| ID | DATA GROUP | NAME | DESCRIPTION | [DATA TYPE](#data_types) | VALUE SET | UNITS | REQ? | DEPENDENT FIELD |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| 01-01 | Reporter | reporting\_jurisdiction | The CDC Epidemiology and Laboratory Capacity (ELC) jurisdiction reporting these data (2-letter abbreviation) | category | CA | [none] | YES |  |
|  |  |  |  |  |  |  |  |  |
| 02-01 | Collection Site | county\_names | 5-digit numeric FIPS codes of all counties and county equivalents served by this sampling site | list (comma-separated integers) | [5-digit integers] | [none] | YES |  |
| 02-02 | Collection Site | other\_jurisdiction | This field has been deprecated. Specify FIPS codes for counties and county equivalents in **'county\_names'**. | list (comma-separated strings) | [empty] | [none] | NO |  |
| 02-03 | Collection Site | zipcode | ZIP code in which this sampling site is located | ZIP code (#####) | [ZIP code] | [none] | YES |  |
| 02-04 | Collection Site | population\_served | Estimated number of persons served by this sampling site | integer | [greater than or equal to 0] | [none] | YES |  |
| 02-05 | Collection Site | sewage\_travel\_time | What is the approximate sewage travel time, on average, from sewage source to this sampling site? This should be specified as a duration in hours, not a time of day. | float | [greater than or equal to 0]; [empty] | hours | NO |  |
| 02-06 | Collection Site | sample\_location | Sample collection location in the wastewater system, whether at a wastewater treatment plant (or other community level treatment infrastructure such as community-scale septic) or upstream in the wastewater system | category | wwtp; upstream | [none] | YES | If **'sample\_location'** is "upstream", specify in '**sample\_location\_specify'** |
| 02-07 | Collection Site | sample\_location\_specify | If **'sample\_location'** is "upstream", specify the collection location in the wastewater system; an arbitrary name may be used if you do not wish to disclose the real name. | string | [string, length less than or equal to 40 characters]; [empty] | [none] | YES | If ‘**sample\_location’** is "upstream", then this must have a non-empty value |
| 02-08 | Collection Site | institution\_type | If this sample represents wastewater from a single institution, facility, or building, specify the institution type; otherwise, specify "not institution specific" | category | [See Valid Values](#institution_type) | [none] | YES |  |
|  |  |  |  |  |  |  |  |  |
| 03-01 | WWTP | epaid | NPDES permit number for the wastewater treatment plant specified in **'wwtp\_name'** | NPDES permit number (<2-letter abbreviation><#######>) | [NPDES permit number] | [none] | NO |  |
| 03-02 | WWTP | wwtp\_name | The name of the Wastewater Treatment Plant (WWTP) to which this wastewater flows. If this wastewater does not flow to a WWTP, specify an identifiable name for the septic or other treatment system to which this wastewater flows. An arbitrary name may be used if you do not wish to disclose the real name. | string | [string, length less than or equal to 40 characters] | [none] | YES |  |
| 03-03 | WWTP | wwtp\_jurisdiction | Jurisdiction name (2-letter abbreviation) in which the wastewater treatment plant provided in **'wwtp\_name'** is located | category | CA | [none] | YES |  |
| 03-04 | WWTP | capacity\_mgd | Wastewater treatment plant design capacity. This should be the capacity for which the plant is permitted. | float | [greater than or equal to 0] | Million gallons per day (MGD) | YES |  |
| 03-05 | WWTP | industrial\_input | Approximate average percentage of wastewater from industrial sources that is received by the wastewater treatment plant specified in **'wwtp\_name'** | float | [0-100]; [empty] | percent | NO |  |
| 03-06 | WWTP | stormwater\_input | Does the wastewater treatment plant specified in **'wwtp\_name'** treat water from a combined sewer system (i.e., a sewer system that collects both sewage and stormwater)? | category | yes; no | [none] | NO |  |
| 03-07 | WWTP | influent\_equilibrated | Is influent to the wastewater treatment plant specified in **'wwtp\_name'** ever stored prior to treatment to equilibrate or modulate the influent flow rate? | category | yes; no | [none] | NO |  |
|  |  |  |  |  |  |  |  |  |
| 04-01 | Collection Method | sample\_type | Type of sample collected, whether grab or composite. If composite, also provide the duration of sampling and type of composite, as listed in the Value Set (e.g., "24-hr flