d3g omicron-variant gene target.  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
```

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

d63g delta-variant gene target { #d63g }
(d63g). d63g delta-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

d796y omicron-variant gene target { #d796y }
(d796y). d796y omicron-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

183

Parts

```
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### d950n delta-variant gene target { #d950n }
(d950n). d950n delta-variant gene target.  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
```

Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Daily count { #daiCo }
(daiCo). Units for describing a population measure of a daily count of new cases of a given
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dataset creation date { #datasetDate }
(datasetDate). Specifies the date a given dataset was created. </br>
Part Type: attributes </br>
Domain: naDomain </br>

185

Parts

Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dataset ID { #datasetID }
(datasetID). The name of the dataset that stores information for MeasureRepor
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dataset table { #datasets }
(datasets). A report table for capturing details about data's parental data set and data cus
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Datasets table column order { #datasetsOrder }
(datasetsOrder). Specifies the order of the columns in a Datasets table. </br>
Part Type: tableSupport </br>

Parts

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 1 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Dataset table required headers { #datasetsRequired }
(datasetsRequired). Specifies the columns required in a Datasets table.  </b
*Part Type:* <a href="#tableSupport">tableSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

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

Data types { #dataTypes }
(dataTypes). The data type for a part. Data types used in the ODM include: varchar, booleen,
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Date { #date }
(date). Date date on which the assayMethod was created or updated (for version update). </br

Parts

Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Datetime data type { #datetime }
(datetime). The data type for date and time data. Only used for the dictionar
Part Type: dataTypes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

190

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Days { #days }
(days). A unit for indicating a length of time in days. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: miscMeas </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: timeUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ddcov_e sars-cov-2 gene target { #ddcovE }

Parts

(ddcovE). ddcov_e sars-cov-2 gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ddcov_n sars-cov-2 gene target { #ddcovN }
(ddcovN). ddcov_n sars-cov-2 gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>

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

Deaths { #death }
(death). Units for describing a population measure of patients who have died from a given ca
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

del143/145 { #del143 }
(del143). 143 or 145 deletion omicron-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

del 157/158 { #del157 }
(del157). 157 or 158 deletion delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

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

del2084/2084   { #del2084 }
(del2084). 2084 or 2084 deletion omicron-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

del212/212 { #del212 }
(del212). 212 or 212 deletion omicron-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

del3674/3676 { #del3674 }
(del3674). 3674 or 3676 deletion omicron-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

196

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

del69/70 { #del6970 }
(del6970). 69 or 70 deletion omicron-variant gene target. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Delta { #delta }
(delta). B.1.617.2 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Depreciated { #depreciated }
(depreciated). Indicator to say that a part is no longer in current use in th
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

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

Derived sample { #derived }
(derived). Specifies a sample that is derrived or made from another sample or material. </b
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Description { #descr }
(descr). A detailed description as an attirbute for describing results or pro
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 200 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Description of change { #descrChange }
(descrChange). A description of change in a part from the previous version.
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>

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

Desk or counter { #desk }
(desk). Desk, table, countertop or other flat working surface. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: surfaceCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dewatered solids { #deso }
(deso). Dewatered solids. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Detected { #det }
(det). Substance detected or not detected. TRUE = detected, FALSE = not detec
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 1 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Access to details deprecated { #detailsDep }
(detailsDep). More details on the existing confidentiality requirements of this measurement.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Development { #development }
(development). Indicator that a part is under development use. See partID = s
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dictionary reference table set { #dictionaryRefTableSet }
(dictionaryRefTableSet). Reference or look-up tables. For example, the parts
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet

204

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Additional dictionary sheets { #dictionarySupport }
(dictionarySupport). Additional sheets for the Excel version of the ODM dictionary. Sheets o
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dictionary set type { #dictSet }
(dictSet). Sets used to describe and group dictionary tables. </br>
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dilution factor { #dilFact }
(dilFact). Specifies the extent to which a sample or aliquot was diluted prio
Part Type: measurements </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>

206

Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: dilution </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Point dillutions { #dillute }
(dillute). Exact concentration or dillutions for generating a standard curve. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: dilution </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>

Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dilution Class { #dilution }
(dilution). Measures and methods relating to dilutions. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: dilution </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Diseases (human) class { #disease }
(disease). Measure and methods related to disease or infection in humans. </
Part Type: classes </br>
Domain: bio </br>

Speciment ID: poSpecimenSet </br>
Compartment Set: humanCompartmentSet </br>
Group: naGroup </br>
Class: disease </br>
Nomenclature: ICD </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: populationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dissolved gas concentration unit set { #dissGasUnitSet }
(dissGasUnitSet). Unit set for carbon dioxide concentrations measurements in water or air.
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: airWaterCompartmentSet </
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: dissGasUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Depth of coverage { #doc }
(doc). The sequencing read depth. Used to interpret the confidence in a prese
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Domain { #domain }
(domain). Domain is the highest level of describing of a measure. The domain
Part Type: attributes </br>

210

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

Domains { #domains }
(domains). There are three domain types: biologic (i.e. Covid-19, chemical (i.e. nitrogen),
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

Parts

Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Higher education domitory or residential building { #dorm }
(dorm). Higher education domitory or residential building </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

e156g delta-variant gene target { #e156g }
(e156g). e156g delta-variant gene target </br>

212

Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

e484a omicron-variant gene target { #e484a }
(e484a). e484a omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Escherichia coli { #ecoli }
(ecoli). Concentration of bacteria that are passed through the faecal excreme
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#surfaceWaterCompartmentSet">surfaceWat
Group: bactMisc </br>
Class: bacteria </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: bacteriaUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Education { #education }

214

(education). A measure or sample taken for education or training. Use this purpose, for exam
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Efficiency { #efficient }
(efficient). The efficiency reported for a standard curve. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>

Parts

Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Contact email { #email }
(email). Contact e-mail address, for the lab. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

European Nucleotide Association { #ena }
(ena). ENA header </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

European Nucleotide Association (ENA) - notes { #enaNotes }
(enaNotes). ENA notes </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

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

Rainfall { #envRnF }
(envRnF). Rainfall, i.e. amount of precipitation in the form of rain. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: siteFeat </br>
Class: precipitation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#precipitationUnitSet">precipitationUnitSet</a
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Ground snow depth { #envSnwD }
(envSnwD). Total depth of snow on the ground. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>
Class: precipitation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: precipitationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Snowfall { #envSnwF }
(envSnwF). Snowfall, i.e. amount of precipitation in the form of snow. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>
Class: precipitation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

Category Set ID: NA </br>
Unit Set: <a href="/sets.html#precipitationUnitSet">precipitationUnitSet</a
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Episode date { #epiDate }
(epiDate). Episode date is the earliest of onset, test or reported date. </l
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

220

Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

ERD table set { #erdTableSet }
(erdTableSet). All tables listed in the Entity Relationship Diagram. The full ODM model is c
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sarbecovirus-specific E sars-cov-2 gene target { #eSarbec }
(eSarbec). Sarbecovirus-specific E sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>

Parts

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Estimated frequency of reads { #estFreqReads }
(estFreqReads). Estimated frequency of reads in a sequencing assay  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#sequence">sequence</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
```

222

Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Estuary, natural water body { #estuary }
(estuary). Estuary, natural water body </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Experiment Failed { #expFail }
(expFail). PCR experiment failed. No value reported. Value should be blank for a measure wit
Part Type: qualityIndicators </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

```
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### 4s method { #extract4s }
(extract4s). Nucleic acid extraction performed using the 4s method.  </br>
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* https://www.protocols.io/view/v-4-direct-wastewater-rna-ca
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
```

224

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Nucleic acid extraction method { #extraction }
(extraction). Description of the nucleic acid extraction method. Description of the method u
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: extractSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Nucleic Acid Extraction set { #extractSet }
(extractSet). set used for storing all the valid category values for the nucleic acid extrac
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>

Parts

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: extractSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Extraction volume of sample { #exvol }
(exvol). Extraction volume of sample. Size of the sample that is analyzed. </
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>

226

Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Fecal matter { #faeces }
(faeces). Fecal matter. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

FALSE { #false }
(false). Boolean data type = FALSE Use these values and their set for any boolean measure or
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>

Parts

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 5 </br>
Maximum Length: 5 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Field sample { #field }
(field). Specifies a sample taken from the field; directly collected from an
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Field sample replicate { #fieldReplicate }
(fieldReplicate). A sample divided into two or more homogeneous parts. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

File location of polygon { #fileLocation }
(fileLocation). The location of the file containing the geometry of the polygon. File path s
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: blob </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 65535 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Filtration { #filt }
(filt). Describes solid separation from a wastewater sample via filtration. I
Part Type: categories </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

First Nation { #fiNa }
(fiNa). Used to categorize a sampleshed that is a First Nation, or on reserve lands. Likely
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

First name of contact { #firstName }
(firstName). Specifies the first name of a given contact. </br>
Part Type: attributes </br>
Domain: naDomain </br>

Parts

```
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### First released version { #firstReleased }
(firstReleased). The version in which a part was first released  </br>
*Part Type:* <a href="#partSupport">partSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
```

232

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Foreign key { #fK }
(fK). Foreign key for a table. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

AI - Inhibition present but addressed { #flagAI }
(flagAI). The original sample was inhibited; however, the inhibition has been addressed thro
Part Type: qualityIndicators </br>

Parts

```
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### B - Trace levels of contamination { #flagB }
(flagB). Analytical result may be subject to "trace" levels of contamination
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

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

FI - Inhibition present and unaddressed { #flagFI }
(flagFI). The original sample was inhibited; however, the inhibition has not been successful
Part Type: qualityIndicators </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

J - Weak signal extrapolation { #flagJ }
(flagJ). Analytical result falls below the lowest concentration of the experiment-specific s

Parts

```
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### ND - Non-detect { #flagND }
(flagND). No amplification occurred in the reaction; non-detect. For the valu
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
```

236

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

UJ - Trace signal extrapolation { #flagUJ }
(flagUJ). Observed quantitation cycle is greater than the experiment-specific standard curve
Part Type: qualityIndicators </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

UQ - Unquantifiable { #flagUQ }

(flagUQ). Unquantifiable, Ct value exceeds the maximum value of the standard
Part Type: qualityIndicators </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Float data type { #float }
(float). The data type for float data. Only used for the dictionary entries o
Part Type: dataTypes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Flow-normalized mean { #floMean }
(floMean). Mean measure normalized to wastewater flow. Mostly used for reporting specific al
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Floor { #floor }
(floor). Floor of a building or room. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#surfaceCompartmentSet">surfaceComparti
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Flow rate { #floRate }
(floRate). Wastewater volumetric flow rate at the sample collection location
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartment$
Group: siteFeat </br>
Class: flow </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: flowUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Flow class { #flow }
(flow). Measures and methods related to flow. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: flow </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: flowUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Flow proportional 24hr sample depreciated { #flow24hDep }
(flow24hDep). A flow proportional 24-hour composite sample generally collecte
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Flow proportional sample { #flowPr }
(flowPr). A flow proportionalcomposite sample generally collected by an autos
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

242

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Volume flow rate unit set { #flowUnitSet }
(flowUnitSet). Unit set for volume flow measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: flowUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Flow volume { #flowVol }
(flowVol). Volume of influent. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: siteFeat </br>
Class: flow </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: flowUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Influenza virus measure { #flu }
(flu). General influenza virus measure This measure should only be used if th
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>

Ontology Reference: <a href="#http://purl.obolibrary.org/obo/MONDO_0005812">http://purl.ob
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Influenza virus A1 { #fluA1 }
(fluA1). Influenza virus A1 type </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>

Parts

Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

influenza virus A2 { #fluA2 }
(fluA2). influenza virus A2 type </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Influenza virus B { #fluB }
(fluB). Influenza virus B type </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>

246

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

Fluidigm digital PCR { #fluiDpcr }
(fluiDpcr). Describes a PCR analysis done using FluidIGM's digital PCR technology. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Foggy { #foggy }
(foggy). Qualitative category for the weather measure, specifying a foggy or
Part Type: categories </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: siteFeat </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Fraction analyzed { #fraction }
(fraction). Fraction of the sample that is analyzed. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: fractionSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sample fraction set { #fractionSet }
(fractionSet). set for the fraction of the sample (solid, liquid, etc.). </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: fractionSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Freyja Script { #freyja }
(freyja). Freyja Script for sequencing.   </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: https://github.com/andersen-lab/Freyja </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

F-Specific RNA bacteriophages { #frna }
(frna). A measure for amount of F-Specific RNA bacteriophages.   </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</

Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

F-Specific RNA bacteriophages, G2 { #frnaG2 }
(frnaG2). A measure for amount of G2 F-Specific RNA bacteriophages. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>

Parts

```
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Sample frozen { #frozen }
(frozen). Sample was frozen before analysis or processing  </br>
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Field sample temperature { #fst }
(fst). Temperature that the sample is stored at while it is being sampled. Th
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#phy">phy</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
```

252

Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: temperature </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Full dictionary sheets set { #fullDictionarySheetSet }
(fullDictionarySheetSet). Worksheets in the full Excel dictionary. The full dictionary is \`
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Funder Contact ID { #funderCont }
(funderCont). A unique identifier for funders. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Funding agency ID { #funderID }
(funderID). The funding agency of the dataset. Use Organization ID to populat
Part Type: attributes </br>
Domain: naDomain </br>

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

g215c delta-variant gene target { #g215c }
(g215c). g215c delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

g339d omicron-variant gene target { #g339d }
(g339d). g339d omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

g496s omicron-variant gene target { #g496s }
(g496s). g496s omicron-variant gene target </br>
Part Type: measurements </br>

Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

g662s delta-variant gene target { #g662s }
(g662s). g662s delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>

Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Gamma { #gam }
(gam). P.1 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Gas class { #gas }
(gas). Measures and methods relating to gas and gases. </br>

Part Type: classes </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: gas </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: dissGasUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Gene copies per copy of crAssphage { #gcCrA }
(gcCrA). Gene or variant copies per copy of crAssphage. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

gene copies per day per 100,000 { #gcD100 }
(gcD100). The unit for measures reflecting the gene copies per day per 100,00
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Gene copies per gram solids { #gCGS }

(gCGS). Gene or variant copies per gram solids. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Gene copies per L { #gcL }
(gcL). Gene or variant copies per litre. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Gene copies per mL { #gcMl }
(gcMl). Gene or variant copies per millilitre of solution. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Gene copies per PMMoV copy { #gcPpmov }
(gcPpmov). Gene or variant copies per copy of PMMoV. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Genetics unit set { #geneticUnitSet }
(geneticUnitSet). Unit set for genetic-related measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

```
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### General missingness set { #genMissingnessSet }
(genMissingnessSet). The general set for missingness values.  </br>
*Part Type:* <a href="#missingnessSets">missingnessSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>
```

Generic quality flag set { #genQualitySet }
(genQualitySet). A quality set to specify any generic quality concerns about a measure or sa
Part Type: qualityIndSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

European Petroleum Survey Group Coordinates { #geoEPSG }
(geoEPSG). The unique EPSG code specifying a given geospatial area. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: miscAttr </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Latitude { #geoLat }
(geoLat). Geographical location, latitude in decimal coordinates, ie.: (45.42
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: miscAttr </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: -90 </br>
Maximum Value: 90 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Longitude { #geoLong }
(geoLong). Geographical location, longitude in decimal coordinates, ie.: (-75.695000) </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: miscAttr </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: -180 </br>
Maximum Value: 180 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Type of geography { #geoType }
(geoType). Type of geography that is represented by the polygon. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

267

Parts

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#geoTypeSet">geoTypeSet</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>

### Geographic set { #geoTypeSet }
(geoTypeSet). set for different type of geographic components.  </br>
*Part Type:* <a href="#mmaSets">mmaSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#geoTypeSet">geoTypeSet</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
```

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Well-known text { #geoWKT }
(geoWKT). Well-known text of the polygon </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 63 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Gram per cubic metre { #gm3 }
(gm3). Density unit. Used for absolute humidity and other measures. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: airCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Geometric mean { #gmn }
(gmn). Geometric mean.   </br>
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>

270

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Government agency { #govt }
(govt). The category of organization type used for government agencies, programs, or crown-c
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Grams { #grams }
(grams). A unit of mass or weight. </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>

Parts

```
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#float">float</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 0 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Gravity settling { #graSet }
(graSet). Describes solid separation from a wastewater sample where the sampl
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#allDo">allDo</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#waterCompartmentSet">waterCompartmentS
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
```

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Grab sample { #grb }
(grb). A single large representative grab sample. If the sample was collected over a series
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Gromstole 1.0 Script { #gromstole }
(gromstole). Gromstole 1.0 Script for sequencing. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* https://github.com/PoonLab/gromstole </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Group { #group }
(group). Unique identifier for a group of measures. Mostly applicable for mea
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
```

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Groups { #groups }
(groups). A collection of related measures. Used primary to group measurements and methods,
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Header { #header }
(header). Header for a table. Also known as a table variable or entiy relationship 'attribut
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Health administration or planning agency { #healthAdm }
(healthAdm). Health adminstrative or planning organization. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Heat inactivated sars-cov-2 virus spike target { #heatInacSARS }
(heatInacSARS). Heat inactivated SARS-CoV-2 virus is used as the recovery efficiency control
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

hep g armored rna { #hepGRna }
(hepGRna). Measure of the amount Hepatitis G Armored RNA. </br>
Part Type: measurements </br>
Domain: bio </br>

Parts

Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

hep g armored rna spike target { #hepGRnaMat }
(hepGRnaMat). Hepatitis G armored RNA is used as the recovery efficiency cont
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

High severity { #high }
(high). Indicates a very sever quality issue, likely meaning the data should not be reported
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sewer Network Health Region { #hlthReg }
(hlthReg). Health region served by the sewer network </br>
Part Type: categories </br>

279

Parts

Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Hand Measurement { #hma }
(hma). Handheld measurement analyzer. A handheld measurement analyzer. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

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

Hollow fiber dead end ultrafiltration { #hollowFiberUF }
(hollowFiberUF). Hollow fiber dead end ultrafiltration </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

General Hospital Admissions { #hosa }
(hosa). Hospital admissions or patients newly admitted to hospital. </br>

Parts

Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Hospital Census { #hosc }
(hosc). Hospital census or the number of people admitted with an ailment. </
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Hospital { #hosptl }
(hosptl). Hospital </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Holding tank wastewater depreciated { #hoTaWa }

(hoTaWa). Wastewater from a holding tank, such as from an airplane or ship De
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Hours { #hours }
(hours). A unit for indicating a length of time in hours. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: miscMeas </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

284

Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Holding tank wastewater { #htSam }
(htSam). Wastewater sampled from a holding tank, such as from an airplane or ship </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Holding tank { #htSite }
(htSite). Holding tank </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Human compartment { #hum }
(hum). A measure or observation made about a human. </br>
Part Type: compartments </br>
Domain: bio </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#humanCompartmentSet">humanCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Human compartment set { #humanCompartmentSet }
(humanCompartmentSet). A compartment set for measures and methods in the human compartment.
Part Type: compartmentSets </br>
Domain: bio </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: humanCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Humidity class { #humid }
(humid). Measures and methods related to humidity. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#airCompartmentSet">airCompartmentSet</
Group: naGroup </br>
Class: humid </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

i1566v omicron-variant gene target { #i1566v }
(i1566v). i1566v omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

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

i3758v omicron-variant gene target { #i3758v }
(i3758v). i3758v omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

i82t delta-variant gene target { #i82t }
(i82t). i82t delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

International Classification of Diseases { #icd }
(icd). Classification system for diseases in humans. </br>
Part Type: nomenclatures </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: <a href="/sets.html#humanCompartmentSet">humanCompartmentS
Group: naGroup </br>
Class: disease </br>
Nomenclature: ICD </br>

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

Intensive care unit patients { #icu }
(icu). Units for describing a population measure of patients who are in intensive care due t
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>

Parts

Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Index { #index }
(index). Index number in case the measurement was taken multiple times. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 50 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Inhibition set { #inhibitionSet }
(inhibitionSet). Category set for inhibition methods. </br>
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: pcr </br>

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: inhibitionSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Inhibition measure { #inhibMe }
(inhibMe). Parameter to report whether or not inhibition was detected in the sample. Detecte
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: miscMeas </br>
Class: sequence </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: booleanUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Inhibition method { #inhibMeth }
(inhibMeth). Description of the method used to evaluate molecular inhibition
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: measGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: inhibitionSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Innovaprep ultrafiltration { #innovaprepUF }
(innovaprepUF). Innovaprep ultrafiltration </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>

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

Input { #input }
(input). Input for a table. Indicates if a part can be used in a table. "Input" is used to i
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Instrument ID { #instrumentID }
(instrumentID). A unique identifier for an instrument. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Instrument table { #instruments }
(instruments). The table that contains information about instruments. adapt
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Instruments table column order { #instrumentsOrder }
(instrumentsOrder). Specifies the order of the columns in the Instruments table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>

Parts

Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Instrutment table required headers { #instrumentsRequired }
(instrumentsRequired). Specifies the columns required in the Instruments tab
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Other instrument { #instrumentTypeOther }
(instrumentTypeOther). Type of instrument other than those included in the Pl
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

298

Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Instrument Type { #insType }
(insType). Type of instrument used to perform the measurement. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: insTypeSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Describe other instrument type, if applicable { #insTypeOth }
(insTypeOth). Description of the instrument in case it is not listed in instr
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Instrument set { #insTypeSet }
(insTypeSet). List of instruments that are used for measures and methods </l
Part Type: mmaSets </br>
Domain: naDomain </br>

300

Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: insTypeSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Integer data type { #integer }
(integer). The data type for integers. Only used for the dictionary entries of parts. </br>
Part Type: dataTypes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Intercept { #inter }
(inter). Intercept value of the calibration curve. Used for storing calibrati
Part Type: measurements </br>
Domain: allDo </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Combined ip2 and ip4 sars-cov-2 gene target { #ip2ip4 }
(ip2ip4). Combined ip2 and ip4 sars-cov-2 gene target </br>
Part Type: measurements </br>

Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ISO639-1 { #iso6391 }
(iso6391). The first part of the ISO 639 series of international standards for language code
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ISO639-2B { #iso6392B }
(iso6392B). A set of international standards that lists short codes for langu
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ISO639-2T { #iso6392T }
(iso6392T). A set of international standards that lists short codes for langu

304

Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ISO639-3 { #iso6393 }
(iso6393). A set of international standards that lists short codes for language names. ISO 6
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ISO639-6 { #iso6396 }
(iso6396). A set of international standards that lists short codes for langua
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

k856r omicron-variant gene target { #k856r }

(k856r). k856r omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Kilogram per second { #kgS }
(kgS). Kilograms per second. </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Kilolitres { #kl }
(kl). Kilolitres of volume </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

308

Litres { #l }
(l). Litres of volume </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

l452r delta-variant gene target { #l452r }
(l452r). l452r delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

l981f omicron-variant gene target { #l981f }
(l981f). l981f omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

310

Laboratory { #lab }
(lab). Laboratory for environmental testing. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Lab ID default depricated { #labDefDep }
(labDefDep). Used as default when a new sample is created by this reporter. See ID in Lab ta
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 10 </br>
*Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

### Laboratory duplicate { #labDuplicate }
(labDuplicate). Second (time or more) processing and analysis of sample. Usua
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Lab ID { #labID }
(labID). Unique identifier for a laboratory. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Lagoon system { #lagoon }
(lagoon). Logoon system for extensive wastewater treatment </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Lake, natural water body { #lake }
(lake). Lake, natural water body </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Lambda { #lamba }
(lamba). C.37 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Language ID { #lang }
(lang). Language code for translation purposes. Specifies the langage for each translation,
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Language family { #langFam }
(langFam). Specifies the language family of a given language for translation
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>

316

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Language name { #langName }
(langName). Specifies the name of the language in roman alphabet characters for translation
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Language Look-up table { #languages }
(languages). Look up table for all languages, used to give structure to the translation tabl
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>

Parts

```
*Class:* <a href="#lookup">lookup</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Language table column order { #languagesOrder }
(languagesOrder). Specifies the order of the columns in the Languages table.
*Part Type:* <a href="#tableSupport">tableSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 1 </br>
```

318

Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Language table required headers { #languagesRequired }
(languagesRequired). Required headers in the Languages table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Last edited { #lastEdited }
(lastEdited). The date the entry was last updated. Use lastEdited if an entry is updated. Le
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#datetime">datetime</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet 
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>

### Last name of contact { #lastName }
(lastName). Specifies the last name of a given contact.  </br>
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet 
```

320

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Last updated version { #lastUpdated }
(lastUpdated). The version in which the part was last updated. Any change to the part of lis
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

LaTeX expression { #latExp }
(latExp). LaTeX expression used to generate formulas, symbols, etc. Mainly relevant for uni
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Parts

Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 20 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Low breadth of coverage { #lBC }
(lBC). The percentage of the genome covered by reads (the breadth) is low.
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Laboratory control sample duplicate { #lcsd }
(lcsd). Known amounts of an analyte or representative compounds are added to a second "clean
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Low depth of coverage { #lDC }
(lDC). Poor coverage, specifically an insufficient number of reads or too many sequencing re
Part Type: qualityIndicators </br>
Domain: naDomain </br>

Parts

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

Leaked sample { #leaked }
(leaked). Sample leaked, some volume and material was lost. </br>
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

324

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Link { #li }
(li). Link to an external reference that describes the geometry of the polygon. Deprecated a
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

License { #license }
(license). The license of a dataset. </br>
Part Type: attributes </br>

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet 
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Linear scale aggregation set { #linearAggrSet }
(linearAggrSet). The aggregation set that contains all aggregations that exis
*Part Type:* <a href="#aggregationSets">aggregationSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

326

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

Liquid fraction { #liq }
(liq). Liquid fraction of a sample. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

List worksheet { #lists }
(lists). Parts lists for template dropdowns and other documentation. Sheets or tabs for the

327

Parts

```
*Part Type:* <a href="#dictionarySupport">dictionarySupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### List set { #listSet }
(listSet). PartTypes that contain categories, sets, or lists. Used to generat
*Part Type:* <a href="#miscSet">miscSet</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#airCompartmentSet">airCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#windSpeedUnitSet">windSpeedUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
```

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

Access to local ha { #localHA }
(localHA). If this is 'no', the, data will not be available to local health authorities. If
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Limit of detection (LOD) { #lod }

(lod). Limit of detection. Limit of detection (LOD) for this method, if one e
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Limit of detection (LOD) - sewage { #lodSewa }
(lodSewa). Limit of detection for sewage samples. Limit of detection (LOD) fo
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>

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

Logarithmic scale aggregation set { #logAggrSet }
(logAggrSet). The aggregation set that contains all aggregations that exist on the logarithm
Part Type: aggregationSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Dictionary tables { #lookup }
(lookup). Tables to describe and support the ODM dictionary. These tables hol
Part Type: classes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: lookup </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Limit of quantification (LOQ) { #loq }
(loq). Loq Limit of quantification (LOQ) for this method if one exists. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: procGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Low severity { #low }
(low). A marker for low severity </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Lower limit of a 95% confidence interval { #lowerCI95 }
(lowerCI95). Specifies the the lower limit of a 95% confidence interval. Shou
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Low-volume sample { #lowVol }
(lowVol). Sample is low-volume, but was run regardless. </br>
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

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

Long-term care facility { #ltcf }
(ltcf). A residential healthcare facility that provides 24-medical care. These are also call
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Long-term care - assisted living or retirement home { #ltcfAl }
(ltcfAl). A residential facility that provides assistance with daily care but
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Other long-term care { #ltcfO }
(ltcfO). Other residential facilities that provide daily and/or medical care
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

336

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Life technologies digital PCR { #ltDpcr }
(ltDpcr). Describes a PCR analysis done using Life Technologies' digital PCR technology.  </
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
```

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Lysis buffer { #lysi }
(lysi). Lysis buffer. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Cubic metres per day { #m3D }
(m3D). Cubic metres per day. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>

338

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Cubic metres per hour { #m3H }
(m3H). Cubic metres per hour. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>

339

Parts

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Cubic metres per second { #m3S }
(m3S). Cubic metre per second. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Manufacturer { #manufacturer }
(manufacturer). Manufacturer of an instrument. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>

340

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Mate pair layout { #mateLay }
(mateLay). Specifies the mate pair layout for a sequencing method. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Maximum length { #maxLength }
(maxLength). The maximum length of the value of a part or measure. </br>
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Maximum value { #maxVal }
(maxVal). Highest value in a range of values for a measure. </br>
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Maximum value part support { #maxValue }
(maxValue). The maximum value of a part. </br>
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Parts

```
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Arithmetic mean { #me }
(me). Arithmetic mean.  </br>
*Part Type:* <a href="#aggregations">aggregations</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>


### Measurement group { #measGrp }
(measGrp). A group of measures that cannot be otherwise categorized.  </br>
*Part Type:* <a href="#groups">groups</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
```

344

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

Other Measure { #measOth }
(measOth). Other measure, not otherwise specified in measures. Add description to categoryOt
Part Type: measurements </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>

Parts

Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Measures quality set { #measQualitySet }
(measQualitySet). A quality set for any measure, includes all the quality fl
Part Type: qualityIndSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Measure { #measure }
(measure). A measurement or observation of any substance including a biologi
Part Type: attributes </br>
Domain: naDomain </br>

Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Measures { #measurements }
(measurements). The attribute to describe a part type of measures. All measures have \`partT
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Report ID { #measureRepID }
(measureRepID). Unique identifier for a measurement. Report IDs cannot be rep
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Measure report table { #measures }
(measures). The table that contains information and details about a given mea
Part Type: tables </br>

348

Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: results </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Measure set report table { #measureSets }
(measureSets). The table that identifies sets of measures. Examples of measure sets include
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: results </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

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

Measure sets table column order { #measureSetsOrder }
(measureSetsOrder). Specifies the order of the columns in a Measure Sets tabl
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Measure Set table required headers { #measureSetsRequired }
(measureSetsRequired). Specifies the columns required in a Measure Sets table

350

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

Measures table column order { #measuresOrder }
(measuresOrder). Specifies the order of the columns in a Measures table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

```
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 1 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Measures table required headers { #measuresRequired }
(measuresRequired). Specifies the columns required in a Measures table.  </b
*Part Type:* <a href="#tableSupport">tableSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Report set ID { #meaureSetRepID }
```

352

(meaureSetRepID). Unique identifier that links together a group of related measures. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Median { #med }
(med). Median. </br>
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

```
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>


### Normalized arithmetic mean { #menr }
(menr). Arithmetic mean, normalized.  </br>
*Part Type:* <a href="#aggregations">aggregations</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>
```

Other Measure Description { #meOthDe }
(meOthDe). Description of other measure (measOtherDesc). </br>
Part Type: measurements </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 60 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Measure license { #mesureLic }
(mesureLic). Specifies the access and use licensing for a given single measurement. Populate
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

```
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Method { #method }
(method). A procedure for collecting a sample or performing a measure.  </br>
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 10 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>
```

Concentration method { #methodConc }
(methodConc). Description of the method to concentrate a wastewater sample. Description of t
Part Type: methods </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: methodConcSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Concentration method set { #methodConcSet }
(methodConcSet). A set a concentration methods. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Methods { #methods }
(methods). Procedures or steps for collecting samples or performing measures
*Part Type:* <a href="#partType">partType</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Membrane filtration with acidification and mgcl2 { #mfAcidmgcl2 }
(mfAcidmgcl2). Membrane filtration with acidification and mgcl2 </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Membrane filtration with acidification and mgcl2, membrane recombined with separated sol
(mfAcidmgcl2SS). Membrane filtration with acidification and mgcl2, membrane recombined with
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

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

Membrane filtration with addition of mgcl2 { #mfMgcl2 }
(mfMgcl2). Membrane filtration with addition of mgcl2 </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Membrane filtration with mgcl2 and separated solids { #mfMgcl2SS }
(mfMgcl2SS). Membrane filtration with addition of mgcl2, membrane recombined with separated
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Membrane filtration with no amendment { #mfNoAmend }
(mfNoAmend). Membrane filtration with no amendment </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

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

Membrane filtration with no amendment, membrane recombined with separated
(mfNoAmendSS). Membrane filtration with no amendment, membrane recombined with
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

362

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Membrane filtration with sample acidification { #mfSampleAcid }
(mfSampleAcid). Membrane filtration with sample acidification </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Membrane filtration with sample acidification, membrane recombined with separated solids
(mfSampleAcidSS). Membrane filtration with sample acidification, membrane recombined with se
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>

Parts

```
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Millions of gallons per day (MG/D) { #mgd }
(mgd). A unit for measuring of design capacity for wastewater treatment plant
*Part Type:* <a href="#units">units</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#float">float</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 0 </br>
```

Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Milligrams per litre { #mgL }
(mgL). Milligrams per litre. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Murine Hepatitis Virus { #mhv }
(mhv). A measure for amount of murine hepatitis viurs. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

```
*Group:* <a href="#virusMisc">virusMisc</a> </br>
*Class:* <a href="#allele">allele</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Multiple issues { #mI }
(mI). Multiple issues have arisen in the sequencing process. When using the
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
```

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Mid-level severity { #mid }
(mid). A marker for med-level severity, where there are some concerns. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Minimum length { #minLength }
(minLength). The maximum value of measure. </br>
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Minutes { #minutes }
(minutes). A unit for indicating a length of time in minutes. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: miscMeas </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>

Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Minimum value { #minVal }
(minVal). Lowest value in a range of values for a measure. </br>
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Minimum value part support { #minValue }
(minValue). The minimum value of part. </br>
Part Type: partSupport </br>
Domain: naDomain </br>

Parts

```
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Miscellaneous attribute group { #miscAttr }
(miscAttr). A group of miscellaneous measurement-like attributes. Examples o
*Part Type:* <a href="#groups">groups</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
```

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Miscellaneous measure group { #miscMeas }
(miscMeas). A group of measures that cannot be otherwise categorized. </br>
Part Type: groups </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Missingness { #missingness }
(missingness). The part type for missingness values. Only used for the dictionary entries of
Part Type: partType </br>

Parts

Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Missingness sets { #missingnessSets }
(missingnessSets). Missingness sets for measures, methods or attributes. Inpu
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

372

Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Mixed/homogenized sample { #mix }
(mix). Mixed or homogenized sample or fraction analyzed. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Millilitres { #ml }
(ml). Millilitres of volume </br>

Parts

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

Megalitres per day (ML/d) { #mld }
(mld). Megalitres per day. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

374

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Millimetres { #mm }
(mm). Unit part for the SI unit of millimetres. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Measure, method, or attribute { #mmaSet }

Parts

(mmaSet). The set for a measure, method, or attribute. Only applicable for ca
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Measure, method, or attribute sets { #mmaSets }
(mmaSets). A set of categories. For example, site type has a list of differer
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

376

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Model { #model }
(model). Model number or version of the instrument. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Parts

Months { #months }
(months). A unit for indicating a length of time in months. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: miscMeas </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Moore swab passive sample { #moorSw }
(moorSw). Moore swab passive sample. Use collectionPeriod to describe how ma
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Metres per second { #ms }
(ms). metres per second. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ms2 coliphage { #ms2Col }
(ms2Col). Measure of the amount of ms2 coliphage. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ms2 coliphage spike target { #ms2ColMat }
(ms2ColMat). ms2 coliphage is used as the recovery efficiency control target
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

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

Matrix spike duplicate { #msd }
(msd). A known amounts of an analyte or representative compounds are added in the laboratory
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Moore swab passive sample depreciated { #mspsDep }
(mspsDep). Moore swab passive sample. Deprecated in version 2, please do not
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Major sewer pipeline { #mSwrPpl }
(mSwrPpl). Major sewer pipeline </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

382

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Mu { #mu }
(mu). B.1.621 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>

Parts

Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

murine coronavirus { #muCo }
(muCo). Measure of the amount of murine coronavirus. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

murine coronavirus spike target { #muCoMat }
(muCoMat). Murine coronavirus is used as the recovery efficiency control targ
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>

384

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

Multiple fraction { #mul }
(mul). Multiple fractions were analyzed separately and aggregated together post-analysis. Th
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Multiple Purpose { #multiple }
(multiple). A measure or sample taken for multiple purposes, not easily captu
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Municipalities or communes { #municipalLevel }
(municipalLevel). Municipalities or communes </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>

386

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

Municipality { #municp }
(municp). A complete municipality, this specifies an entire metropolitan area, either a city
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Mutations class { #mutation }
(mutation). Measures and methods related to mutations. </br>
Part Type: classes </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

N sars-cov-2 gene target { #n }
(n). N sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</

388

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

Combined N1 and N2 sars-cov-2 gene target { #n1n2 }
(n1n2). Combined N1 and N2 sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

n211i omicron-variant gene target { #n211i }
(n211i). n211i omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

n679k omicron-variant gene target { #n679k }
(n679k). n679k omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

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

n856k omicron-variant gene target { #n856k }
(n856k). n856k omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>

Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

n969k omicron-variant gene target { #n969k }
(n969k). n969k omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Not applicable { #NA }
(NA). The field for which the expected value is not a property of the descri
Part Type: missingness </br>
Domain: naDomain </br>

```
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>

### Aggregation not applicable { #naAggr }
(naAggr). Not applicable for aggregations. Used for parts for which an aggregation value is
*Part Type:* <a href="#aggregations">aggregations</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
```

393

Parts

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Aggregation scale not applicable { #naAggrScale }
(naAggrScale). Not application for aggregation sets. Used for parts for whic
Part Type: aggregationScales </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Aggregation set not applicable { #naAggrSet }
(naAggrSet). Not application for aggregation sets. Used for parts for which a
Part Type: aggregationSets </br>

394

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Class not applicable { #naClass }
(naClass). Class is not applicable. Use this for all parts that don't have classes (most nor
*Part Type:* <a href="#classes">classes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

Parts

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

Compartment not applicable { #naCompartment }
(naCompartment). Compartment not applicable. </br>
Part Type: compartments </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 13 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Compartment set not applicable { #naCompartmentSet }
(naCompartmentSet). Compartment not applicable. </br>

396

Part Type: compartmentSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 13 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Domain not applicable { #naDomain }
(naDomain). Not applicable. Use 'not applicable' when there is no domain for the part </br>
Part Type: domains </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

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

Group not applicable { #naGroup }
(naGroup). Used when there is no group; ie. group is not applicable. Use 'not
Part Type: groups </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Name { #name }

(name). Name of a domain, specimen, group, class, attribute, unit, nomeclature or other enti
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Not a number { #nan }
(nan). The outcome of a measurement is not a valid number (plus or minus infinity, error, ..
Part Type: missingness </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Nomenclature not applicable { #naNomenclature }
(naNomenclature). Not applicable. Use 'not applicable' when there is no nomen
Part Type: nomenclatures </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

400

Specimen not applicable { #naSpecimen }
(naSpecimen). Non applicable specimen. Use 'not applicable' when there is no specimen/set fo
Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Specimen set not applicable { #naSpecimenSet }
(naSpecimenSet). A specimen set for when specimen/specimen set is not applicable. Use 'not a
Part Type: compartmentSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

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

Native Name { #natName }
(natName). The native name of the language, i.e. what the language is called
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

402

Unit not applicable { #naUnit }
(naUnit). Not appliable for units. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Unit set not applicable { #naUnitSet }
(naUnitSet). Not applicable for unit sets. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

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

National Center for Biotechnology Information { #ncbi }
(ncbi). NCBI header </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

NCBI - notes { #ncbiNotes }
(ncbiNotes). NCBI notes </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Neighbourhood { #neigh }
(neigh). A municipal neighbourhood, this specifies a sub-section of a larger municipality.
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

405

Parts

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

Local administrative units or neighborhoods { #neighborLevel }
(neighborLevel). Local administrative units or neighborhoods </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: ISCU </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#nrNAMissingnessSet">nrNAMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

406

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population of newly vaccinated persons { #newVax }
(newVax). Population of newly vaccinated persons </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

NextClade nomenclature { #nextclade }
(nextclade). Specifies variant or genetic nomenclature as set out by NextClade. </br>
Part Type: nomenclatures </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

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

Normalized geometric mean { #ngmn }
(ngmn). Geometric mean, normalized. </br>
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Ammonium Nitrogen { #nH4N }
(nH4N). Ammonium nitrogen concentration, as N. </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

niid_2019-ncov_n sars-cov-2 gene target { #niid19 }
(niid19). niid_2019-ncov_n sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>

Parts

```
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### No quality concerns { #noConcern }
(noConcern). A flag to indicate there is are no quality concern about the mea
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 1 </br>
```

Maximum Value: 1 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sample not labelled { #noLabel }
(noLabel). Sample had no label </br>
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

No liquid concentration, liquid recombined with separated solids { #noliquid }
(noliquid). No liquid concentration, liquid recombined with separated solids </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Nomenclature { #nomenclature }
(nomenclature). A classification system to report the measure class. Only ap
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
```

412

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Nomenclatures { #nomenclatures }
(nomenclatures). A classification system to report the measure class. See partID = nomenclat
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

NORMAN { #norman }
(norman). NORMAN header </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Parts

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

NORMAN - notes { #normanNote }
(normanNote). Norman notes </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

414

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Norovirus G1 { #noroG1 }
(noroG1). Norovirus genogroup 1 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Norovirus G2 { #noroG2 }
(noroG2). Norovirus genogroup 2 </br>
Part Type: measurements </br>
Domain: bio </br>

Parts

Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Notes { #notes }
(notes). A note used to describe details that are not captured in other attri
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 200 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample missing time stamp { #noTime }
(noTime). Sample is missing the autosampler time; incomplete metadata on collection. </br>
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Not reported { #nr }
(nr). A value could have been recorded, however, it was not. Missing value indicator for dat
Part Type: missingness </br>

Parts

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>

### Not reported, Not applicable missing set { #nrNAMissingnessSet }
(nrNAMissingnessSet). Not reported, Not applicable missing set.  </br>
*Part Type:* <a href="#missingnessSets">missingnessSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

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

Sarbecovirus-specific N sars-cov-2 gene target { #nSarbec }
(nSarbec). Sarbecovirus-specific N sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Nephelometric turbidity unit { #ntu }
(ntu). Nephelometric Turbidity Units, a unit used in the measurement of turbidity (see "turb

680nm) and 90° incident angle. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: https://www.sciencedirect.com/topics/engineering/nephelomet
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Nuclisens automated magnetic bead extraction kit { #nucAuto }
(nucAuto). Nucleic acid extraction performed using the nuclisens automated ma
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Nuclisens manual magnetic bead extraction kit { #nucManu }
(nucManu). Nucleic acid extraction performed using the nuclisens manual magnetic bead extrac
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Null { #null }
(null). A logical representation of a statement that is neither TRUE nor FALS
Part Type: missingness </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

National Wastewater Surveillance System { #nwss }
(nwss). NWSS header </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

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

NWSS - notes { #nwssNotes }
(nwssNotes). NWSS notes </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

NWSS - process { #nwssProcess }
(nwssProcess). NWSS process </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Water { #nww }
(nww). Non-wastewater, coming from any kind of water body </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

coronavirus OC43 { #oc43 }
(oc43). Measure of the amount of coronavirus OC43. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

oc43 spike target { #oc43Mat }
(oc43Mat). Human coronavirus OC43 is used as the recovery efficiency control
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Ocean, natural water body { #ocean }
(ocean). Ocean, natural water body </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

426

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Other Collection depreciated { #oColDep }
(oColDep). Other type of collection method. Add description to collectionOther. Deprecated a
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Lab Analysis { #ola }
(ola). Offline laboratory analysis. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Omicron BA.1 { #omicr1 }
(omicr1). Omicron B.1.1.529 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: sarsCov2 </br>
Class: variant </br>

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

Omicron BA.2 { #omicr2 }
(omicr2). Omicron BA.2 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>

Parts

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Omicron BA.2.75 { #omicr275 }
(omicr275). Omicron BA.2.75 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Omicron BA.4 { #omicr4 }
(omicr4). Omicron BA.4 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>

430

Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Omicron BA.5 { #omicr5 }
(omicr5). Omicron BA.5 </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: who </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>

431

Parts

Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Onset date { #onsDate }
(onsDate). Earliest that symptoms were reported for this case. This data is c
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Online Sensor { #onse }
(onse). Online sensor An online sensor </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>


### Ontology reference { #ontologyRef }
(ontologyRef). Ontology reference for a part. This field contains a link to an existing onto
*Part Type:* <a href="#partSupport">partSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
```

Parts

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 200 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Orthophosphates { #ophos }
(ophos). Ortho-phosphate concentration. </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Other residential building { #orb }
(orb). Individual residential buildings or institutions not captured in othe
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

434

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

OR Boolean aggregation { #orBoo }
(orBoo). "OR" aggreation. If any value in the aggregation is "TRUE" then the OR aggregation
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ORF1a sars-cov-2 gene target { #orf1a }
(orf1a). ORF1a sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ORF1ab sars-cov-2 gene target { #orf1ab }
(orf1ab). ORF1ab sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>

436

Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ORF1b sars-cov-2 gene target { #orf1b }
(orf1b). ORF1b sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization ID { #organizationID }
(organizationID). A unique identifier for the organization to which the repor
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Organization table { #organizations }
(organizations). The table that contains information about a laboratory. adap
Part Type: tables </br>

438

Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Organizations table column order { #organizationsOrder }
(organizationsOrder). Specifies the order of the columns in a Organizations table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

Parts

Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organziation table required headers { #organizationsRequired }
(organizationsRequired). Specifies the columns required in a Organizations ta
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization level { #orgLevel }
(orgLevel). The geographic level of an organization. There are six levels bas

440

Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: orgLevelSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: nrNAMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization level set { #orgLevelSet }
(orgLevelSet). Categories of organization levels. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization sector { #orgSector }
(orgSector). The sector of an organization </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: orgSectorSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#nrNAMissingnessSet">nrNAMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization sector set { #orgSectorSet }

442

(orgSectorSet). Cateogries of organization sectors. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization Type { #orgType }
(orgType). Specifies the type or purpose of a given organization. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: orgTypeSet </br>
Unit Set: naUnitSet </br>

Parts

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#nrNAMissingnessSet">nrNAMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Organization type set { #orgTypeSet }
(orgTypeSet). The set for storing organization types. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

444

Sample origin { #origin }
(origin). An attribute of a sample specifying the origin. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample Origin set { #originSet }
(originSet). The set for storing the valid categorical values of sample origin. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

```
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Other Collection depreciated { #otco }
(otco). Other type of collection method. Add description to collectionOther.
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#NA">NA</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.
```

446

Other aggregation scale { #othAgg }
(othAgg). Specifies an aggregation scale that can't be described as either "qualitative" or
Part Type: aggregationScales </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Other { #other }
(other). Other Other category. A categorical response for several variables in version 1. Al
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 2.0.0. Last updated: 2.0.0.

Other aggregation set { #otherAggrSet }
(otherAggrSet). Aggregation set used for unitless measures. </br>
Part Type: aggregationSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Other aggregation depricated { #otherDep }
(otherDep). Other aggregation method. Add description to aggregationOther Deprecated as of v
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Access to other prov depricated { #otherProvDep }
(otherProvDep). If this is 'no', this data will not be available to other data providers not
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#booleanSet">booleanSet</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#boolean">boolean</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 1 </br>
*Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

### Other report table set { #otherReportTableSet }
(otherReportTableSet). Additional tables that form the full data model.  </br
*Part Type:* <a href="#dictSets">dictSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
```

450

Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Variants Other { #otherV }
(otherV). Used for reporting variants detected for which a specific measureID doesn't alread
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: variant </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Other Site - sample depreciated { #otsisaDep }
(otsisaDep). Other type of site. Add description to typeOther. Deprecated as of version 2, p
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Other Site - Site depreciated { #otsisiDep }
(otsisiDep). Other site type. Add description to typeOther </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

452

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Other Unit depricated { #otunDep }
(otunDep). Other measurement of viral copies or wastewater treatment plant parameter. Add de
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Outbreak { #outb }
(outb). Measure to indicate outbreak status. Given that when outbreaks occur, full data on c
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: humanCompartmentSet </br>
Group: miscMeas </br>

453

Parts

Class: outbreak </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: outbreakSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Outbreak End { #outbEnd }
(outbEnd). Indicates an outbreak has ended. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Outbreak - on-going { #outbOngoing }
(outbOngoing). Indicates an outbreak is on-going. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Outbreak class { #outbreak }
(outbreak). Measures and methods relating to public health outbreaks. </br>
Part Type: classes </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#outbreak">outbreak</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#unitlessUnitSet">unitlessUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Outbreak set { #outbreakSet }
(outbreakSet). set for the valid values of the outbreak measure.  </br>
*Part Type:* <a href="#mmaSets">mmaSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#outbreakSet">outbreakSet</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
```

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Outbreak start { #outbStart }
(outbStart). Indicates an outbreak began. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

p100l delta-variant gene target { #p100l }
(p100l). p100l delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

Parts

```
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### p2046l delta-variant gene target { #p2046l }
(p2046l). p2046l delta-variant gene target  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#sarsCov2">sarsCov2</a> </br>
*Class:* <a href="#mutation">mutation</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
```

458

Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

p2287s delta-variant gene target { #p2287s }
(p2287s). p2287s delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

p3395h omicron-variant gene target { #p3395h }
(p3395h). p3395h omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>

Parts

Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

p681r delta-variant gene target { #p681r }
(p681r). p681r delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

460

Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Paired Layout { #pairLay }
(pairLay). Specifies the paired layout for a sequencing method </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Pangolin nomenclature { #pangolin }
(pangolin). Specifies variant or genetic nomenclature as set out by the Phylogenetic Assignm
Part Type: nomenclatures </br>

Parts

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Parent dataset ID { #parDatasetID }
(parDatasetID). The datasetID that is a parent to another datasetID.  </br>
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

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

Parent sample ID { #parent }
(parent). If this sample has been pooled into one big sample for analysis this indicates the
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.1.0. Last updated: 2.0.0. </br>

Parent Site ID { #parSiteID }
(parSiteID). The siteID that is a parent to another siteID; usually the sub-site will be con

Parts

```
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Part description { #partDesc }
(partDesc). The description of the part. Provides description of the part, us
*Part Type:* <a href="#partSupport">partSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
```

464

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

Part identifier { #partID }
(partID). The unique identify of any entity within the dictionary. Every entity in the ODM h
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 28 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Part instruction { #partInstr }

(partInstr). Additional notes and instructions on how a part is used and/or (
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 200 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Label { #partLabel }
(partLabel). A human readable label of a part. Typically, a part label has no
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts Look-up table { #parts }
(parts). Look up table containing all parts in of the data model. Contains all parts, includ
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: lookup </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Parts table column order { #partsOrder }
(partsOrder). Order of headers in the Parts table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts table required headers { #partsRequired }
(partsRequired). Required headers in the Parts table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

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

Part types { #partType }
(partType). Part types describe the purpose or use of the part. Enivornment data has three n
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Primary Clarifier Effluent depreciated { #pceDep }
(pceDep). Effluent obtained after primary clarifiers. Deprecated in version
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Postal or Zip Code { #pCode }
(pCode). The zip code or postal code for a given address, specifying a speci
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

470

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

qPCR Class { #pcr }
(pcr). Measures and methods relating to qPCR. </br>
Part Type: classes </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

PCR method { #pcrmeth }
(pcrmeth). Description of the PCR method. Description of the PCR method used
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: measGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: pcrSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

PCR quality set { #pcrQualitySet }
(pcrQualitySet). Quality set for PCR measures. </br>
Part Type: qualityIndSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

472

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

PCR sequencingsSelection method { #pcrSeq }
(pcrSeq). Specifies the PCR selection method for sequencing, ie. that a pre-determined prime
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

PCR Method set { #pcrSet }
(pcrSet). The set capturing containing all of the valid methods for the PCR r
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: pcrSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Primary Clarifier Sludge depreciated { #pcs }
(pcs). Sludge produced by primary clarifiers. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>

474

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Primary clarifier effluent { #pEfflu }
(pEfflu). Effluent obtained after primary clarifiers </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Polyethyleneglycol (PEG) precipitation { #peg }
(peg). Peg precipitation </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Percent { #perc }
(perc). Percentage. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>

```
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#float">float</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 0 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>
```

Percent recovery { #percRec }

```
(percRec). Percent of the surrogate recovery for a recovery efficiency control assay. Use th
*Part Type:* <a href="#units">units</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a> </br>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
```

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

pH { #ph }
(ph). pH measurement </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: miscMeas </br>
Class: pHClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: 1 </br>
Maximum Value: 14 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Access to phac { #phac }
(phac). If this is 'no', the data will not be available to employees of the
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

478

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

PHAGE { #phage }
(phage). PHAGE header </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

479

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

PHAGE - notes { #phageNotes }
(phageNotes). PHAGE notes </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

pH class { #pHClass }
(pHClass). Measures and methods relating to pH. </br>
Part Type: classes </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>

Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: pHClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Phenol chloroform { #phenCl }
(phenCl). Nucleic acid extraction performed using phenol chloroform. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Pseudomonas virus phi6 { #phi6 }
(phi6). Measure of the amount of pseudomonas virus phi6. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

phi6 spike target { #phi6Mat }
(phi6Mat). Pseudomonas virus phi6is used as the recovery efficiency control t
Part Type: categories </br>
Domain: bio </br>

Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Contact phone { #phone }
(phone). Contact phone number, for the lab. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 10 </br>
Maximum Length: 12 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Total phosphorous { #phos }
(phos). Total phosphorous </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Total Phosphates { #phostot }
(phostot). Total phosphates </br>
Part Type: measurements </br>

484

```
*Domain:* <a href="#phy">phy</a> </br>
*Speciment ID:* <a href="/sets.html#siSaSpecimenSet">siSaSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#waterCompartmentSet">waterCompartmentSet</a> </br>
*Group:* <a href="#miscMeas">miscMeas</a> </br>
*Class:* <a href="#standardConc">standardConc</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet </a> </br>
*Minimum Value:* seeUnitVal </br>
*Maximum Value:* seeUnitVal </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 1.1.0. Last updated: 2.0.0. </br>

### PHRED quality score { #phred }
(phred). PHRED Quality Score For Sequencing  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a> </br>
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#sequence">sequence</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Physical property { #phy }
(phy). A physical property or object not characterized by life or chemistry.
Part Type: domains </br>
Domain: phy </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Physical class { #physical }
(physical). Measures and methods related to generic physical properties. </l

486

Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Primary key { #pK }
(pK). Primary key for a table. All report tables have a primary key. Each row in a report ta
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

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

PMMoV- and flow-normalized mean { #pmFloMean }
(pmFloMean). Mean measure normalized to amount of PMMoV and wastewater flow.
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

PMMoV-normalized mean { #pmmovNorm }

488

(pmmovNorm). Mean measure normalized to amount of PMMoV. Mostly used for reporting specific
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population { #po }
(po). An measure or observation for a geographic area or population. Examples include human
Part Type: specimens </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Post-Grit depreciated { #pogr }
(pogr). Raw wastewater after a treatment plant's headworks. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

490

Polygon ID { #polygonID }
(polygonID). Unique identifier for the polygon. A polygon is a geographic are representing t
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Polygon table { #polygons }
(polygons). The table that contains information about the geometry of a geographic area. </
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Polygons table column order { #polygonsOrder }
(polygonsOrder). Specifies the order of the columns in a Polygons table. </l
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

492

Polygon table required headers { #polygonsRequired }
(polygonsRequired). Specifies the columns required in a Polygons table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Polygon Population { #polyPop }
(polyPop). An attribute of a polygon, which specifies the population of that polygon. A roug
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Pooled { #pooled }
(pooled). Is this a pooled sample, and therefore composed of multiple child s
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

494

Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Type of date for case reporting depreciated { #popDateTypeDep }
(popDateTypeDep). Type of date used for confirmed cases. Typically, report or episode are re
Part Type: attributes </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: humanCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: methodConcSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Case reporting date set { #popDateTypeSet }
(popDateTypeSet). set for the date of case reporting. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

Ontology Reference: NA </br>
Category Set ID: popDateTypeSet </
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Population equivalents { #popEq }
(popEq). A unit for measuring of design capacity for wastewater treatment pla
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>

496

Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Population group { #popGrp }
(popGrp). A group of measures/methods related to population-level factors. Examples might be
Part Type: groups </br>
Domain: allDo </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: popGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population Served { #popServ }
(popServ). An attribute of a site, which specifies the population of/population served by a
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population unit set { #populationUnitSet }
(populationUnitSet). Unit set for hospital-related measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#humanCompartmentSet">humanCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: populationUnitSet </br
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population or sample set { #poSaSpecimenSet }
(poSaSpecimenSet). A specimen set that inculdes population or sample specimen. </br>
Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: poSaSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population or site set { #poSiSpecimenSet }
(poSiSpecimenSet). A specimen set that inculdes population or site specimen. </br>
Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: poSiSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>

Parts

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population specimen set { #poSpecimenSet }
(poSpecimenSet). A specimen set that inculdes only a population specimen. </
Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

500

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Percent positive { #pp }
(pp). Percent positive of sample measures. Can use for Moore swabs, etc. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

parts per million { #ppm }
(ppm). Parts per million. </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#quantAggScale">quantAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#float">float</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 0 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>

### PMMoV-CP { #ppmv }
(ppmv). Pepper mild mottle virus capsid protein gene region  </br>
*Part Type:* <a href="#measurements">measurements</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#virusMisc">virusMisc</a> </br>
*Class:* <a href="#allele">allele</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#geneticUnitSet">geneticUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#seeUnitData">seeUnitData</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet 
```

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Percent positivity rate { #pprt }
(pprt). Percent positivity rate of tests conducted within a day in a given region. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Percent primary sludge { #pps }
(pps). Percentage of total solids, for primary sludge. </br>
Part Type: units </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>

503

Parts

Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Precipitation class { #precipation }
(precipation). Measures and methods related to precipitation. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: precipitation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#precipitationUnitSet">precipitationUnitSet</a
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Precipitation unit set { #precipitationUnitSet }
(precipitationUnitSet). Unit set for percipitation measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: precipitationUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Pretreatment { #pretreat }
(pretreat). Was the sample chemically treated in anyway with the addition of stabilizers or
Part Type: methods </br>
Domain: allDo </br>

Parts

```
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#booleanSet">booleanSet</a> </br>
*Unit Set:* <a href="/sets.html#unitlessUnitSet">unitlessUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet 
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 1 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>

### Genetic primer { #primer }
(primer). Method ID used for indicating the primer used for a PCR or sequenc
*Part Type:* <a href="#methods">methods</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#measGrp">measGrp</a> </br>
*Class:* <a href="#sequence">sequence</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#primerSet">primerSet</a> </br>
*Unit Set:* <a href="/sets.html#unitlessUnitSet">unitlessUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
```

Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Genetic primer set { #primerSet }
(primerSet). The set for genetic primers used in sequencing or PCR assays. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: primerSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Private sector { #priv }
(priv). The category of organization type used for private sector or non-profit groups that
Part Type: categories </br>

Parts

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 10 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Processing group { #procGrp }
(procGrp). A group of measures/methods related to processing samples for anal
*Part Type:* <a href="#groups">groups</a> </br>
*Domain:* <a href="#allDo">allDo</a> </br>
*Speciment ID:* <a href="/sets.html#siSaSpecimenSet">siSaSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a>
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

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

Program decription tables { #programDescr }
(programDescr). Tables used to describe surveillance and testing programs. Program descripti
Part Type: classes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

promega automated tna kit { #promAuto }
(promAuto). Nucleic acid extraction performed using the promega automated tna kit. </br>

Parts

Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

promega ht tna kit { #promHt }
(promHt). Nucleic acid extraction performed using the promega ht tna kit. <
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

510

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

promega manual tna kit { #promManu }
(promManu). Nucleic acid extraction performed using the promega manual tna kit. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

promega wastewater large volume tna capture kit { #promWW }

(promWW). Nucleic acid extraction performed using the promega wastewater larg
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Proportion of total { #prop }
(prop). Proportion as a precent of total. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Proportion of variant in sample { #propV }
(propV). Proportion of a variant as percent of total variants. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Parts

Protocol ID { #protocolID }
(protocolID). A unique identifier for a given protocol. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol ID container { #protocolIDContainer }
(protocolIDContainer). Unique identifier for the protocol and the steps and
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

514

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol ID object { #protocolIDObj }
(protocolIDObj). The object of the relationship between one protocol and another protocol or
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol ID subject { #protocolIDSub }
(protocolIDSub). The subject of the relationship between one protocol and and
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol relationships table { #protocolRelationships }
(protocolRelationships). The table that contains the organizational informati
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

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

Protocol relationships table column order { #protocolRelationshipsOrder }
(protocolRelationshipsOrder). Specifies the order of the columns in the Protocol Organizatio
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol Relationship table required headers { #protocolRelationshipsRequired
(protocolRelationshipsRequired). Specifies the columns required in the Protoc
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol Relationships set { #protocolRelSet }
(protocolRelSet). set for valid values of relationshipID in the protocolRelat
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

518

Ontology Reference: NA </br>
Category Set ID: protocolRelSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocols table { #protocols }
(protocols). The table for protocols. </br>
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocols table column order { #protocolsOrder }
(protocolsOrder). Specifies the order of the columns in the Protocols table.
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocols table required headers { #protocolsRequired }
(protocolsRequired). Specifies the columns required in the Protocols table.
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>

520

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

Protocol steps table { #protocolSteps }
(protocolSteps). The table for collecting metadata on individual steps in a protocol, method
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: programDescr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

```
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>
```

Protocol steps table column order { #protocolStepsOrder }
```
(protocolStepsOrder). Specifies the order of the columns in a Protocol Steps
*Part Type:* <a href="#tableSupport">tableSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 1 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>
```

Protocol steps table required headers { #protocolStepsRequired }
```
(protocolStepsRequired). Specifies the columns required in a Protocol Steps
*Part Type:* <a href="#tableSupport">tableSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
```

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

Protocol table set { #protocolTableSet }
(protocolTableSet). Tables holding information on the methods used for sample collection or
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol version { #protocolVersion }
(protocolVersion). Specifies the version of a method set. Version of the met}
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Access to prov ha { #provHA }
(provHA). If this is 'no', this data will not be available to provincial heal
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

524

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Provisional report { #provisional }
(provisional). A provisional or interm report. Use for measurement that are not yet finalize
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Primary clarifier sludge { #pSludge }
(pSludge). Sludge produced by primary clarifiers </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Pumping station { #pStat }
(pStat). Pumping station </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Post-grit { #pstGrit }
(pstGrit). Raw wastewater after a treatment plant's headworks (post grit or removal of large
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Pretreatment description - depreciated { #ptDescDep }
(ptDescDep). If preTreatment then describe the treatment that was performed.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 255 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Number of positive tests { #ptot }
(ptot). Number of positive tests conducted within a day in a given region.
Part Type: units </br>
Domain: bio </br>

Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Public healith agency { #pubHealth }
(pubHealth). Public health agency. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Access to public { #public }
(public). If this is 'no', this data will not be available to the public. If
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Puro virus { #puro }
(puro). Measure of the amount of puro virus. </br>
Part Type: measurements </br>

530

Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Puro virus spike target { #puroMat }
(puroMat). Puro Virus is used as the recovery efficiency control target. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

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

Purpose { #purpose }
(purpose). The reason the measure or sample was taken. See allowed categories
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: purposeSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Purpose set { #purposeSet }
(purposeSet). Purpose set for a sample or measure. </br>

Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: purposeSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

q19e omicron-variant gene target { #q19e }
(q19e). q19e omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

q493r omicron-variant gene target { #q493r }
(q493r). q493r omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

q498r omicron-variant gene target { #q498r }

(q498r). q498r omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

q954h omicron-variant gene target { #q954h }
(q954h). q954h omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>

Parts

Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quaility assurance method { #qaqc }
(qaqc). Quality assurance and quality control method. Description of the qua
Part Type: methods </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

Quality concerns { #qf1 }
(qf1). A flag to indicate there is a quality concern, not otherwise sepcified. </br>
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 0 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

qiagen allprep dna/rna kit { #qgDNARNA }
(qgDNARNA). Nucleic acid extraction performed using the qiagen allprep dna/rna kit. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

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

qiagen digital PCR { #qgDpcr }
(qgDpcr). Describes a PCR analysis done using Qiagen's digital PCR technology
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

qiagen ez1 virus mini kit v2.0 { #qgEz1 }
(qgEz1). Nucleic acid extraction performed using the qiagen ez1 virus mini kit v2.0. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

qiagen allprep powerfecal dna/rna kit { #qgPwrFecal }
(qgPwrFecal). Nucleic acid extraction performed using the qiagen allprep powerfecal dna/rna
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### qiagen allprep powerviral dna/rna kit { #qgPwrViral }
(qgPwrViral). Nucleic acid extraction performed using the qiagen allprep powe
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

qiagen powerwater kit { #qgPwrWtr }
(qgPwrWtr). Nucleic acid extraction performed using the qiagen powerwater kit. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

qiagen qiaamp buffers with epoch columns { #qgQiAmp }
(qgQiAmp). Nucleic acid extraction performed using the qiagen qiaamp buffers with epoch colu
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### qiagen rneasy kit { #qgRneasy }
(qgRneasy). Nucleic acid extraction performed using the qiagen rneasy kit.
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
```

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

qiagen rneasy powermicrobiome kit { #qgRneasyPwr }
(qgRneasyPwr). Nucleic acid extraction performed using the qiagen rneasy powermicrobiome kit
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quantitative PCR { #qpcr }
(qpcr). Real-time PCR, also called 'quantAggScale' PCR </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

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

Qualitative { #qualAggScale }
(qualAggScale). The qualitative aggregation scale. </br>
Part Type: aggregationScales </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: qualAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality control { #qualityControl }
(qualityControl). A measure or sample taken for the purpose of quality control. Measures wit
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality flag { #qualityFlag }
(qualityFlag). A field for reporting any quality concerns - of lack thereof - for a sample c
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>

Parts

```
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Quality report ID { #qualityID }
(qualityID). A unique identifier for a given quality report.  </br>
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
```

546

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality indicators { #qualityIndicators }
(qualityIndicators). A measure of the quality of a reported value or sample. Only used for t
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality indicator sets { #qualityIndSets }
(qualityIndSets). Sets of quality indicators or measures. For example, PCR have a quality me
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 15 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Quality reports table { #qualityReports }
(qualityReports). The table for recording the various quality metrics and inc
*Part Type:* <a href="#tables">tables</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#results">results</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
```

548

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality rerpots table column order { #qualityReportsOrder }
(qualityReportsOrder). Specifies the order of the columns in the Quality Reports table. </b
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality report table required headers { #qualityReportsRequired }
(qualityReportsRequired). Specifies the columns required in the Quality Reports table. </br
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Parts

Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quality set { #qualitySetID }
(qualitySetID). The quality set that corresponds to a given part. Only appli
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Quantitative { #quantAggScale }
(quantAggScale). The "quantAggScale" aggregation scale. </br>
Part Type: aggregationScales </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

R squared { #r2 }
(r2). R-squared value of the calibration curve. Used for storing calibration curve informati
Part Type: measurements </br>
Domain: allDo </br>

Parts

Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

r203m delta-variant gene target { #r203m }
(r203m). r203m delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Raindance digital PCR { #rainDpcr }
(rainDpcr). Describes a PCR analysis done using Raindance's digital PCR technology. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Rainy { #rainy }
(rainy). Qualitative category for the weather measure, specifying a rainy day. </br>
Part Type: categories </br>

Parts

```
*Domain:* <a href="#phy">phy</a> </br>
*Speciment ID:* <a href="/sets.html#siSpecimenSet">siSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#siteFeat">siteFeat</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Random sequencing selection method { #ranSeq }
(ranSeq). Specifies the random selection method for sequencing No primer set
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

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

Ratio { #ratio }
(ratio). Ratio (unitless) Report as a real number or fration. i.e 10:2 ratio is reported as
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Raw wastewater { #raws }
(raws). Raw wastes water sample </br>

Parts

Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Raw sewage at site { #rawWW }
(rawWW). Wastewater without any form of treatment </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

556

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Raw sewage downstream from a site { #rawWWdown }
(rawWWdown). Downstream from a site. See partType = rawWWup. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Raw sewage upstream from a site { #rawWWup }

(rawWWup). Upstream from a site. Used when there is not direct access to a si
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

IP2 rdrp sars-cov-2 gene target { #rdrpIP2 }
(rdrpIP2). IP2 rdrp sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>

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

IP4 rdrp sars-cov-2 gene target { #rdrpIP4 }
(rdrpIP4). IP4 rdrp sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Date sample recieved { #recDate }
(recDate). The date the sample was received at the laboratory for analysis.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Recovered patients { #recov }
(recov). Units for describing a population measure of patients who have recov
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Reference link { #refLink }
(refLink). Link to the reference material for a part. May link to literature on a method, me
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 255 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Regular { #regular }
(regular). A measure or sample taken for surveillance or epidemiology. A 'reg
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Regular reports table set { #regularReportTableSet }
(regularReportTableSet). Tables used for daily reporting of new measurements
Part Type: dictSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Relative humidity { #relHum }
(relHum). The unit of relative humidity, or the air-water mixture. The ratio of the partial
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>
Class: humid </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: relHumidUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Relative humidity unit set { #relHumidUnitSet }
(relHumidUnitSet). Unit set for relative humidity measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: relHumidUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Representative grab sample { #repGrab }
(repGrab). A single large representative grab sample. Deprecated in version 2
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Replicate Type set { #replicateSet }
(replicateSet). The set for storing valid categorical values of replicate type. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: replicateSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

replicate number { #repNum }
(repNum). The replicate number for a Ct or Cq value - used for specifying out
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Primary reporting authority { #repOrg1 }
(repOrg1). The primary or most responsible authority for routine surveillan
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>

566

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Secondary reporting authority { #repOrg2 }
(repOrg2). The secondary, additional or alternative authority for rountine surveillance repo
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Reportable { #reportable }
(reportable). Flag for whether a measure is reportable or not, based on confi
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Report date { #reportDate }
(reportDate). The date a measure was reported. This date is the first date t
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>

568

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Reporter ID depreciated { #reporterIDDep }
(reporterIDDep). Unique identifier for the person or organization that is reporting the data
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>

569

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.1.0. Last updated: 2.0.0. ~

Reporter table depreciated { #reportersDep }
(reportersDep). The table that contains information about a reporter of a san
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. ~

Replicate Type { #repType }
(repType). Attirbute of a sample, specifying whether the sample is unique, or
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

570

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: replicateSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Resuspend COSCa filter collection { #resCosca }
(resCosca). Nucleic acid extraction via resuspension of a sample collected using the COSCa b
Part Type: categories </br>
Domain: bio </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Parts

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 10 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Results tables { #results }
(results). Tables used to record samples, measures and quality reports. These
Part Type: classes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: results </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Retention pond { #retPond }
(retPond). Retention pond </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

572

Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

River, natural water body { #river }
(river). River, natural water body </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Role of contact { #role }
(role). Specifies the organizational role of a given contact.   </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Rate per 100,000 { #rP100 }
(rP100). Units for describing a population measure of a rate of case incidenc
Part Type: units </br>
Domain: bio </br>

574

Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Raw post-pasteurized wastewater { #rppw }
(rppw). Raw wastewater sample post-pasteurization </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Respiratory syncytial virus { #rsv }
(rsv). Respiratory syncytial virus. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: virusMisc </br>
Class: allele </br>
Nomenclature: naNomenclature </br>
Ontology Reference: <a href="#http://purl.obolibrary.org/obo/NCIT_C14267">
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

s2083i omicron-variant gene target { #s2083i }
(s2083i). s2083i omicron-variant gene target </br>
Part Type: measurements </br>

576

Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

s371l omicron-variant gene target { #s371l }
(s371l). s371l omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>

Parts

Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

s373p omicron-variant gene target { #s373p }
(s373p). s373p omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

s375f omicron-variant gene target { #s375f }
(s375f). s375f omicron-variant gene target </br>

578

Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

s477n omicron-variant gene target { #s477n }
(s477n). s477n omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample { #sa }
(sa). A measure made on a compartment or property from a sample of a substanc
Part Type: specimens </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample material { #saMaterial }

580

(saMaterial). Type of sample. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: sampleMatSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sample ID { #sampleID }
(sampleID). Unique identifier for a sample. Suggestion:siteID-date-index. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Sample ID object { #sampleIDObject }
(sampleIDObject). Populated by \`sampleID\` - this specifies the object of a
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

582

Sample ID subject { #sampleIDSubject }
(sampleIDSubject). Populated by \`sampleID\` - this specifies the subject of a sample relati
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample material set { #sampleMatSet }
(sampleMatSet). set for the types of material that can be found in a sample. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: sampleMatSet </br>

Parts

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample quality set { #sampleQualitySet }
(sampleQualitySet). Quality set for a sample. </br>
Part Type: qualityIndSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

584

Sample relationships table { #sampleRelationships }
(sampleRelationships). Table for recording the relationships between samples. Samples can be
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: results </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample relationships table column order { #sampleRelationshipsOrder }
(sampleRelationshipsOrder). Specifies the order of the columns in a Sample Relationships tab
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#integer">integer</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* 1 </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Sample relationships table required headers { #sampleRelationshipsRequire
(sampleRelationshipsRequired). Specifies the columns required in a Sample Rel
*Part Type:* <a href="#tableSupport">tableSupport</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

586

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample relationship { #sampleRelID }
(sampleRelID). Attribute for specifying the relationship between a sample subject and object
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: <a href="/sets.html#sampleRelSet, protocolRelSet">sampleRelSet, protocolR
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample relationships set { #sampleRelSet }
(sampleRelSet). set for valid values of relationshipID in the sampleRelationships table. Use
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

Ontology Reference: NA </br>
Category Set ID: sampleRelSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample report table { #samples }
(samples). The table that contains information about a sample. A sample is de
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: results </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

588

Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sample shed { #sampleShed }
(sampleShed). A geographic area, physical space, or structure. A sample is taken from a samp
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: shedSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Samples table column order { #samplesOrder }
(samplesOrder). Specifies the order of the columns in a Samples table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

589

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample table required headers { #samplesRequired }
(samplesRequired). Specifies the columns required in a Samples table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

590

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Collection other depreciated { #sampleTypeOther }
(sampleTypeOther). Description for other type of method not listed in collection. depreciate
Part Type: methods </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

SARS-CoV-2 { #sarsCov2 }
(sarsCov2). A group of measures/methods related to the SARS-CoV-2 virus. SARS-CoV-2 measures
Part Type: groups </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>

Parts

```
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#http://purl.obolibrary.org/obo/NCIT_C169076">
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Sample specimen set { #saSpecimenSet }
(saSpecimenSet). A specimen set that inculdes only a sample specimen.  </br>
*Part Type:* <a href="#specimenSets">specimenSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
```

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sparse coverage { #sC }
(sC). Sequencing shows sparse coverage, ie. numerical breadth of coverage shows as adequate
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Secondary clarifier effluent depreciated { #sce }
(sce). Effluent obtained after secondary clarifiers. Deprecated in version 2, please do not
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>

Parts

Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Standard curve frequency { #scf }
(scf). A method for specifying the frequecy over which a standard curve (or
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: timeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

School { #school }
(school). A school serving students in the kindergarten to 12th grade range </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sequencing script version set { #scriptSet }
(scriptSet). The set for script versions </br>
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

Parts

Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: scriptSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Genetic sequencing script version { #scriptVersion }
(scriptVersion). Used to specify the script or script version used to extract
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: sequence </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: scriptSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>

596

Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Secondary clarifier sludge depreciated { #scsDep }
(scsDep). Sludge produced by secondary clarifiers. Deprecated in version 2, please do not us
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Standard deviation { #sd }
(sd). Standard deviation. </br>
Part Type: aggregations </br>
Domain: naDomain </br>

Parts

Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Normalized standard deviation { #sdn }
(sdn). Standard deviation, normalized. </br>
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sea, natural water body { #sea }
(sea). Sea, natural water body </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

See unit (aggregation scales) { #seeUnitAggScale }
(seeUnitAggScale). A value for aggregation scale to be used when the aggregation scale deper
Part Type: aggregationScales </br>

Parts

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### See unit (data type) { #seeUnitData }
(seeUnitData). The data type entry when the data type for a given entry is sp
*Part Type:* <a href="#dataTypes">dataTypes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

600

Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

See unit (value) { #seeUnitVal }
(seeUnitVal). A value for maximum or minimum value in the dictionary, use when the maximum o
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Secondary clarifier effluent { #sEfflu }
(sEfflu). Effluent obtained after secondary clarifiers </br>

Parts

Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Access to self { #self }
(self). If this is 'no', this data will not be shown on the portal when this
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Date sample was sent { #sentDate }
(sentDate). The date the sample was sent for analyses at a laboratory. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: datetime </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Septic tank wastewater { #septage }

(septage). Wastewater from within a septic tank </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Septic tank { #septTnk }
(septTnk). Septic tank </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sequencing Layout { #seqLay }
(seqLay). The layout of genetic material used in sequencing. </br>
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: sequence </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: seqLaySet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Sequencing Layout set { #seqLaySet }
(seqLaySet). The set for the layout of genetic material used in sequencing
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: seqLaySet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sequencing quality set { #seqQualitySet }
(seqQualitySet). Quality set for sequencing measures </br>
Part Type: qualityIndSets </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sequencing selection method { #seqSel }
(seqSel). The primer sequence selection method used in sequencing. </br>
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: sequence </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: seqSelSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sequencing selection method set { #seqSelSet }
(seqSelSet). The set for the selection method used in sequencing </br>
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: seqSelSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sequencing Strategy { #seqStrat }
(seqStrat). The sequencing strategy used for an analysis. </br>
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</br>
Group: procGrp </br>
Class: sequence </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: seqStratSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sequencing Strategy set { #seqStratSet }
(seqStratSet). The set for the sequencing strategy used for an analysis </br>
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: seqStratSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Genetic sequences class { #sequence }
(sequence). Measures and methods related to genetic sequencing. </br>
Part Type: classes </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: sequence </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Serial dilution { #serialDilution }
(serialDilution). The serial dilution method for assessing inhibition. </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: procGrp </br>
Class: dilution </br>
Nomenclature: naNomenclature </br>

610

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

Sewer Sediments Depcreciated { #seseDep }
(seseDep). Sediments obtained in sewer. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. ↵

Set ID { #setID }
(setID). The unique identifier of a value set. A set is a group of units, att
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet ↵
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 28 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sets look-up table { #sets }
(sets). Look up table for all sets, managing how categorical inputs for vario
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: lookup </br>

612

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

Sets table column order { #setsOrder }
(setsOrder). Specifies the order of the columns in the Sets table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>

Parts

Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sets table required headers { #setsRequired }
(setsRequired). Required headers in the Sets table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Settled solids { #settsol }
(settsol). Amount of settled solids from a wastewater sample. May be a volume
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>

Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Set type { #setType }
(setType). The type of set. i.e. quality set, aggregation set, unit set </br>
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Parts

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Set Value { #setValue }
(setValue). The partID for the set value or category. Populated by any part u
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Severity indicator { #severity }
(severity). An indicator of the severity or seriousness of a quality flag.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

616

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

Severity set { #sevSet }
(sevSet). A set for severity indicators. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: sevSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Parts

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sewer network file link depreciated { #sewerNetworkFileBLOB }
(sewerNetworkFileBLOB). Link to a file that has any detailed information abou
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

S sars-cov-2 gene target { #sGene }
(sGene). S sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

618

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

Sampleshed set { #shedSet }
(shedSet). The set for all valid values of sampleshed. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Ship { #ship }
(ship). A cruise ship or other ship. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Shipped on ice { #shipOnIce }
(shipOnIce). Was the sample kept cool while being shipped to the lab </br>
Part Type: methods </br>
Domain: allDo </br>

Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: booleanSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Short names { #shortName }
(shortName). Shortened names for tables and other important parts for use in wide names. </
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

Parts

Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Site { #si }
(si). A measure made on a compartment or property at a site. An example is tl
Part Type: specimens </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Single { #sin }
(sin). A value that is not an aggregate measurement (ie. not a mean, median,
Part Type: aggregations </br>

622

Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Single Layout { #sinLay }
(sinLay). Specifies the single layout for a sequencing method </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

Parts

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

Site or sample specimen set { #siSaSpecimenSet }
(siSaSpecimenSet). A specimen set that inculdes site or sample specimen. </b
Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Site specimen set { #siSpecimenSet }
(siSpecimenSet). A specimen set that inculdes only a site specimen. </br>

624

Part Type: specimenSets </br>
Domain: naDomain </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Site ID default { #siteDef }
(siteDef). Used as default when a new sample is created by this reporter. See ID in Site tab
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Site features group { #siteFeat }
(siteFeat). A group of environmental measures/methods and those pertaining to
Part Type: groups </br>
Domain: allDo </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: siteFeat </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Site ID { #siteID }

626

(siteID). Unique identifier for the location where a sample was taken. </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Site measure ID { #siteMeasureID }
(siteMeasureID). Unique identifier for wide table only. Use when all measures are performed
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

Parts

```
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0. <

### Sites table { #sites }
(sites). The table that contains information about a site; the location where
*Part Type:* <a href="#tables">tables</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#programDescr">programDescr</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>
```

628

Sites table column order { #sitesOrder }
(sitesOrder). Specifies the order of the columns in a Sites table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sites table required headers { #sitesRequired }
(sitesRequired). Specifies the columns required in a Sites table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

```
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Site Type { #siteType }
(siteType). Type of site or institution where sample was taken.  </br>
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#colGrp">colGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/sets.html#siteTypeSet">siteTypeSet</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 1.0.0. Last updated: 2.0.0. </br>
```

630

Site set { #siteTypeSet }
(siteTypeSet). set for the type of sampling site. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: siteTypeSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Skimmed milk flocculation { #skimMilkFloc }
(skimMilkFloc). Skimmed milk flocculation </br>
Part Type: categories </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

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

slope { #slope }
(slope). Slope value of the calibration curve. Used for storing calibration
Part Type: measurements </br>
Domain: allDo </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

632

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sewer network file link depreciated 2 { #snfl }
(snfl). Link to a file that has any detailed information about the sewer network associated
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Snowy { #snowy }
(snowy). Qualitative category for the weather measure, specifying a snowy day. </br>
Part Type: categories </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

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

Solid fraction { #sol }
(sol). Solid fraction of a sample. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Solid seperation { #solidSep }
(solidSep). Process used to separate solid and liquid phases of the sample. Solid seperation
Part Type: methods </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: solidSeparationSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Solid separation set { #solidSeparationSet }
(solidSeparationSet). set for the separation of solids. </br>
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: <a href="/sets.html#solidSeparationSet">solidSeparationSet
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Source Protocol ID { #sourceProtocol }
(sourceProtocol). A protocol that served as a basis for another protocol. Thi
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>

636

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol step source ID { #sourceStep }
(sourceStep). Specifies the protocol step which serves as a basis for a given protocol step.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Specific humidity { #specHum }
(specHum). Measure for specific humidity, the unit is the ratio of the mass of water vapour
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>

Parts

Class: humid </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: specHumidUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Specific humidity unit set { #specHumidUnitSet }
(specHumidUnitSet). Unit set for specific humidity. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: specHumidUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

638

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Specifies { #specifies }
(specifies). Specifies that the object step or protocol occurs specifies details for the sub
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Specimen { #specimen }
(specimen). The substance or thing upon which the observation was made. Specimens include: s
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>

Parts

```
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet <
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 12 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Specimens { #specimens }
(specimens). Measures or observations are taken from three types of substance
*Part Type:* <a href="#partType">partType</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#categorical">categorical</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
```

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Specimen sets { #specimenSets }
(specimenSets). Sets of specimens. Specimen sets are used when a measure or attribute can be
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Speed class { #speed }
(speed). Measures and methods relating to speed. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>

Parts

Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: speed </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: windSpeedUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Spike matrix and recovery { #spike }
(spike). The spike matrix and recovery method for assessing inhibition. </br
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: procGrp </br>
Class: pcr </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Spike material { #spikeMat }
(spikeMat). Material into which the recovery efficiency control target is spiked. </br>
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: spikeMatSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 4 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Spike material set { #spikeMatSet }
(spikeMatSet). set for spikeMat (aterial into which the recovery efficiency control target i
Part Type: mmaSets </br>
Domain: naDomain </br>

Parts

Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: spikeMatSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Recovery efficiency spike target { #spikeTarget }
(spikeTarget). Method specifying the recovery efficiency control target. This
Part Type: methods </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: spikeTargetSet </l
Unit Set: unitlessUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>

644

Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Recovery efficiency spike target set { #spikeTargetSet }
(spikeTargetSet). The set capturing containing all of the valid categories for the recovery
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: spikeTargetSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample spilled { #spill }
(spill). Sample contents spilled from container. </br>
Part Type: qualityIndicators </br>

Parts

Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Secondary clarifier sludge { #sSludge }
(sSludge). Sludge produced by secondary clarifiers </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>

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

Social services shelter { #sss }
(sss). Other type of social services shelter </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Stabilization pond { #stabPnd }
(stabPnd). Specifies a site type which is a pond designed and built for wastewater treatment

Parts

Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Standard concentrations class { #standardConc }
(standardConc). Measures and methods relating to standard conentrations. </l
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>

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

Standard curve class { #standardCurve }
(standardCurve). Measures and methods relating to generating or recording a standard curve.
Part Type: classes </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: standardCurve </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Departments, states, or provinces { #stateProvLevel }

Parts

(stateProvLevel). Departments, states, or provinces </br>
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: ISCU </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#nrNAMissingnessSet">nrNAMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

State, Province, or Region { #stateProvReg }
(stateProvReg). The state, province, or region where a site or organization
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>

650

Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Status { #status }
(status). Whether the part is still active and can be used in the most current ODM version.
Part Type: partSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: statusSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Parts

Status set { #statusSet }
(statusSet). A set for partID = Status to indicate whether a part is in curre
Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Standard concentration unit set { #stdConcentrationUnitSet }
(stdConcentrationUnitSet). Unit set for concentration measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Storage temp { #sTemp }
(sTemp). Temperature that the sample is stored at in Celsius. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: temperature </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Protocol Step ID { #stepID }
(stepID). The unique identifier for a specific protocol step. Protocol Steps
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Step ID Object { #stepIDObj }
(stepIDObj). The object of the relationship between one protocol step and and
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Step ID Subject { #stepIDSub }
(stepIDSub). The subject of the relationship between one protocol step and another step or p
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>

Parts

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Method step parent ID { #stepProvenanceID }
(stepProvenanceID). A method step that served as a basis for another method s
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Protocol step version { #stepVer }
(stepVer). Specifies the version of a given protocol step. Version of the met
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

656

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 50 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sewer network file blob { #storTempDef }
(storTempDef). A file blob that has any detailed information about the sewer network associa
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: blob </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Parts

Maximum Length: 65535 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Storage time { #stoTim }
(stoTim). Length of time that a sample was in storage. </br>
Part Type: measurements </br>
Domain: allDo </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: procGrp </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: timeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sub-variant or lineage { #subVar }
(subVar). A unit used to report a specific genetic lineage, or to specify tha
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: virusMisc </br>
Class: variant </br>

658

Nomenclature: pangolin </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Summary { #summ }
(summ). Short description of the assay and how it is different from the other assay methods.
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 255 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Summary worksheet { #summary }
(summary). Summary sheet of the dictionary.xlxs file. The summary sheet conta
Part Type: dictionarySupport </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sunny { #sunny }
(sunny). Qualitative category for the weather measure, specifying a clear an
Part Type: categories </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: siteFeat </br>

660

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

Surface compartment { #surf }
(surf). A measure or observation made from a substance on a surface. </br>
Part Type: compartments </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: surfaceCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Other surface { #surface }
(surface). Surface other than floor or desk. See also categories for floor ar
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#surfaceCompartmentSet">surfaceCompartm
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Surface compartment set { #surfaceCompartmentSet }
(surfaceCompartmentSet). A compartment set for measures and methods in the su
Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#surfaceCompartmentSet">surfaceCompartm

662

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Surface and water compartment set { #surfaceWaterCompartmentSet }
(surfaceWaterCompartmentSet). A compartment set for measures and methods in the surface or w
Part Type: compartmentSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: <a href="/sets.html#surfaceWaterCompartmentSet">surfaceWaterCompartmentSe
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Surface swab { #surfSw }
(surfSw). Surface swab. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#surfaceCompartmentSet">surfaceCompartm
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sewage truck { #swgTrck }
(swgTrck). Sewage truck </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sewer sediment { #swrSed }
(swrSed). Sediments obtained in sewer </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Parts

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Sewer catchment area { #swrSet }
(swrSet). Sewer catchment area. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Synthetic sample { #synthetic }
(synthetic). Specifies a synthetic, or artificially derrived sample. </br>
Part Type: categories </br>
Domain: naDomain </br>

666

Speciment ID: `<a href="/sets.html#naSpecimenSet">naSpecimenSet</a>` </br>
Compartment Set: `<a href="/sets.html#naCompartmentSet">naCompartmentSet</a>` </br>
Group: `<a href="#naGroup">naGroup</a>` </br>
Class: `<a href="#naClass">naClass</a>` </br>
Nomenclature: `<a href="#naNomenclature">naNomenclature</a>` </br>
Ontology Reference: `<a href="#NA">NA</a>` </br>
Category Set ID: `<a href="/parts.html#NA">NA</a>` </br>
Unit Set: `<a href="/sets.html#naUnitSet">naUnitSet</a>` </br>
Aggregation Scale: `<a href="#NA">NA</a>` </br>
Quality Set: `<a href="/parts.html#NA">NA</a>` </br>
Reference Link: NA </br>
Data Type: `<a href="#varchar">varchar</a>` </br>
Missingness Set: `<a href="/parts.html#NA">NA </a>` </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

t19r delta-variant gene target { #t19r }
(t19r). t19r delta-variant gene target </br>
Part Type: `<a href="#measurements">measurements</a>` </br>
Domain: `<a href="#bio">bio</a>` </br>
Speciment ID: `<a href="/sets.html#saSpecimenSet">saSpecimenSet</a>` </br>
Compartment Set: `<a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a>` </br>
Group: `<a href="#sarsCov2">sarsCov2</a>` </br>
Class: `<a href="#mutation">mutation</a>` </br>
Nomenclature: `<a href="#naNomenclature">naNomenclature</a>` </br>
Ontology Reference: `<a href="#NA">NA</a>` </br>
Category Set ID: `<a href="/parts.html#NA">NA</a>` </br>
Unit Set: `<a href="/sets.html#geneticUnitSet">geneticUnitSet</a>` </br>
Aggregation Scale: `<a href="#seeUnitAggScale">seeUnitAggScale</a>` </br>
Quality Set: `<a href="/parts.html#NA">NA</a>` </br>
Reference Link: NA </br>

Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

t3646a delta-variant gene target { #t3646a }
(t3646a). t3646a delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

t547k omicron-variant gene target { #t547k }
(t547k). t547k omicron-variant gene target </br>
Part Type: measurements </br>

Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

t9i omicron-variant gene target { #t9i }
(t9i). t9i omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>

Parts

Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Tables { #tables }
(tables). Tables are where measures, methods and attributes are recorded. Tal
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Table column set { #tableSet }
(tableSet). The set for valid inputs in table columns. These categories are u

670

Part Type: mmaSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: tableSet </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

TaqPath N sars-cov-2 gene target { #taqpatN }
(taqpatN). TaqPath N sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

TaqPath S sars-cov-2 gene target { #taqpatS }
(taqpatS). TaqPath N sars-cov-2 gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample temperature { #temp }

(temp). Temperature of the sample measured in degrees Celcius </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: miscMeas </br>
Class: temperature </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Temperature class { #temperature }
(temperature). Measures and methods related to temperatures. </br>
Part Type: classes </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: temperature </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </br>

Parts

Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Temperature unit set { #temperatureUnitSet }
(temperatureUnitSet). Unit set for temperature measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</a
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

674

Nucleic acid template volume { #tempVol }
(tempVol). The volume of DNA or RNA template used for PCR. </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Airport terminal { #terminal }
(terminal). Airport terminal sample shed category type </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

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

Test date { #tesDate }
(tesDate). Date that the covid-19 test was performed. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

676

Number of tests performed { #test }
(test). Number of tests performed. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Testing { #testing }
(testing). A measure or sample taken to test a new method. These measures are typically used
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### thermo magmax microbiome ultra nucleic acid isolation kit { #thermMag }
(thermMag). Nucleic acid extraction performed using the thermo magmax microbi:
*Part Type:* <a href="#categories">categories</a> </br>
*Domain:* <a href="#bio">bio</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
*Group:* <a href="#procGrp">procGrp</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Time class { #time }
(time). Measures and methods relating to time. </br>
Part Type: classes </br>
Domain: allDo </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: timeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Time proportional sample { #timePr }
(timePr). A time proportionalcomposite sample generally collected by an autosampler. Use col
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

Parts

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Time unit set { #timeUnitSet }
(timeUnitSet). The unit set for measures of time. </br>
Part Type: unitSets </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: miscMeas </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: timeUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

680

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Total Kjeldahl Nitrogen { #tkn }
(tkn). A measure of Total Kjeldahl Nitrogen; ie. the sum of nitrogen bound in organic substa
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Total Nitrogen { #tn }
(tn). Total nitrogen concentration, as N. </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: standardConc </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Time Proportional 24hr sample { #tp24s }
(tp24s). A time proportional 24-hour composite sample generally collected by
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

682

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Translation look-up table { #translations }
(translations). Look up table for translations of the description, label, and instruction fc
Part Type: tables </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: lookup </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Translation table column order { #translationsOrder }
(translationsOrder). Specifies the order of the columns in the Translation table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>

Parts

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 1 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Translation table required headers { #translationsRequired }
(translationsRequired). Required headers in the Translations table. </br>
Part Type: tableSupport </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

trizol, zymo mag beads w/ zymo clean and concentrator { #trizol }
(trizol). Nucleic acid extraction performed using the trizol, zymo mag beads w/ zymo clean a
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

TRUE { #true }
(true). Boolean data type = TRUE Use only "TRUE" (case sensitive) </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>

Parts

Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: boolean </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 4 </br>
Maximum Length: 4 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Total solids concentration { #ts }
(ts). Total solids concentration </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <

Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Total suspended solids { #tss }
(tss). Total suspended solids </br>
Part Type: measurements </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Concentration of total suspended solids { #tssConc }
(tssConc). Total suspended solids concentration of the wastewater. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>

Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUni
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Tubidity { #turb }
(turb). A measure for the turbidity of water, or a liquid sample, quanitfying
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: turbidity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: turbidityUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>

Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Turburdity class { #turbidity }
(turbidity). Measures and methods relating to water and wastewater turbidity. </br>
Part Type: classes </br>
Domain: che </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: turbidity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: turbidityUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Turbidity unit set { #turbidityUnitSet }
(turbidityUnitSet). Unit set for turbidity measurements. </br>
Part Type: unitSets </br>
Domain: naDomain </br>

Parts

Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: turbidityUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Tube weight empty { #tWeighE }
(tWeighE). The weight of the tube used for analysis while empty. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: procGrp </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

690

Data Type: integer </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Tube weight full { #tWeighF }
(tWeighF). The weight of the tube used for analysis while full of analyte. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: procGrp </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Type other depreciate { #tyOtDep }
(tyOtDep). Description for other type of sample not listed in </br>
Part Type: methods </br>

Parts

```
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 100 </br>
*Part Status:* **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

### Type other depreciate2 { #tyOtDep2 }
(tyOtDep2). Description of the site when the site is not listed. See siteType
*Part Type:* <a href="#attributes">attributes</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
```

Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 100 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

University campus { #uCampus }
(uCampus). Universityor college campus - comprising an entire campus or part of a campus. Se
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Undisclosed { #undisc }
(undisc). A value has been recorded, however it was not included in the dataset. Missing val

Parts

Part Type: missingness </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Unique sample { #unique }
(unique). A unique sample, not duplicated. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>

694

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

Unit { #unit }
(unit). The units of a measurement. Different units that are used to describe measurement va
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Unitless measure { #unitless }

(unitless). A unit for unitless measures, like pH. </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Unitless unit set { #unitlessUnitSet }
(unitlessUnitSet). Unit set for measurements that does not have units. </br>
Part Type: unitSets </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: unitlessUnitSet </br>

Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Units { #units }
(units). The unit of the measurement. Every measurement must have a unit. Meaning, \`units\`
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Parts

Unit set { #unitSet }
(unitSet). An idenfication of a set of units that can be used for a measure
Part Type: attributes </br>
Domain: che </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: procGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Unit sets { #unitSets }
(unitSets). Sets of units. Contains units that are associated with part types
Part Type: partType </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Ultracentrifugation { #untracent }
(untracent). Ultracentrifugation Should typically be linked to a lower limit, and some indic
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Upper limit of a 95% confidence interval { #upperCI95 }
(upperCI95). Specifies the the upper limit of a 95% confidence interval. A ca
Part Type: aggregations </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Upstream sites { #upstream }
(upstream). A general site type for upstream wastewater sampling sites. </br
Part Type: categories </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.1.0. Last updated: 2.0.0. </br>

Micro-Siemens per centimetre { #uSCm }
(uSCm). Micro-siemens per centimetre. Deprecated in version 2, please do not use. MeasureID
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 12 </br>

Parts

Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. ·

U site measure ID { #uSiteMeasureID }
(uSiteMeasureID). Unique identifier for each measurement for a site. </br>
Part Type: attributes </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet ·
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

v2930l delta-variant gene target { #v2930l }
(v2930l). v2930l delta-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>

702

Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Validation study { #validationStudy }
(validationStudy). A meaure or sample taken for a validation study. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Value { #value }
(value). Value of a measure, observation or attribute. Only used for the dict
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Variable character data type { #varchar }
(varchar). The data type for variable character data. Measured by sequencing
Part Type: dataTypes </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<
Group: naGroup </br>
Class: naClass </br>

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: 100 </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Frequency of variants detected { #varFreq }
(varFreq). A description of the frequency of a variants detected. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: variant </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

Parts

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Variants class { #variant }
(variant). Measures and methods relating to variants. </br>
Part Type: classes </br>
Domain: bio </br>
Speciment ID: poSaSpecimenSet </br>
Compartment Set: anyCompartmentSet
Group: naGroup </br>
Class: variant </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population with 1 dose of vaccine { #vax1 }
(vax1). A measure of the population with a single dose of vaccine. </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>

Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population with 2 doses of vaccine { #vax2 }
(vax2). Population with 2 doses of vaccine </br>
Part Type: units </br>
Domain: bio </br>
Speciment ID: poSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>

Parts

Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Population with 3 doses of vaccine { #vax3 }
(vax3). Population with 3 doses of vaccine </br>
Part Type: units </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ODM V1 category { #version1Category }
(version1Category). ODM V1 category </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet

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

ODM V1 location { #version1Location }
(version1Location). ODM V1 location </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>

Parts

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ODM V1 table { #version1Table }
(version1Table). ODM V1 table </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

ODM version 1 to 2 changes { #version1to2Changes }
(version1to2Changes). Changes for part between ODM v1 and V2 </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>

710

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

ODM V1 variable { #version1Variable }
(version1Variable). ODM V1 variable \</br>
Part Type: \crosswalkTableSet\ \</br>
Domain: \bio\ \</br>
Speciment ID: \naSpecimenSet\ \</br>
Compartment Set: \anyCompartmentSet\ \</br>
Group: \virusMisc\ \</br>
Class: \naClass\ \</br>
Nomenclature: \naNomenclature\ \</br>
Ontology Reference: \NA\ \</br>
Category Set ID: \NA\ \</br>
Unit Set: \naUnitSet\ \</br>
Aggregation Scale: \seeUnitAggScale\ \</br>
Quality Set: \NA\ \</br>
Reference Link: NA \</br>
Data Type: \varchar\ \</br>

Parts

Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Miscellaneous viruses group { #virusMisc }
(virusMisc). A group of measures/methods related to miscellaneous viruses. T
Part Type: groups </br>
Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: measGrp </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Size in volume { #vol }
(vol). Total volume of water or sludge sampled. Used for water or air testing
Part Type: measurements </br>
Domain: phy </br>

712

Speciment ID: saSpecimenSet </br>
Compartment Set: airWaterCompartmentSet </
Group: colGrp </br>
Class: physical </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: volumeUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Volume proportional sample { #volPr }
(volPr). A volume proportional sample generally collected by an autosampler. </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>

Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Volume unit set { #volumeUnitSet }
(volumeUnitSet). Unit set of volume measurements. </br>
Part Type: unitSets </br>
Domain: che </br>
Speciment ID: siSaSpecimenSet </br
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: miscMeas </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: <a href="/sets.html#stdConcentrationUnitSet">stdConcentrationUnit
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Volatile suspended solids { #vss }
(vss). Volatile suspended solids </br>
Part Type: measurements </br>

Domain: phy </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: measGrp </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Volatile suspended solids - ignition { #vssIg }
(vssIg). A water quality measure, captured by via the loss on ignition of the mass of measur
Part Type: measurements </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: measGrp </br>
Class: standardConc </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: stdConcentrationUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>

Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 1 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Water compartment { #wat }
(wat). A measure or observation made from a substance in the water, including
Part Type: compartments </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: NA </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0.

Water depreciated { #water }
(water). Non-wastewater, coming from any kind of water body. </br>

Part Type: categories </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 15 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Water compartment set { #waterCompartmentSet }
(waterCompartmentSet). A compartment set for measures and methods in the water compartment.
Part Type: compartmentSets </br>
Domain: phy </br>
Speciment ID: siSaSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: miscMeas </br>
Class: temperature </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: temperatureUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>

717

Parts

Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Wastewater temperature { #watTemp }
(watTemp). Temperature of the wastewater. </br>
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: siteFeat </br>
Class: weather </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: weathSet </br>
Unit Set: temperatureUnitSet <
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: float </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: 0 </br>
Maximum Value: 40 </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Weather { #weath }

718

(weath). A measure for weather captured through qualitative categories; part of a larger sui
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>
Class: weather </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: weathSet </br>
Unit Set: unitlessUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: categorical </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Weather class { #weather }
(weather). Measures and methods relating to weather. </br>
Part Type: classes </br>
Domain: allDo </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: weather </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: unitlessUnitSet </br>

Parts

Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Weather set { #weathSet }
(weathSet). A set of the valid qualitative categories for the qualitative wea
Part Type: mmaSets </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet</
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: NA </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Whole genome sequencing { #wgs }
(wgs). Specifies the whole genome sequencing (WGS) strategy for genetic sequencing </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

WHO nomenclature { #who }
(who). Specifies variant or genetic nomenclature as set out by the World Health Organization
Part Type: nomenclatures </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>

Parts

```
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>


### Wide 95% interval { #wI }
(wI). The 95% interval is too wide, low confidence in results.  </br>
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#saSpecimenSet">saSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* NA </br>
*Maximum Length:* NA </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>
```

Wide name table { #wideNames }
(wideNames). The table for wide names. </br>
Part Type: tables </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: siteFeat </br>
Class: speed </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: windSpeedUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: seeUnitData </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: seeUnitVal </br>
Maximum Value: seeUnitVal </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Wind Speed { #wind }
(wind). A measure for wind speed; part of a larger suite of weather measures that may be use
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: airCompartmentSet </br>
Group: siteFeat </br>
Class: speed </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>

Parts

```
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#windSpeedUnitSet">windSpeedUnitSet</a> </br>
*Aggregation Scale:* <a href="#seeUnitAggScale">seeUnitAggScale</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Wind speed unit set { #windSpeedUnitSet }
(windSpeedUnitSet). Unit set for wind speed measurements.  </br>
*Part Type:* <a href="#unitSets">unitSets</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/sets.html#genMissingnessSet">genMissingnessSet
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
```

724

Part Status: **depreciated**. First released: 1.0.0. Last updated: 2.0.0. </br>

Measure identification (wide table) { #wMeasureID }
(wMeasureID). Unique identifier for wide table only. Use when all measures are performed on
Part Type: attributes </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Sample stored incorrectly { #wrongStorage }
(wrongStorage). Sample was stored inappropriately. </br>
Part Type: qualityIndicators </br>
Domain: naDomain </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>

725

Parts

```
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
*Maximum Length:* 30 </br>
*Part Status:* active. First released: 2.0.0. Last updated: 2.0.0. </br>

### Sample stored at wrong temperature { #wrongTemp }
(wrongTemp). Sample was stored at an inappropriate temperature.  </br>
*Part Type:* <a href="#qualityIndicators">qualityIndicators</a> </br>
*Domain:* <a href="#naDomain">naDomain</a> </br>
*Speciment ID:* <a href="/sets.html#naSpecimenSet">naSpecimenSet</a> </br>
*Compartment Set:* <a href="/sets.html#naCompartmentSet">naCompartmentSet</a>
*Group:* <a href="#naGroup">naGroup</a> </br>
*Class:* <a href="#naClass">naClass</a> </br>
*Nomenclature:* <a href="#naNomenclature">naNomenclature</a> </br>
*Ontology Reference:* <a href="#NA">NA</a> </br>
*Category Set ID:* <a href="/parts.html#NA">NA</a> </br>
*Unit Set:* <a href="/sets.html#naUnitSet">naUnitSet</a> </br>
*Aggregation Scale:* <a href="#NA">NA</a> </br>
*Quality Set:* <a href="/parts.html#NA">NA</a> </br>
*Reference Link:* NA </br>
*Data Type:* <a href="#varchar">varchar</a> </br>
*Missingness Set:* <a href="/parts.html#NA">NA </a> </br>
*Minimum Value:* NA </br>
*Maximum Value:* NA </br>
*Minimum Length:* 0 </br>
```

Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

World Sphere (W-SPHERE) { #wSphere }
(wSphere). World Sphere header </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: naCompartmentSet </br>
Group: naGroup </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

World Sphere (W-SPHERE) notes { #wSphereNotes }
(wSphereNotes). W-Shere notes </br>
Part Type: crosswalkTableSet </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>

Parts

Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Wastewater treatment plant { #wwtp }
(wwtp). A general site type for wastewater treatment plants. Used as a catch-
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>

728

Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Back-up wastewater treatment site { #wwtpBack }
(wwtpBack). Indicates a wastewater treatment plant where multiple labs are or were sampling,
Part Type: categories </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: siteFeat </br>
Class: capacity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Wastewater treatment plant designed capacity { #wwtpCap }
(wwtpCap). A measure for the designed capacity of a wastewater treatment plant, in terms of
Part Type: measurements </br>
Domain: phy </br>
Speciment ID: siSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>

729

Parts

Class: capacity </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: capacityUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Industrial wastewater treatment plant { #wwtpInd }
(wwtpInd). Industrial wastewater treatment plant </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: <a href="/sets.html#waterCompartmentSet">waterCompartmentS
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>

730

Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Municipal wastewater treatment plant for combined sewage { #wwtpMuC }
(wwtpMuC). Municipal wastewater treatment plant for combined sewage </br>
Part Type: categories </br>
Domain: naDomain </br>
Speciment ID: naSpecimenSet </br>
Compartment Set: waterCompartmentSet </br>
Group: colGrp </br>
Class: naClass </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: NA </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: NA </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 1.0.0. Last updated: 2.0.0. </br>

Municipal wastewater treatment plant for sanitary dewage only { #wwtpMuS }
(wwtpMuS). Municipal wastewater treatment plant for sanitary sewage only </br>
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet </br>

Parts

Group: sarsCov2 </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

y505h omicron-variant gene target { #y505h }
(y505h). y505h omicron-variant gene target </br>
Part Type: measurements </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: <a href="/sets.html#anyCompartmentSet">anyCompartmentSet<,
Group: procGrp </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: geneticUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet <

732

Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

Years { #years }
(years). A unit for indicating a length of time in years. </br>
Part Type: units </br>
Domain: allDo </br>
Speciment ID: anySpecimenSet </br>
Compartment Set: anyCompartmentSet </br>
Group: miscMeas </br>
Class: time </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: quantAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: integer </br>
Missingness Set: NA </br>
Minimum Value: 0 </br>
Maximum Value: NA </br>
Minimum Length: NA </br>
Maximum Length: NA </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

zymo environ water rna kit/ zymo environ water rna kit (cat. r2042) { #zymoEnv }
(zymoEnv). Nucleic acid extraction performed using the zymo environ water rna kit/ zymo envi
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>

Parts

Compartment Set: anyCompartmentSet</br>
Group: procGrp </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>
Missingness Set: <a href="/sets.html#genMissingnessSet">genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

zymo quick-rna fungal/bacterial miniprep #r2014 { #zymoQuick }
(zymoQuick). Nucleic acid extraction performed using the zymo quick-rna funga
Part Type: categories </br>
Domain: bio </br>
Speciment ID: saSpecimenSet </br>
Compartment Set: anyCompartmentSet</br>
Group: procGrp </br>
Class: mutation </br>
Nomenclature: naNomenclature </br>
Ontology Reference: NA </br>
Category Set ID: NA </br>
Unit Set: naUnitSet </br>
Aggregation Scale: seeUnitAggScale </br>
Quality Set: NA </br>
Reference Link: NA </br>
Data Type: varchar </br>

Missingness Set: genMissingnessSet </br>
Minimum Value: NA </br>
Maximum Value: NA </br>
Minimum Length: 0 </br>
Maximum Length: 30 </br>
Part Status: active. First released: 2.0.0. Last updated: 2.0.0. </br>

`<!-- quarto-file-metadata: eyJyZXNvdXJjZURpciI6Ii4ifQ== -->`{=html}

```{=html}
<!-- quarto-file-metadata: eyJyZXNvdXJjZURpciI6Ii4iLCJib29rSXRlbVR5cGUiOiJjaGFwdGVyIiwiYm9va va
```

Sets

Warning in get_latest_dictionary(): Multiple dictionaries found only one
dictionary should be stored.

Dictionary 2.0.0.

Sets are lists of categories and other parts. For example, `Collection category set` ([colle

Sets can have parts that are reused. For example, there are different quality measures for s

::: {.cell}

:::

Aggregations { #aggregations }
(aggregations). Statistical measures used to report a

 AND Boolean aggregation (andBoo). "AND" aggregation
 Flow-normalized mean (floMean). Mean measure norm
 Geometric mean (gmn). Geometric mean. </br>Status: ad
 Lower limit of a 95% confidence interval <a href="/parts.html#lowerCI95">(lowerCI95
 Maximum value (maxVal). Highest value in a range o

 Arithmetic mean (me). Arithmetic mean.
 Median (med). Median. </br>Status: act
 Normalized arithmetic mean (menr). Ar
 Minimum value (minVal). Lowest valu
 Aggregation not applicable (naAggr)
 Normalized geometric mean (ngmn). Geo
 OR Boolean aggregation (orBoo). "OR"
 Other aggregation depricated <a href="/parts.html#otherDep">(otherDe
 PMMoV- and flow-normalized mean <a href="/parts.html#pmFloMean">(pmI
 PMMoV-normalized mean <a href="/parts.html#pmmovNorm">(pmmovNorm)</a
 Standard deviation (sd). Standard devia
 Normalized standard deviation (sdn). S
 Single (sin). A value that is not an a
 Upper limit of a 95% confidence interval <a href="/parts.html#upperC

Aggregation scales { #aggregationScales }
(aggregationScales). The scale of

 Aggregation scale not applicable <a href="/parts.html#naAggrScale">
 Other aggregation scale (othAgg). S
 Qualitative (qualAggScale). T
 Quantitative <a href="/parts.html#quantAggScale">(quantAggScale)</a
 See unit (aggregation scales) <a href="/parts.html#seeUnitAggScale">

Aggregation sets { #aggregationSets }
(aggregationSets). Sets of aggregat

Boolean aggregation set { #booleanAggrSet }
(booleanAggrSet)Aggreagation set for
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 AND Boolean aggregation (andBoo). "
 OR Boolean aggregation (orBoo). "OR"
 Single (sin). A value that is not an a

Linear scale aggregation set { #linearAggrSet }
(linearAggrSet)The aggregation set that contains all
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Flow-normalized mean (floMean). Mean measure norm
 Lower limit of a 95% confidence interval <a href="/parts.html#lowerCI95">(lowerCI95
 Maximum value (maxVal). Highest value in a range c
 Arithmetic mean (me). Arithmetic mean. </br>Status: ac
 Median (med). Median. </br>Status: active. First rele
 Normalized arithmetic mean (menr). Arithmetic mean,
 Minimum value (minVal). Lowest value in a range of
 PMMoV- and flow-normalized mean (pmFloMean). Me
 PMMoV-normalized mean (pmmovNorm). Mean measure
 Standard deviation (sd). Standard deviation. </br>Stat
 Normalized standard deviation (sdn). Standard deviati
 Single (sin). A value that is not an aggregate measur
 Upper limit of a 95% confidence interval <a href="/parts.html#upperCI95">(upperCI95

Logarithmic scale aggregation set { #logAggrSet }
(logAggrSet)The aggregation set that contains all aggre
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Flow-normalized mean (floMean). Mean measure norm
 Geometric mean (gmn). Geometric mean. </br>Status: ac
 Lower limit of a 95% confidence interval <a href="/parts.html#lowerCI95">(lowerCI95
 Maximum value (maxVal). Highest value in a range c
 Minimum value (minVal). Lowest value in a range of
 Normalized geometric mean (ngmn). Geometric mean, no
 PMMoV- and flow-normalized mean (pmFloMean). Me
 PMMoV-normalized mean (pmmovNorm). Mean measure
 Single (sin). A value that is not an aggregate measur

739

 Upper limit of a 95% confidence interval <a href="/parts.html#upper(

Aggregation set not applicable { #naAggrSet }
(naAggrSet)Not application for aggregatio
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Aggregation not applicable (naAggr)

Other aggregation set { #otherAggrSet }
(otherAggrSet)Aggregation set used fo
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Flow-normalized mean (floMean). Me
 Geometric mean (gmn). Geometric mean.
 Lower limit of a 95% confidence interval <a href="/parts.html#lower(
 Maximum value (maxVal). Highest val
 Arithmetic mean (me). Arithmetic mean.
 Median (med). Median. </br>Status: act
 Normalized arithmetic mean (menr). Ar
 Minimum value (minVal). Lowest valu
 Aggregation not applicable (naAggr)
 Normalized geometric mean (ngmn). Geo
 Standard deviation (sd). Standard devia
 Normalized standard deviation (sdn). S
 Single (sin). A value that is not an a
 Upper limit of a 95% confidence interval <a href="/parts.html#upper(

Attributes { #attributes }
(attributes). Attributes describe the wh

 Analysis date (aDate). Date the meas
 Analysis date end (aDateEnd). Dat

 Analysis date start (aDateStart). Date the mea
 Address Line 1 (addL1). Line 1 (the street name, nu
 Address Line 2 (addL2). Line 2 (the unit number) fo
 Address ID (addressID). A unique identifier for
 Administrative regions (admRegLevel). Adminis
 Aggregation scale (aggragationScale). A
 Aggregation (aggregation). Statistical measur
 Aggregation set (aggregationSet). The aggr
 Alias depreciated (aliasDep). ID of an assay tha
 Alias ID depreciated (aliasIDDep). Alias id </
 Access to all org (allOrgs). If this is 'no', thi
 Assay method id default depreciated (amDefDep).
 Assay ID (asID). Links with the AssayMethod used to
 City (city). The city where a site or organization i
 Class (class). A unique identifier for a class, whi
 Collection date time (collDT). For grab samples th
 Collection date time end (collDTEnd). For integ
 Collection date time start (collDTStart). For
 Collection number (collNum). The number of subsam
 Collection number and period (collNumPer). Com
 Collection period (collPer). Collection period. T
 Sample collection type (collType). The type of c
 Column name depreciiated (columnNameDep). N
 Compartment (compartment). The attribute ide
 Contact ID (contactID). A unique identifier for
 Contact name (contactName). Contact person or
 Country (country). The country where a site or or
 Countries or sovereign states (countryLevel)
 Districts, counties, regions (countyLevel). D
 Covid-19 population measurement date (cphDate). d
 Cphd ID (cphid). Unique identifier for the table. <
 Custody Contact ID (custodyCont). A unique id
 Data custodian ID (custodyID). The data custodi
 Dataset creation date (datasetDate). Specifie

 Dataset ID (datasetID). The name
 Date (date). Date </br>Status: depre
 Description (descr). A detailed desc
 Access to details deprecated <a href="/parts.html#detailsDep">(deta:
 Domain (domain). Domain is the hig
 Contact email (email). Contact e-ma:
 File location of polygon <a href="/parts.html#fileLocation">(fileLod
 First name of contact <a href="/parts.html#firstName">(firstName)</a
 Fraction analyzed (fraction). Fra
 Funder Contact ID (funderCont)
 Funding agency ID (funderID). The
 European Petroleum Survey Group Coordinates <a href="/parts.html#ged
 Latitude (geoLat). Geographical lod
 Longitude (geoLong). Geographical
 Type of geography (geoType). Type
 Well-known text (geoWKT). Well-knou
 Group (group). Unique identifier for
 Index (index). Index number in case
 Instrument ID (instrumentID)
 Instrument Type (insType). Type of
 Describe other instrument type, if applicable <a href="/parts.html#:
 ISO639-1 (iso6391). The first part
 ISO639-2B (iso6392B). A set of in
 ISO639-2T (iso6392T). A set of in
 ISO639-3 (iso6393). A set of inter
 ISO639-6 (iso6396). A set of inter
 Lab ID default depricated <a href="/parts.html#labDefDep">(labDefDep
 Lab ID (labID). Unique identifier for
 Language ID (lang). Language code for
 Language family (langFam). Specif:
 Language name (langName). Specif:
 Last edited (lastEdited). The d
 Last name of contact (lastName).
 Link (li). Link to an external referend

742

 License (license). The license of a dataset. </br
 Access to local ha (localHA). If this is 'no', th
 Manufacturer (manufacturer). Manufacturer of
 Measure (measure). A measurement or observation o
 Report ID (measureRepID). Unique identifier
 Report set ID (meaureSetRepID). Unique ide
 Measure license (mesureLic). Specifies the acce
 Method (method). A procedure for collecting a samp
 Measure, method, or attribute (mmaSet). The set fo
 Model (model). Model number or version of the instr
 Municipalities or communes <a href="/parts.html#municipalLevel">(municipalLevel)</a
 Name (name). Name of a domain, specimen, group, clas
 Native Name (natName). The native name of the lan
 Local administrative units or neighborhoods <a href="/parts.html#neighborLevel">(ne
 Nomenclature (nomenclature). A classificatio
 Notes (notes). A note used to describe details that
 Organization ID (organizationID). A unique
 Organization level (orgLevel). The geographic le
 Organization sector (orgSector). The sector of
 Organization Type (orgType). Specifies the type o
 Sample origin (origin). An attribute of a sample s
 Access to other prov depricated <a href="/parts.html#otherProvDep">(otherProvDep)</
 Parent dataset ID (parDatasetID). The datase
 Parent sample ID (parent). If this sample has been
 Parent Site ID (parSiteID). The siteID that is
 Postal or Zip Code (pCode). The zip code or postal
 Access to phac (phac). If this is 'no', the data wil
 Contact phone (phone). Contact phone number, for th
 Polygon ID (polygonID). Unique identifier for t
 Polygon Population (polyPop). An attribute of a p
 Pooled (pooled). Is this a pooled sample, and ther
 Type of date for case reporting depreciated <a href="/parts.html#popDateTypeDep">(p
 Population Served (popServ). An attribute of a si
 Protocol ID (protocolID). A unique identifier

 Protocol ID container <a href="/parts.html#protocolIDContainer">(pro
 Protocol ID object <a href="/parts.html#protocolIDObj">(protocolIDO
 Protocol ID subject <a href="/parts.html#protocolIDSub">(protocolIDS
 Protocol version <a href="/parts.html#protocolVersion">(protocolVers
 Access to prov ha (provHA). If this
 Pretreatment description - depreciated <a href="/parts.html#ptDesc
 Access to public (public). If this
 Purpose (purpose). The reason the
 Quality flag (qualityFlag). A
 Quality report ID (qualityID). A
 Quality set (qualitySetID). T
 Date sample recieved (recDate). Th
 Reference link (refLink). Link to
 Primary reporting authority <a href="/parts.html#repOrg1">(repOrg1)
 Secondary reporting authority <a href="/parts.html#repOrg2">(repOrg2
 Reportable (reportable). Flag
 Report date (reportDate). The
 Reporter ID depreciated <a href="/parts.html#reporterIDDep">(reporte
 Replicate Type (repType). Attirbut
 Role of contact (role). Specifies the
 Sample material (saMaterial). T
 Sample ID (sampleID). Unique ider
 Sample ID object <a href="/parts.html#sampleIDObject">(sampleIDObjec
 Sample ID subject <a href="/parts.html#sampleIDSubject">(sampleIDSub
 Sample relationship <a href="/parts.html#sampleRelID">(sampleRelID)
 Sample shed (sampleShed). A geo
 Access to self (self). If this is 'no
 Date sample was sent (sentDate).
 Set ID (setID). The unique identifie
 Set Value (setValue). The partID
 Severity indicator (severity). An
 Sewer network file link depreciated <a href="/parts.html#sewerNetwor
 Site ID default (siteDef). Used as
 Site ID (siteID). Unique identifier

 Site measure ID (siteMeasureID). Unique ide
 Site Type (siteType). Type of site or institutio
 Sewer network file link depreciated 2 (snfl). Link t
 Source Protocol ID (sourceProtocol). A pro
 Protocol step source ID (sourceStep). Specifie
 Specimen (specimen). The substance or thing upor
 Departments, states, or provinces <a href="/parts.html#stateProvLevel">(stateProvLe
 State, Province, or Region (stateProvReg). T
 Protocol Step ID (stepID). The unique identifier f
 Step ID Object (stepIDObj). The object of the r
 Step ID Subject (stepIDSub). The subject of the
 Method step parent ID (stepProvenanceID)
 Protocol step version (stepVer). Specifies the ve
 Sewer network file blob (storTempDef). A file
 Summary (summ). Short description of the assay and h
 Type other depreciate2 (tyOtDep2). Description c
 Unit (unit). The units of a measurement. </br>Status
 Unit set (unitSet). An idenfication of a set of u
 U site measure ID (uSiteMeasureID). Unique
 Value (value). Value of a measure, observation or a
 Measure identification (wide table) <a href="/parts.html#wMeasureID">(wMeasureID)</

Classes { #classes }
(classes). A class is a collection of one or more related

 Alleles class (allele). Measures and methods relat
 Bacteria Class (bacteria). Measures and methods
 Capacity class (capacity). Measures and methods
 Conductivity class (conductivity). Measures
 Dilution Class (dilution). Measures and methods
 Diseases (human) class (disease). Measure and met
 Flow class (flow). Measures and methods related to f
 Gas class (gas). Measures and methods relating to gas
 Humidity class (humid). Measures and methods relate

745

 Dictionary tables (lookup). Tables
 Mutations class (mutation). Measu
 Class not applicable (naClass). Cl
 Outbreak class (outbreak). Measur
 qPCR Class (pcr). Measures and methods
 pH class (pHClass). Measures and m
 Physical class (physical). Measur
 Precipitation class <a href="/parts.html#precipation">(precipation)
 Program decription tables <a href="/parts.html#programDescr">(progra
 Results tables (results). Tables u
 Genetic sequences class <a href="/parts.html#sequence">(sequence)</a
 Speed class (speed). Measures and me
 Standard concentrations class <a href="/parts.html#standardConc">(st
 Standard curve class <a href="/parts.html#standardCurve">(standardCu
 Temperature class <a href="/parts.html#temperature">(temperature)</a
 Time class (time). Measures and metho
 Turburdity class (turbidity). Me
 Variants class (variant). Measures
 Weather class (weather). Measures

Compartments { #compartments }
(compartments). The substance from whi

 Human compartment (hum). A measure or
 Compartment not applicable <a href="/parts.html#naCompartment">(naCo
 Surface compartment (surf). A measure
 Water compartment (wat). A measure or

Compartment sets { #compartmentSets }
(compartmentSets). Sets of compartm

Air compartment set { #airCompartmentSet }
(airCompartmentSet)A compartment
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

746

```
<ul>
<li> **Air compartment** <a href="/parts.html#air">(air)</a>. A measure or observation made
</ul>
```

Air and surface compartment set { #airSurfaceCompartmentSet }
```
<a href="/parts.html#airSurfaceCompartmentSet">(airSurfaceCompartmentSet)</a>A compartment s
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Air compartment** <a href="/parts.html#air">(air)</a>. A measure or observation made
<li> **Surface compartment** <a href="/parts.html#surf">(surf)</a>. A measure or observation
</ul>
```

Air and water compartment set { #airWaterCompartmentSet }
```
<a href="/parts.html#airWaterCompartmentSet">(airWaterCompartmentSet)</a>A compartment set f
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Air compartment** <a href="/parts.html#air">(air)</a>. A measure or observation made
</ul>
```

Any compartment set { #anyCompartmentSet }
```
<a href="/parts.html#anyCompartmentSet">(anyCompartmentSet)</a>A compartment set for measure
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Air compartment** <a href="/parts.html#air">(air)</a>. A measure or observation made
<li> **Surface compartment** <a href="/parts.html#surf">(surf)</a>. A measure or observation
<li> **Water compartment** <a href="/parts.html#wat">(wat)</a>. A measure or observation mad
</ul>
```

Human compartment set { #humanCompartmentSet }
```
<a href="/parts.html#humanCompartmentSet">(humanCompartmentSet)</a>A compartment set for mea
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Human compartment** <a href="/parts.html#hum">(hum)</a>. A measure or observation mad
</ul>
```

Compartment set not applicable { #naCompartmentSet }
(naCompartmentSet)Compartment not
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Compartment not applicable <a href="/parts.html#naCompartment">(naCo

Surface compartment set { #surfaceCompartmentSet }
(surfaceCompartmentSet)A comp
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Surface compartment (surf). A measure

Surface and water compartment set { #surfaceWaterCompartmentSet }
<a href="/parts.html#surfaceWaterCompartmentSet">(surfaceWaterCompartmentSet)
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Surface compartment (surf). A measure
 Water compartment (wat). A measure or

Water compartment set { #waterCompartmentSet }
(waterCompartmentSet)A compartm
Status: active. First Released: 1.0.0. Last updated: 2.0.0.

 Water compartment (wat). A measure or

Data types { #dataTypes }
(dataTypes). The data type for a part. Da

 Binary Large Object (BLOB) data type <a href="/parts.html#blob">(blo
 Boolean data type (boolean). The d

748

```
<li> **Categorical data type** <a href="/parts.html#categorical">(categorical)</a>. The data
<li> **Datetime data type** <a href="/parts.html#datetime">(datetime)</a>. The data type for
<li> **Float data type** <a href="/parts.html#float">(float)</a>. The data type for float da
<li> **Integer data type** <a href="/parts.html#integer">(integer)</a>. The data type for in
<li> **See unit (data type)** <a href="/parts.html#seeUnitData">(seeUnitData)</a>. The data
<li> **Variable character data type** <a href="/parts.html#varchar">(varchar)</a>. The data
</ul>
## Domains { #domains }
<a href="/parts.html#domains">(domains)</a>. There are three domain types: biologic (i.e. Co
<ul>
<li> **All domains** <a href="/parts.html#allDo">(allDo)</a>. Domain that specifies that it
<li> **Biologic** <a href="/parts.html#bio">(bio)</a>. A living organism or biological subst
<li> **Chemical** <a href="/parts.html#che">(che)</a>. A chemical compound. </br>Status: act
<li> **Domain not applicable** <a href="/parts.html#naDomain">(naDomain)</a>. Not applicable
<li> **Physical property** <a href="/parts.html#phy">(phy)</a>. A physical property or objec
</ul>
## Groups { #groups }
<a href="/parts.html#groups">(groups)</a>. A collection of related measures. Used primary to
<ul>
<li> **Miscellaneous bacteria group** <a href="/parts.html#bactMisc">(bactMisc)</a>. A group
<li> **Collection group** <a href="/parts.html#colGrp">(colGrp)</a>. A group of measurement-
<li> **Measurement group** <a href="/parts.html#measGrp">(measGrp)</a>. A group of measures
<li> **Miscellaneous attribute group** <a href="/parts.html#miscAttr">(miscAttr)</a>. A grou
<li> **Miscellaneous measure group** <a href="/parts.html#miscMeas">(miscMeas)</a>. A group
<li> **Group not applicable** <a href="/parts.html#naGroup">(naGroup)</a>. Used when there i
<li> **Population group** <a href="/parts.html#popGrp">(popGrp)</a>. A group of measures/met
<li> **Processing group** <a href="/parts.html#procGrp">(procGrp)</a>. A group of measures/m
<li> **SARS-CoV-2** <a href="/parts.html#sarsCov2">(sarsCov2)</a>. A group of measures/metho
<li> **Site features group** <a href="/parts.html#siteFeat">(siteFeat)</a>. A group of envir
<li> **Miscellaneous viruses group** <a href="/parts.html#virusMisc">(virusMisc)</a>. A grou
</ul>
## Measures { #measurements }
<a href="/parts.html#measurements">(measurements)</a>. The attribute to describe a part type
<ul>
```

Sets

 a1306s delta-variant gene target <a href="/parts.html#a1306s">(a1306
 a1918v delta-variant gene target <a href="/parts.html#a1918v">(a1918
 a2710t omicron-variant gene target <a href="/parts.html#a2710t">(a2
 a63t omicron-variant gene target <a href="/parts.html#a63t">(a63t)</
 a67v omicron-variant gene target <a href="/parts.html#a67v">(a67v)</
 Absolute humidity (absHum). A measu
 Environmental temperature <a href="/parts.html#airTemp">(airTemp)</a
 Arrival temperature (arTemp). The t
 bcov (bcov). Measure of the amount o:
 Beta (beta). B.1.351 </br>Status: act
 5-Day carbonaceous kiochemical oxygen demand <a href="/parts.html#bc
 5-day total biochemical oxygen demand <a href="/parts.html#bod5t">(k
 Bovine respiratory syncytial virus group <a href="/parts.html#brsv">
 BRSV-N (brsvN). bovine respiratory s
 Carbon Dioxide (co2). A measure of an
 Chemical Oxygen Demand (cod). Chemical
 Water conductivity (cond). Measuremen
 Covid-19 (cov). Covid-19 infection. </
 SARS-CoV-2 measure (cov2Me). Measu:
 SARS-CoV-2-B.1.1.7 (covB117). Var:
 SARS-CoV-2-B.1.351 (covB135). Var:
 SARS-CoV-2-E (covE). SARS-CoV-2 E ger
 SARS-CoV-2-N1 (covN1). SARS-CoV-2 nu
 SARS-CoV-2-N2 (covN2). SARS-CoV-2 nu
 SARS-CoV-2-N3 (covN3). SARS-CoV-2 nu
 SARS-CoV-2-P.1 (covP1). Variant P.1
 SARS-CoV-2-RdRp (covRdrp). SARS-Co
 crAssphage-N (cra). crAssphage virus
 Cycle threshold or quantification cycle (Ct or Cq) <a href="/parts.l
 d377y delta-variant gene target <a href="/parts.html#d377y">(d377y)·
 d3g omicron-variant gene target <a href="/parts.html#d3g ">(d3g)</a
 d63g delta-variant gene target (d63g)
 d796y omicron-variant gene target <a href="/parts.html#d796y ">(d796
 d950n delta-variant gene target <a href="/parts.html#d950n">(d950n)·

750

 ddcov_e sars-cov-2 gene target (ddcovE). ddcov_e s
 ddcov_n sars-cov-2 gene target (ddcovN). ddcov_n
 **del143/145 ** (del143). 143 or 145 deletion omicron-
 del 157/158 (del157). 157 or 158 deletion delta-va
 **del2084/2084 ** (del2084). 2084 or 2084 deletion om
 **del212/212 ** (del212). 212 or 212 deletion omicron-
 **del3674/3676 ** (del3674). 3674 or 3676 deletion om
 del69/70 (del6970). 69 or 70 deletion omicron-var
 Delta (delta). B.1.617.2 </br>Status: active. First
 Dilution factor (dilFact). Specifies the extent t
 Point dillutions (dillute). Exact concentration o
 e156g delta-variant gene target (e156g). e156g delt
 e484a omicron-variant gene target (e484a). e484a
 Escherichia coli (ecoli). Concentration of bacteria
 Efficiency (efficient). The efficiency reported
 Rainfall (envRnF). Rainfall, i.e. amount of precip
 Ground snow depth (envSnwD). Total depth of snow
 Snowfall (envSnwF). Snowfall, i.e. amount of prec
 Sarbecovirus-specific E sars-cov-2 gene target <a href="/parts.html#eSarbec">(eSarb
 Estimated frequency of reads (estFreqReads).
 Extraction volume of sample (exvol). Extraction vol
 Flow rate (floRate). Wastewater volumetric flow r
 Flow volume (flowVol). Volume of influent. </br>S
 Influenza virus measure (flu). General influenza viru
 Influenza virus A1 (fluA1). Influenza virus A1 type
 influenza virus A2 (fluA2). influenza virus A2 type
 Influenza virus B (fluB). Influenza virus B type </b
 F-Specific RNA bacteriophages (frna). A measure for
 F-Specific RNA bacteriophages, G2 (frnaG2). A meas
 Field sample temperature (fst). Temperature that the
 g215c delta-variant gene target (g215c). g215c delt
 g339d omicron-variant gene target (g339d). g339d
 g496s omicron-variant gene target (g496s). g496s
 g662s delta-variant gene target (g662s). g662s delt

751

 Gamma (gam). P.1 </br>Status: active.
 hep g armored rna (hepGRna). Meas
 i1566v omicron-variant gene target <a href="/parts.html#i1566v ">(i
 i3758v omicron-variant gene target <a href="/parts.html#i3758v ">(i3
 i82t delta-variant gene target (i82t)
 Inhibition measure (inhibMe). Par
 Intercept (inter). Intercept value
 Combined ip2 and ip4 sars-cov-2 gene target <a href="/parts.html#ip2
 k856r omicron-variant gene target <a href="/parts.html#k856r ">(k856
 l452r delta-variant gene target <a href="/parts.html#l452r">(l452r)
 l981f omicron-variant gene target <a href="/parts.html#l981f ">(l981
 Lambda (lamba). C.37 </br>Status: ac
 Limit of detection (LOD) (lod). Limit
 Limit of detection (LOD) - sewage <a href="/parts.html#lodSewa">(lod
 Limit of quantification (LOQ) (loq).
 Other Measure (measOth). Other mea
 Other Measure Description <a href="/parts.html#meOthDe">(meOthDe)</a
 Murine Hepatitis Virus (mhv). A measu
 ms2 coliphage (ms2Col). Measure of
 Mu (mu). B.1.621 </br>Status: active.
 murine coronavirus (muCo). Measure o
 N sars-cov-2 gene target (n). N sars-co
 Combined N1 and N2 sars-cov-2 gene target <a href="/parts.html#n1n2"
 n211i omicron-variant gene target <a href="/parts.html#n211i ">(n211
 n679k omicron-variant gene target <a href="/parts.html#n679k ">(n679
 n856k omicron-variant gene target <a href="/parts.html#n856k ">(n856
 n969k omicron-variant gene target <a href="/parts.html#n969k ">(n969
 Ammonium Nitrogen (nH4N). Ammonium n
 niid_2019-ncov_n sars-cov-2 gene target <a href="/parts.html#niid19
 Norovirus G1 (noroG1). Norovirus ge
 Norovirus G2 (noroG2). Norovirus ge
 Sarbecovirus-specific N sars-cov-2 gene target <a href="/parts.html#
 coronavirus OC43 (oc43). Measure of t
 Omicron BA.1 (omicr1). Omicron B.1

752

```
<li> **Omicron BA.2** <a href="/parts.html#omicr2">(omicr2)</a>. Omicron BA.2 </br>Status: a
<li> **Omicron BA.2.75** <a href="/parts.html#omicr275">(omicr275)</a>. Omicron BA.2.75 </br
<li> **Omicron BA.4** <a href="/parts.html#omicr4">(omicr4)</a>. Omicron BA.4 </br>Status: a
<li> **Omicron BA.5** <a href="/parts.html#omicr5">(omicr5)</a>. Omicron BA.5 </br>Status: a
<li> **Orthophosphates** <a href="/parts.html#ophos">(ophos)</a>. Ortho-phosphate concentrat
<li> **ORF1a sars-cov-2 gene target** <a href="/parts.html#orf1a">(orf1a)</a>. ORF1a sars-co
<li> **ORF1ab sars-cov-2 gene target** <a href="/parts.html#orf1ab">(orf1ab)</a>. ORF1ab sar
<li> **ORF1b sars-cov-2 gene target** <a href="/parts.html#orf1b">(orf1b)</a>. ORF1b sars-co
<li> **Variants Other** <a href="/parts.html#otherV">(otherV)</a>. Used for reporting varian
<li> **Outbreak** <a href="/parts.html#outb">(outb)</a>. Measure to indicate outbreak status
<li> **p100l delta-variant gene target** <a href="/parts.html#p100l">(p100l)</a>. p100l delt
<li> **p2046l delta-variant gene target** <a href="/parts.html#p2046l">(p2046l)</a>. p2046l
<li> **p2287s delta-variant gene target** <a href="/parts.html#p2287s">(p2287s)</a>. p2287s
<li> **p3395h omicron-variant gene target** <a href="/parts.html#p3395h ">(p3395h )</a>. p33
<li> **p681r delta-variant gene target** <a href="/parts.html#p681r">(p681r)</a>. p681r delt
<li> **pH** <a href="/parts.html#ph">(ph)</a>. pH measurement </br>Status: active. First rel
<li> **Pseudomonas virus phi6** <a href="/parts.html#phi6">(phi6)</a>. Measure of the amount
<li> **Total phosphorous** <a href="/parts.html#phos">(phos)</a>. Total phosphorous </br>Sta
<li> **Total Phosphates** <a href="/parts.html#phostot">(phostot)</a>. Total phosphates </br
<li> **PHRED quality score** <a href="/parts.html#phred">(phred)</a>. PHRED Quality Score Fo
<li> **PMMoV-CP** <a href="/parts.html#ppmv">(ppmv)</a>. Pepper mild mottle virus capsid pro
<li> **Puro virus** <a href="/parts.html#puro">(puro)</a>. Measure of the amount of puro vir
<li> **q19e omicron-variant gene target** <a href="/parts.html#q19e ">(q19e )</a>. q19e omic
<li> **q493r omicron-variant gene target** <a href="/parts.html#q493r ">(q493r )</a>. q493r
<li> **q498r omicron-variant gene target** <a href="/parts.html#q498r ">(q498r )</a>. q498r
<li> **q954h omicron-variant gene target** <a href="/parts.html#q954h ">(q954h )</a>. q954h
<li> **R squared** <a href="/parts.html#r2">(r2)</a>. R-squared value of the calibration cur
<li> **r203m delta-variant gene target** <a href="/parts.html#r203m">(r203m)</a>. r203m delt
<li> **IP2 rdrp sars-cov-2 gene target** <a href="/parts.html#rdrpIP2">(rdrpIP2)</a>. IP2 rd
<li> **IP4 rdrp sars-cov-2 gene target** <a href="/parts.html#rdrpIP4">(rdrpIP4)</a>. IP4 rd
<li> **Relative humidity** <a href="/parts.html#relHum">(relHum)</a>. The unit of relative h
<li> **replicate number** <a href="/parts.html#repNum">(repNum)</a>. The replicate number fo
<li> **Respiratory syncytial virus** <a href="/parts.html#rsv">(rsv)</a>. Respiratory syncyt
<li> **s2083i omicron-variant gene target** <a href="/parts.html#s2083i ">(s2083i )</a>. s20
```

753

 s371l omicron-variant gene target <a href="/parts.html#s371l ">(s37
 s373p omicron-variant gene target <a href="/parts.html#s373p ">(s373
 s375f omicron-variant gene target <a href="/parts.html#s375f ">(s375
 s477n omicron-variant gene target <a href="/parts.html#s477n ">(s477
 Settled solids (settsol). Amount o
 S sars-cov-2 gene target (sGene). S
 slope (slope). Slope value of the ca
 Specific humidity (specHum). Measu
 Storage temp (sTemp). Temperature th
 Storage time (stoTim). Length of ti
 Sub-variant or lineage (subVar). A
 t19r delta-variant gene target <a href="/parts.html#t19r">(t19r)</a
 t3646a delta-variant gene target <a href="/parts.html#t3646a">(t3646
 t547k omicron-variant gene target <a href="/parts.html#t547k ">(t547
 t9i omicron-variant gene target <a href="/parts.html#t9i ">(t9i)</a
 TaqPath N sars-cov-2 gene target <a href="/parts.html#taqpatN">(taqp
 TaqPath S sars-cov-2 gene target <a href="/parts.html#taqpatS">(taqp
 Sample temperature (temp). Temperatur
 Nucleic acid template volume <a href="/parts.html#tempVol">(tempVol)
 Total Kjeldahl Nitrogen (tkn). A measu
 Total Nitrogen (tn). Total nitrogen con
 Total solids concentration (ts). Total
 Total suspended solids (tss). Total su
 Concentration of total suspended solids <a href="/parts.html#tssConc
 Tubidity (turb). A measure for the tu
 Tube weight empty (tWeighE). The w
 Tube weight full (tWeighF). The we
 v2930l delta-variant gene target <a href="/parts.html#v2930l">(v2930
 Size in volume (vol). Total volume of
 Volatile suspended solids (vss). Volat
 Volatile suspended solids - ignition <a href="/parts.html#vssIg">(vs
 Wastewater temperature (watTemp).
 Weather (weath). A measure for weath
 Wind Speed (wind). A measure for wind

 Wastewater treatment plant designed capacity <a href="/parts.html#wwtpCap">(wwtpCap
 y505h omicron-variant gene target (y505h). y505h

Methods { #methods }
(methods). Procedures or steps for collecting samples or p

 Nucleic acid extraction method (extraction). D
 Inhibition method (inhibMeth). Description of t
 Concentration method (methodConc). Description
 PCR method (pcrmeth). Description of the PCR meth
 Pretreatment (pretreat). Was the sample chemical
 Genetic primer (primer). Method ID used for indica
 Quaility assurance method (qaqc). Quality assurance
 Collection other depreciated <a href="/parts.html#sampleTypeOther">(sampleTypeOther
 Standard curve frequency (scf). A method for specifyi
 Genetic sequencing script version <a href="/parts.html#scriptVersion">(scriptVersio
 Sequencing Layout (seqLay). The layout of genetic
 Sequencing selection method (seqSel). The primer s
 Sequencing Strategy (seqStrat). The sequencing s
 Shipped on ice (shipOnIce). Was the sample kept
 Solid seperation (solidSep). Process used to sep
 Spike material (spikeMat). Material into which t
 Recovery efficiency spike target <a href="/parts.html#spikeTarget">(spikeTarget)</a
 Type other depreciate (tyOtDep). Description for

Missingness { #missingness }
(missingness). The part type for missingness values. [

 Not applicable (NA). The field for which the expected
 Not a number (nan). The outcome of a measurement is n
 Not reported (nr). A value could have been recorded, h
 Null (null). A logical representation of a statement
 Undisclosed (undisc). A value has been recorded, h

755

Missingness sets { #missingnessSets }
(missingnessSets). Missingness set

General missingness set { #genMissingnessSet }
(genMissingnessSet)The general se
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Not applicable (NA). The field for whic
 Not a number (nan). The outcome of a n
 Not reported (nr). A value could have l
 Null (null). A logical representation
 Undisclosed (undisc). A value has l

Not reported, Not applicable missing set { #nrNAMissingnessSet }
(nrNAMissingnessSet)Not reported
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Not applicable (NA). The field for whic
 Not reported (nr). A value could have l

Measure, method, or attribute sets { #mmaSets }
(mmaSets). A set of categories. For example

Boolean value set { #booleanSet }
(booleanSet)Set that contains the valid
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 FALSE (false). Boolean data type = F
 TRUE (true). Boolean data type = TRUE

Sample collection set { #collectSet }
(collectSet)Methods for collection sampl

Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Area proportional sample (areaPr). An area proport
 Composite sample - archival (comp). A composite samp
 COSCa ball (cosca). COSCa passive sampling device.
 Flow proportional sample (flowPr). A flow proporti
 Grab sample (grb). A single large representative grab
 Moore swab passive sample (moorSw). Moore swab pas
 Surface swab (surfSw). Surface swab. </br>Status:
 Time proportional sample (timePr). A time proporti
 Volume proportional sample (volPr). A volume propor

Nucleic Acid Extraction set { #extractSet }
(extractSet)set used for storing all the valid category
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Amicon filter, extract with MP96 (amiMP96). Nucle
 Bead beating, extract with MP96 (bbMP96). Nucleaic
 Chemagic viral dna/rna 300 kit (chemVir). Nucleic
 4s method (extract4s). Nucleic acid extraction
 Nuclisens automated magnetic bead extraction kit <a href="/parts.html#nucAuto">(nuc
 Nuclisens manual magnetic bead extraction kit <a href="/parts.html#nucManu">(nucMan
 Phenol chloroform (phenCl). Nucleic acid extractio
 promega automated tna kit (promAuto). Nucleic ac
 promega ht tna kit (promHt). Nucleic acid extracti
 promega manual tna kit (promManu). Nucleic acid
 promega wastewater large volume tna capture kit <a href="/parts.html#promWW">(promW
 qiagen allprep dna/rna kit (qgDNARNA). Nucleic a
 qiagen ez1 virus mini kit v2.0 (qgEz1). Nucleic aci
 qiagen allprep powerfecal dna/rna kit <a href="/parts.html#qgPwrFecal">(qgPwrFecal)
 qiagen allprep powerviral dna/rna kit <a href="/parts.html#qgPwrViral">(qgPwrViral)
 qiagen powerwater kit (qgPwrWtr). Nucleic acid e
 qiagen qiaamp buffers with epoch columns <a href="/parts.html#qgQiAmp">(qgQiAmp)</a

757

 qiagen rneasy kit (qgRneasy). Nuc
 qiagen rneasy powermicrobiome kit <a href"/parts.html#qgRneasyPwr">
 Resuspend COSCa filter collection <a href="/parts.html#resCosca">(re
 thermo magmax microbiome ultra nucleic acid isolation kit <a href=",
 trizol, zymo mag beads w/ zymo clean and concentrator <a href="/part
 zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)
 zymo quick-rna fungal/bacterial miniprep #r2014 <a href="/parts.html

Sample fraction set { #fractionSet }
(fractionSet)set for the fraction of t
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Liquid fraction (liq). Liquid fractio
 Mixed/homogenized sample (mix). Mixed
 Solid fraction (sol). Solid fraction c

Geographic set { #geoTypeSet }
(geoTypeSet)set for different type of ge
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Sewer Network Health Region <a href="/parts.html#hlthReg">(hlthReg)
 Sewer catchment area (swrSet). Sewe

Inhibition set { #inhibitionSet }
(inhibitionSet)Category set for inhi
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Serial dilution <a href="/parts.html#serialDilution">(serialDilutio
 Spike matrix and recovery (spike).

758

Instrument set { #insTypeSet }
(insTypeSet)List of instruments that are used for measu
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Atline Analyzer (aas). Atline analyzer with sampler.
 Hand Measurement (hma). Handheld measurement analyzer
 Other instrument <a href="/parts.html#instrumentTypeOther">(instrumentTypeOther)</a
 Lab Analysis (ola). Offline laboratory analysis. </br
 Online Sensor (onse). Online sensor </br>Status: act

Concentration method set { #methodConcSet }
(methodConcSet)A set a concentration methods. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Aloh3 precipitation (aloh3). Aloh3 precipitation </
 Amicon ultrafiltration (amiconUf). Amicon ultraf
 Beef extract flocculation (beeExtractFloc)
 Centricon ultrafiltration (centriconUf). Cent
 Ceres nanotrap (ceres). Ceres nanotrap. </br>Status
 Hollow fiber dead end ultrafiltration <a href="/parts.html#hollowFiberUF">(hollowFi
 Innovaprep ultrafiltration (innovaprepUF). I
 Polyethyleneglycol (PEG) precipitation (peg). Peg pre
 Skimmed milk flocculation (skimMilkFloc). Sk
 Ultracentrifugation (untracent). Ultracentrifug

Organization level set { #orgLevelSet }
(orgLevelSet)Categories of organization levels. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Administrative regions (admRegLevel). Adminis
 Countries or sovereign states (countryLevel)
 Districts, counties, regions (countyLevel). D

```
<li> **Municipalities or communes** <a href="/parts.html#municipalLevel">(mu
<li> **Local administrative units or neighborhoods** <a href="/parts.html#nei
<li> **Departments, states, or provinces** <a href="/parts.html#stateProvLeve
</ul>
```

Organization sector set { #orgSectorSet }
```
<a href="/parts.html#orgSectorSet">(orgSectorSet)</a>Cateogries of organizati
```
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
```
<ul>
<li> **Airport** <a href="/parts.html#airport">(airport)</a>. Airport sample
<li> **Long-term acute care hospital** <a href="/parts.html#ccc">(ccc)</a>. A
<li> **Higher education domitory or residential building** <a href="/parts.ht
<li> **First Nation** <a href="/parts.html#fiNa">(fiNa)</a>. Used to categori
<li> **Health administration or planning agency** <a href="/parts.html#health
<li> **Laboratory** <a href="/parts.html#lab">(lab)</a>. Laboratory for envir
<li> **Long-term care facility** <a href="/parts.html#ltcf">(ltcf)</a>. A res
<li> **Long-term care - assisted living or retirement home** <a href="/parts
<li> **Public healith agency** <a href="/parts.html#pubHealth">(pubHealth)</a
<li> **School** <a href="/parts.html#school">(school)</a>. A school serving s
<li> **Social services shelter** <a href="/parts.html#sss">(sss)</a>. Other t
<li> **University campus** <a href="/parts.html#uCampus">(uCampus)</a>. Unive
</ul>
```

Organization type set { #orgTypeSet }
```
<a href="/parts.html#orgTypeSet">(orgTypeSet)</a>The set for storing organiza
```
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
```
<ul>
<li> **Academic institution** <a href="/parts.html#academ">(academ)</a>. The
<li> **Government agency** <a href="/parts.html#govt">(govt)</a>. The categor
<li> **Private sector** <a href="/parts.html#priv">(priv)</a>. The category o
</ul>
```

Sample Origin set { #originSet }
```
<a href="/parts.html#originSet">(originSet)</a>The set for storing the valid
```

Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Derived sample (derived). Specifies a sample that
 Field sample (field). Specifies a sample taken from
 Synthetic sample (synthetic). Specifies a synth

Outbreak set { #outbreakSet }
(outbreakSet)set for the valid values of the outbreak
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Outbreak End (outbEnd). Indicates an outbreak has
 Outbreak - on-going (outbOngoing). Indicates
 Outbreak start (outbStart). Indicates an outbre

PCR Method set { #pcrSet }
(pcrSet)The set capturing containing all of the valid metho
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Digital droplet emulsification PCR <a href="/parts.html#bioRadDdpcr">(bioRadDdpcr)<
 Fluidigm digital PCR (fluiDpcr). Describes a PCR
 Life technologies digital PCR (ltDpcr). Describes
 qiagen digital PCR (qgDpcr). Describes a PCR analy
 Quantitative PCR (qpcr). Real-time PCR, also called
 Raindance digital PCR (rainDpcr). Describes a PC

Genetic primer set { #primerSet }
(primerSet)The set for genetic primers used in sequencin
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Use of the articV3 primer (articV3). Initial impl
 Use of the articV4 primer (articV4). Artic V4 seq

Sets

```
</ul>

### Protocol Relationships set { #protocolRelSet }
<a href="/parts.html#protocolRelSet">(protocolRelSet)</a>set for valid values
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Is Before** <a href="/parts.html#before">(before)</a>. Specifies that
<li> **Is concurrent to** <a href="/parts.html#concurrent">(concurrent)</a>.
<li> **Specifies** <a href="/parts.html#specifies">(specifies)</a>. Specifies
</ul>

### Purpose set { #purposeSet }
<a href="/parts.html#purposeSet">(purposeSet)</a>Purpose set for a sample or
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Education** <a href="/parts.html#education">(education)</a>. A measure
<li> **Multiple Purpose** <a href="/parts.html#multiple">(multiple)</a>. A me
<li> **Provisional report** <a href="/parts.html#provisional">(provisional)</
<li> **Quality control** <a href="/parts.html#qualityControl">(qualityControl
<li> **Regular** <a href="/parts.html#regular">(regular)</a>. A measure or sa
<li> **Testing** <a href="/parts.html#testing">(testing)</a>. A measure or sa
<li> **Validation study** <a href="/parts.html#validationStudy">(validationSt
</ul>

### Replicate Type set { #replicateSet }
<a href="/parts.html#replicateSet">(replicateSet)</a>The set for storing vali
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Co-located sample** <a href="/parts.html#colocated">(colocated)</a>. S
<li> **Field sample replicate** <a href="/parts.html#fieldReplicate">(fieldRe
<li> **Laboratory duplicate** <a href="/parts.html#labDuplicate">(labDuplicat
<li> **Laboratory control sample duplicate** <a href="/parts.html#lcsd">(lcsd
<li> **Matrix spike duplicate** <a href="/parts.html#msd">(msd)</a>. A known
<li> **Unique sample** <a href="/parts.html#unique">(unique)</a>. A unique sa
```

762

```
</ul>
```

Sample material set { #sampleMatSet }
(sampleMatSet)set for the types of material that can
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
```
<ul>
```
 Air filter (afu). Air filter as part of filtration or
 Desk or counter (desk). Desk, table, countertop or c
 Fecal matter (faeces). Fecal matter. </br>Status:
 Floor (floor). Floor of a building or room. </br>St
 Holding tank wastewater (htSam). Wastewater sampled
 Water (nww). Non-wastewater, coming from any kind of
 Primary clarifier effluent (pEfflu). Effluent obta
 Primary clarifier sludge (pSludge). Sludge produc
 Post-grit (pstGrit). Raw wastewater after a treat
 Raw sewage at site (rawWW). Wastewater without any
 Raw sewage downstream from a site (rawWWdown).
 Raw sewage upstream from a site (rawWWup). Upstre
 Secondary clarifier effluent (sEfflu). Effluent ob
 Septic tank wastewater (septage). Wastewater from
 Secondary clarifier sludge (sSludge). Sludge prod
 Other surface (surface). Surface other than floor
 Sewer sediment (swrSed). Sediments obtained in sew
```
</ul>
```

Sample relationships set { #sampleRelSet }
(sampleRelSet)set for valid values of relationshipID
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
```
<ul>
```
 Child relationship (child). Indicated that this is
 Co-located sample (colocated). Second or multip
 Field sample replicate (fieldReplicate). A
 Laboratory duplicate (labDuplicate). Second
 Laboratory control sample duplicate (lcsd). Known am

Sets

 Matrix spike duplicate (msd). A known

Sequencing script version set { #scriptSet }
(scriptSet)The set for script versions
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Freyja Script (freyja). Freyja Scr
 Gromstole 1.0 Script <a href="/parts.html#gromstole">(gromstole)</a

Sequencing Layout set { #seqLaySet }
(seqLaySet)The set for the layout of gene
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Mate pair layout (mateLay). Speci
 Paired Layout (pairLay). Specifies
 Single Layout (sinLay). Specifies t

Sequencing selection method set { #seqSelSet }
(seqSelSet)The set for the selection meth
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 PCR sequencingsSelection method <a href="/parts.html#pcrSeq">(pcrSeq
 Random sequencing selection method <a href="/parts.html#ranSeq">(ran

Sequencing Strategy set { #seqStratSet }
(seqStratSet)The set for the sequencing
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Amplicon sequencing (amp). Specifies t
 Whole genome sequencing (wgs). Specifi

Severity set { #sevSet }
(sevSet)A set for severity indicators. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 High severity (high). Indicates a very sever quality
 Low severity (low). A marker for low severity </br>St
 Mid-level severity (mid). A marker for med-level seve

Sampleshed set { #shedSet }
(shedSet)The set for all valid values of sampleshed. </br
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Airplane (airpln). Airplane sample shed category t
 Airport (airport). Airport sample shed category t
 Long-term acute care hospital (ccc). Acute care hospi
 Child day care (cdc). Child day care facility. </br>S
 Cphd ID (corFcil). Correctional facility </br>Sta
 Higher education domitory or residential building <a href="/parts.html#dorm">(dorm)
 First Nation (fiNa). Used to categorize a sampleshed
 Hospital (hosptl). Hospital </br>Status: active. F
 Long-term care facility (ltcf). A residential health
 Long-term care - assisted living or retirement home <a href="/parts.html#ltcfAl">(l
 Other long-term care (ltcfO). Other residential fac
 Municipality (municp). A complete municipality, th
 Neighbourhood (neigh). A municipal neighbourhood, t
 Other residential building (orb). Individual resident
 School (school). A school serving students in the
 Ship (ship). A cruise ship or other ship. </br>Statu
 Social services shelter (sss). Other type of social s
 Airport terminal (terminal). Airport terminal sa
 University campus (uCampus). Universityor college

Sets

```
</ul>

### Site set { #siteTypeSet }
<a href="/parts.html#siteTypeSet">(siteTypeSet)</a>set for the type of sampli
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Branch sewer pipleline** <a href="/parts.html#bSwrPpl">(bSwrPpl)</a>.
<li> **Building cleanout** <a href="/parts.html#buildCO">(buildCO)</a>. Spec
<li> **Estuary, natural water body** <a href="/parts.html#estuary">(estuary)
<li> **Holding tank** <a href="/parts.html#htSite">(htSite)</a>. Holding tan
<li> **Lagoon system** <a href="/parts.html#lagoon">(lagoon)</a>. Logoon syst
<li> **Lake,  natural water body** <a href="/parts.html#lake">(lake)</a>. Lal
<li> **Major sewer pipeline** <a href="/parts.html#mSwrPpl">(mSwrPpl)</a>. Ma
<li> **Ocean, natural water body** <a href="/parts.html#ocean">(ocean)</a>. (
<li> **Pumping station** <a href="/parts.html#pStat">(pStat)</a>. Pumping sta
<li> **Retention pond** <a href="/parts.html#retPond">(retPond)</a>. Retentio
<li> **River, natural water body** <a href="/parts.html#river">(river)</a>. !
<li> **Sea, natural water body** <a href="/parts.html#sea">(sea)</a>. Sea, na
<li> **Septic tank** <a href="/parts.html#septTnk">(septTnk)</a>. Septic tanl
<li> **Stabilization pond** <a href="/parts.html#stabPnd">(stabPnd)</a>. Spec
<li> **Sewage truck** <a href="/parts.html#swgTrck">(swgTrck)</a>. Sewage tru
<li> **Upstream sites** <a href="/parts.html#upstream">(upstream)</a>. A gene
<li> **Wastewater treatment plant** <a href="/parts.html#wwtp">(wwtp)</a>. A
<li> **Back-up wastewater treatment site** <a href="/parts.html#wwtpBack">(wv
<li> **Industrial wastewater treatment plant** <a href="/parts.html#wwtpInd">
<li> **Municipal wastewater treatment plant for combined sewage** <a href="/p
<li> **Municipal wastewater treatment plant for sanitary dewage only** <a hre
</ul>

### Solid separation set { #solidSeparationSet }
<a href="/parts.html#solidSeparationSet">(solidSeparationSet)</a>set for the
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Centrifugation** <a href="/parts.html#cent">(cent)</a>. Describes sol
```

766

 Filtration (filt). Describes solid separation from a
 Gravity settling (graSet). Describes solid separat
 Membrane filtration with acidification and mgcl2 <a href="/parts.html#mfAcidmgcl2">
 **Membrane filtration with acidification and mgcl2, membrane recombined with separated
 Membrane filtration with addition of mgcl2 <a href="/parts.html#mfMgcl2">(mfMgcl2)<
 Membrane filtration with mgcl2 and separated solids <a href="/parts.html#mfMgcl2SS
 Membrane filtration with no amendment <a href="/parts.html#mfNoAmend">(mfNoAmend)</
 Membrane filtration with no amendment, membrane recombined with separated solids <a
 Membrane filtration with sample acidification <a href="/parts.html#mfSampleAcid">(m
 **Membrane filtration with sample acidification, membrane recombined with separated sol
 No liquid concentration, liquid recombined with separated solids <a href="/parts.ht

Spike material set { #spikeMatSet }
(spikeMatSet)set for spikeMat (aterial into which the
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Clarified sample (clari). Clarified sample. </br>St
 Sample concentrate (conc). Sample concentrate. </br>
 Dewatered solids (deso). Dewatered solids. </br>Stat
 Lysis buffer (lysi). Lysis buffer. </br>Status: acti
 Raw wastewater (raws). Raw wastes water sample </br>
 Raw post-pasteurized wastewater (rppw). Raw wastewat

Recovery efficiency spike target set { #spikeTargetSet }
(spikeTargetSet)The set capturing containing all of
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 bcov culture spike target (bcovCul). Cultured bov
 bcov vaccine spike target (bcovVac). The bovine c
 brsv culture spike target (brsvCul). Cultured bov
 brsv vaccine spike target (brsvVac). The bovine r
 Heat inactivated sars-cov-2 virus spike target <a href="/parts.html#heatInacSARS">(

 hep g armored rna spike target <a href="/parts.html#hepGRnaMat">(hep
 ms2 coliphage spike target <a href="/parts.html#ms2ColMat">(ms2ColMa
 murine coronavirus spike target <a href="/parts.html#muCoMat">(muCoM
 oc43 spike target (oc43Mat). Human
 phi6 spike target (phi6Mat). Pseud
 Puro virus spike target (puroMat)

Status set { #statusSet }
(statusSet)A set for partID = Status to
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Active (active). Indicator that a
 Depreciated (depreciated). Ind
 Development (development). Ind

Table column set { #tableSet }
(tableSet)The set for valid inputs in tab
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Foreign key (fK). Foreign key for a tab
 Header (header). Header for a table
 Input (input). Input for a table. I
 Primary key (pK). Primary key for a tab

Weather set { #weathSet }
(weathSet)A set of the valid qualitative
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Cloudy (cloudy). Qualitative catego
 Foggy (foggy). Qualitative category
 Rainy (rainy). Qualitative category

 Snowy (snowy). Qualitative category for the weather
 Sunny (sunny). Qualitative category for the weather

Nomenclatures { #nomenclatures }
(nomenclatures). A classification system to report t

 International Classification of Diseases (icd). Class
 Nomenclature not applicable <a href="/parts.html#naNomenclature">(naNomenclature)</
 NextClade nomenclature (nextclade). Specifies v
 Pangolin nomenclature (pangolin). Specifies vari
 WHO nomenclature (who). Specifies variant or genetic

Quality indicators { #qualityIndicators }
(qualityIndicators). A measure of the quality of

 Experiment Failed (expFail). PCR experiment faile
 AI - Inhibition present but addressed (flagAI). Th
 B - Trace levels of contamination (flagB). Analytic
 FI - Inhibition present and unaddressed (flagFI).
 J - Weak signal extrapolation (flagJ). Analytical r
 ND - Non-detect (flagND). No amplification occurre
 UJ - Trace signal extrapolation (flagUJ). Observed
 UQ - Unquantifiable (flagUQ). Unquantifiable, Ct v
 Sample frozen (frozen). Sample was frozen before a
 Low breadth of coverage (lBC). The percentage of the
 Low depth of coverage (lDC). Poor coverage, specifica
 Leaked sample (leaked). Sample leaked, some volume
 Low-volume sample (lowVol). Sample is low-volume,
 Multiple issues (mI). Multiple issues have arisen in t
 No quality concerns (noConcern). A flag to indi
 Sample not labelled (noLabel). Sample had no labe
 Sample missing time stamp (noTime). Sample is miss
 Quality concerns (qf1). A flag to indicate there is a
 Sparse coverage (sC). Sequencing shows sparse coverage

 Sample spilled (spill). Sample conte

 Wide 95% interval (wI). The 95% interva

 Sample stored incorrectly <a href="/parts.html#wrongStorage">(wrongS

 Sample stored at wrong temperature <a href="/parts.html#wrongTemp">

Quality indicator sets { #qualityIndSets }

(qualityIndSets). Sets of quality i

Generic quality flag set { #genQualitySet }

(genQualitySet)A quality set to spec

Status: active. First Released: 1.0.0. Last updated: 2.0.0.

 Multiple issues (mI). Multiple issues

 No quality concerns (noConcern)

 Quality concerns (qf1). A flag to indi

Measures quality set { #measQualitySet }

(measQualitySet)A quality set for a

Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Experiment Failed (expFail). PCR

 AI - Inhibition present but addressed <a href="/parts.html#flagAI">

 B - Trace levels of contamination <a href="/parts.html#flagB">(flag

 FI - Inhibition present and unaddressed <a href="/parts.html#flagFI"

 J - Weak signal extrapolation <a href="/parts.html#flagJ">(flagJ)</a

 ND - Non-detect (flagND). No ampli

 UJ - Trace signal extrapolation <a href="/parts.html#flagUJ">(flagUJ

 UQ - Unquantifiable (flagUQ). Unqua

 Low breadth of coverage (lBC). The per

 Low depth of coverage (lDC). Poor cove

 Multiple issues (mI). Multiple issues

 No quality concerns (noConcern)

 Sample missing time stamp (noTime)

770

 Quality concerns (qf1). A flag to indicate there is a
 Sparse coverage (sC). Sequencing shows sparse coverage

PCR quality set { #pcrQualitySet }
(pcrQualitySet)Quality set for PCR measures. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Experiment Failed (expFail). PCR experiment faile
 AI - Inhibition present but addressed (flagAI). Th
 B - Trace levels of contamination (flagB). Analytic
 FI - Inhibition present and unaddressed (flagFI).
 J - Weak signal extrapolation (flagJ). Analytical r
 ND - Non-detect (flagND). No amplification occurre
 UJ - Trace signal extrapolation (flagUJ). Observed
 UQ - Unquantifiable (flagUQ). Unquantifiable, Ct v
 No quality concerns (noConcern). A flag to indi

Sample quality set { #sampleQualitySet }
(sampleQualitySet)Quality set for a sample. </br
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Sample frozen (frozen). Sample was frozen before a
 Leaked sample (leaked). Sample leaked, some volume
 Low-volume sample (lowVol). Sample is low-volume,
 No quality concerns (noConcern). A flag to indi
 Sample not labelled (noLabel). Sample had no labe
 Sample missing time stamp (noTime). Sample is miss
 Sample spilled (spill). Sample contents spilled fro
 Sample stored incorrectly (wrongStorage). Sa
 Sample stored at wrong temperature (wrongTemp).

Sequencing quality set { #seqQualitySet }
(seqQualitySet)Quality set for sequer
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Experiment Failed (expFail). PCR e
 Low breadth of coverage (lBC). The per
 Low depth of coverage (lDC). Poor cove
 No quality concerns (noConcern)
 Sample missing time stamp (noTime)
 Sparse coverage (sC). Sequencing shows

Specimens { #specimens }
(specimens). Measures or observations are

 Population (po). An measure or observat
 Sample (sa). A measure made on a compar
 Site (si). A measure made on a compartr

Specimen sets { #specimenSets }
(specimenSets). Sets of specimens. Spe

Any specimen set { #anySpecimenSet }
(anySpecimenSet)A specimen set that
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Population (po). An measure or observat
 Sample (sa). A measure made on a compar
 Site (si). A measure made on a compartr

Specimen set not applicable { #naSpecimenSet }
(naSpecimenSet)A specimen set for whe
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

772

 Specimen not applicable (naSpecimen). Non appl

Population or sample set { #poSaSpecimenSet }
(poSaSpecimenSet)A specimen set that inculdes popu
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Population (po). An measure or observation for a geogr
 Sample (sa). A measure made on a compartment or proper

Population or site set { #poSiSpecimenSet }
(poSiSpecimenSet)A specimen set that inculdes popu
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Population (po). An measure or observation for a geogr
 Site (si). A measure made on a compartment or property

Population specimen set { #poSpecimenSet }
(poSpecimenSet)A specimen set that inculdes only a p
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Population (po). An measure or observation for a geogr

Sample specimen set { #saSpecimenSet }
(saSpecimenSet)A specimen set that inculdes only a s
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Sample (sa). A measure made on a compartment or proper

Site or sample specimen set { #siSaSpecimenSet }

773

Sets

(siSaSpecimenSet)A specimen set tha
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Sample (sa). A measure made on a compar
 Site (si). A measure made on a compartr

Site specimen set { #siSpecimenSet }
(siSpecimenSet)A specimen set that i
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Site (si). A measure made on a compartr

Tables { #tables }
(tables). Tables are where measures, methods

 Address table (addresses). The t
 Contact table (contacts). The tal
 Dataset table (datasets). A repor
 Instrument table (instruments)
 Language Look-up table <a href="/parts.html#languages">(languages)</
 Measure report table (measures).
 Measure set report table <a href="/parts.html#measureSets">(measureS
 Organization table <a href="/parts.html#organizations">(organizatio
 Parts Look-up table (parts). Look up
 Polygon table (polygons). The tal
 Protocol relationships table <a href="/parts.html#protocolRelationsh
 Protocols table (protocols). The
 Protocol steps table <a href="/parts.html#protocolSteps">(protocolSt
 Quality reports table <a href="/parts.html#qualityReports">(qualityR
 Reporter table depreciated <a href="/parts.html#reportersDep">(repor
 Sample relationships table <a href="/parts.html#sampleRelationships"
 Sample report table (samples). The
 Sets look-up table (sets). Look up ta

774

 Sites table (sites). The table that contains inform
 Translation look-up table (translations). Lo
 Wide name table (wideNames). The table for wide

Units { #units }
(units). The unit of the measurement. Every measurement must

 Number of active cases (acti). Number of active case
 Breadth of coverage (>=5x depth) (boc). Positions wit
 Degrees Celcius (cel). Degrees Celsius. </br>Status:
 CFU per 100 ml (cfu). Colony forming units per 100 ml
 Centimetres (cm). Unit part for the SI unit of centime
 Confirmed Cases Case report date (conCase). Date
 Number of confirmed cases (conf). Number of confirme
 Confirmed cases episode date (confEp). Episode dat
 Confirmed Cases Onset date (confOn). Earliest that
 Confirmed cases test date (conTest). Date that th
 Cumulative count (cuCo). Units for describing a popu
 Daily count (daiCo). Units for describing a populat
 Days (days). A unit for indicating a length of time
 Deaths (death). Units for describing a population m
 Detected (det). Substance detected or not detected. <
 Depth of coverage (doc). The sequencing read depth. <
 Gene copies per copy of crAssphage (gcCrA). Gene or
 gene copies per day per 100,000 (gcD100). The unit
 Gene copies per gram solids (gCGS). Gene or variant
 Gene copies per L (gcL). Gene or variant copies per l
 Gene copies per mL (gcMl). Gene or variant copies pe
 Gene copies per PMMoV copy (gcPpmov). Gene or var
 Gram per cubic metre (gm3). Density unit. </br>Status
 Grams (grams). A unit of mass or weight. </br>Statu
 General Hospital Admissions (hosa). Hospital admissi
 Hospital Census (hosc). Hospital census or the numbe
 Hours (hours). A unit for indicating a length of ti

 Intensive care unit patients (icu). Un
 Kilogram per second (kgS). Kilograms p
 Kilolitres (kl). Kilolitres of volume <
 Litres (l). Litres of volume </br>Status
 Cubic metres per day (m3D). Cubic metr
 Cubic metres per hour (m3H). Cubic met
 Cubic metres per second (m3S). Cubic m
 Millions of gallons per day (MG/D) <a href="/parts.html#mgd">(mgd)</
 Milligrams per litre (mgL). Milligrams
 Minutes (minutes). A unit for ind
 Millilitres (ml). Millilitres of volum
 Megalitres per day (ML/d) (mld). Megal
 Millimetres (mm). Unit part for the SI
 Months (months). A unit for indica
 Metres per second (ms). metres per sec
 Unit not applicable (naUnit). Not a
 Population of newly vaccinated persons <a href="/parts.html#newVax">
 Nephelometric turbidity unit (ntu). Ne
 Other Unit depricated (otunDep). O
 Percent (perc). Percentage. </br>Stat
 Percent recovery (percRec). Percen
 Population equivalents (popEq). A un
 Percent positive (pp). Percent positive
 parts per million (ppm). Parts per mil
 Percent positivity rate (pprt). Perce
 Percent primary sludge (pps). Percenta
 Proportion of total (prop). Proportio
 Proportion of variant in sample <a href="/parts.html#propV">(propV)<
 Number of positive tests (ptot). Numb
 Ratio (ratio). Ratio (unitless) </br
 Recovered patients (recov). Units fo
 Rate per 100,000 (rP100). Units for
 Number of tests performed (test). Num
 Unitless measure (unitless). A un

 Micro-Siemens per centimetre (uSCm). Micro-siemens p
 Frequency of variants detected (varFreq). A descr
 Population with 1 dose of vaccine (vax1). A measure
 Population with 2 doses of vaccine (vax2). Populatio
 Population with 3 doses of vaccine (vax3). Populatio
 Years (years). A unit for indicating a length of ti

Unit sets { #unitSets }
(unitSets). Sets of units. Contains units that are associ

Absolute humidity unit set { #absHumidUnitSet }
(absHumidUnitSet)Unit set for absolute humidity me
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Gram per cubic metre (gm3). Density unit. </br>Status

Allele unit set { #alleleUnitSet }
(alleleUnitSet)Unit set for alleles. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Cycle threshold or quantification cycle (Ct or Cq) <a href="/parts.html#ct">(ct)</a
 Detected (det). Substance detected or not detected. <
 Depth of coverage (doc). The sequencing read depth. <
 Gene copies per copy of crAssphage (gcCrA). Gene or
 gene copies per day per 100,000 (gcD100). The unit
 Gene copies per gram solids (gCGS). Gene or variant
 Gene copies per mL (gcMl). Gene or variant copies pe
 Gene copies per PMMoV copy (gcPpmov). Gene or var

Bacteria unit set { #bacteriaUnitSet }
(bacteriaUnitSet)Unit set for bacteria-related mea
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

Sets

```
<ul>
<li> **CFU per 100 ml** <a href="/parts.html#cfu">(cfu)</a>. Colony forming u
</ul>
```

Capacity unit set { #capacityUnitSet }

```
<a href="/parts.html#capacityUnitSet">(capacityUnitSet)</a>Unit set for capac
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Millions of gallons per day (MG/D)** <a href="/parts.html#mgd">(mgd)<,
<li> **Megalitres per day (ML/d)** <a href="/parts.html#mld">(mld)</a>. Megal
<li> **Population equivalents** <a href="/parts.html#popEq">(popEq)</a>. A u
</ul>
```

Conductivity unit set { #conductivityUnitSet }

```
<a href="/parts.html#conductivityUnitSet">(conductivityUnitSet)</a>Unit set
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Micro-Siemens per centimetre** <a href="/parts.html#uSCm">(uSCm)</a>.
</ul>
```

Dissolved gas concentration unit set { #dissGasUnitSet }

```
<a href="/parts.html#dissGasUnitSet">(dissGasUnitSet)</a>Unit set for carbon
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Milligrams per litre** <a href="/parts.html#mgL">(mgL)</a>. Milligrams
<li> **parts per million** <a href="/parts.html#ppm">(ppm)</a>. Parts per mil
</ul>
```

Volume flow rate unit set { #flowUnitSet }

```
<a href="/parts.html#flowUnitSet">(flowUnitSet)</a>Unit set for volume flow
Status: active. First Released: 2.0.0. Last updated: 2.0.0.
<ul>
<li> **Kilogram per second** <a href="/parts.html#kgS">(kgS)</a>. Kilograms
<li> **Cubic metres per day** <a href="/parts.html#m3D">(m3D)</a>. Cubic metr
```

 Cubic metres per hour (m3H). Cubic metres per hour. <
 Cubic metres per second (m3S). Cubic metre per second
 Millions of gallons per day (MG/D) (mgd). A unit for
 Megalitres per day (ML/d) (mld). Megalitres per day.

Genetics unit set { #geneticUnitSet }
(geneticUnitSet)Unit set for genetic-related measur
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Breadth of coverage (>=5x depth) (boc). Positions wit
 Detected (det). Substance detected or not detected. <
 Depth of coverage (doc). The sequencing read depth. <
 Gene copies per L (gcL). Gene or variant copies per l
 Percent recovery (percRec). Percent of the surrog
 Proportion of total (prop). Proportion as a precent
 Proportion of variant in sample (propV). Proportion

Unit set not applicable { #naUnitSet }
(naUnitSet)Not applicable for unit sets. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Unit not applicable (naUnit). Not appliable for ur

Population unit set { #populationUnitSet }
(populationUnitSet)Unit set for hospital-related
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Number of active cases (acti). Number of active case
 Confirmed Cases Case report date (conCase). Date
 Number of confirmed cases (conf). Number of confirme
 Confirmed cases episode date (confEp). Episode dat

779

Sets

 Confirmed Cases Onset date <a href="/parts.html#confOn">(confOn)</a
 Confirmed cases test date <a href="/parts.html#conTest">(conTest)</a
 Cumulative count (cuCo). Units for de
 Daily count (daiCo). Units for descr
 Deaths (death). Units for describing
 General Hospital Admissions (hosa). U
 Hospital Census (hosc). Hospital cens
 Intensive care unit patients (icu). Un
 Population of newly vaccinated persons <a href="/parts.html#newVax">
 Percent positivity rate (pprt). Perce
 Number of positive tests (ptot). Numb
 Recovered patients (recov). Units fo
 Rate per 100,000 (rP100). Units for
 Number of tests performed (test). Num
 Population with 1 dose of vaccine <a href="/parts.html#vax1">(vax1)
 Population with 2 doses of vaccine <a href="/parts.html#vax2">(vax2)
 Population with 3 doses of vaccine <a href="/parts.html#vax3">(vax3)

Precipitation unit set { #precipitationUnitSet }
(precipitationUnitSet)Unit set
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Centimetres (cm). Unit part for the SI
 Millimetres (mm). Unit part for the SI

Relative humidity unit set { #relHumidUnitSet }
(relHumidUnitSet)Unit set for relat
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Percent (perc). Percentage. </br>Stat

780

Specific humidity unit set { #specHumidUnitSet }
(specHumidUnitSet)Unit set for specific humidity.
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Ratio (ratio). Ratio (unitless) </br>Status: active

Standard concentration unit set { #stdConcentrationUnitSet }
(stdConcentrationUnitSet)Unit set for conc
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Milligrams per litre (mgL). Milligrams per litre. </b
 parts per million (ppm). Parts per million. </br>Stat
 Percent primary sludge (pps). Percentage of total sol

Temperature unit set { #temperatureUnitSet }
(temperatureUnitSet)Unit set for temperature me
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Degrees Celcius (cel). Degrees Celsius. </br>Status:

Time unit set { #timeUnitSet }
(timeUnitSet)The unit set for measures of time. </br>
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Days (days). A unit for indicating a length of time
 Hours (hours). A unit for indicating a length of ti
 Minutes (minutes). A unit for indicating a length
 Months (months). A unit for indicating a length of
 Years (years). A unit for indicating a length of ti

781

Turbidity unit set { #turbidityUnitSet }
(turbidityUnitSet)Unit set for tur
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Nephelometric turbidity unit (ntu). Ne

Unitless unit set { #unitlessUnitSet }
(unitlessUnitSet)Unit set for measu
Status: active. First Released: 2.0.0. Last updated: 2.0.0.

 Unitless measure (unitless). A un

Volume unit set { #volumeUnitSet }
(volumeUnitSet)Unit set of volume mea
Status: active. First Released: 1.0.0. Last updated: 2.0.0.

 Grams (grams). A unit of mass or wei
 Kilolitres (kl). Kilolitres of volume
 Litres (l). Litres of volume </br>Status
 Millilitres (ml). Millilitres of volume
 Millimetres (mm). Unit part for the SI
 Percent positive (pp). Percent positive
 Sub-variant or lineage (subVar). A
 Frequency of variants detected <a href="/parts.html#varFreq">(varFre

Wind speed unit set { #windSpeedUnitSet }
(windSpeedUnitSet)Unit set for wir
Status: depreciated. First Released: 1.0.0. Last updated: 2.0.0.

 Metres per second (ms). metres per seco

782

`` `<!-- quarto-file-metadata: eyJyZXNvdXJjZURpciI6Ii4ifQ== -->`{=html} ``

```{=html}
<!-- quarto-file-metadata: eyJyZXNvdXJjZURpciI6Ii4iLCJib29rSXRlbVR5cGUiOiJjaGFwdGVyIiwiYm9va
```

Tables

```
Warning in get_latest_dictionary(): Multiple dictionaries found only one
dictionary should be stored.
```

Dictionary 2.0.0. "'

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.

> **i** Data storage
>
> Store all ODM data in the 21 recommended tables to ensure optimal interoprablity 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.

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

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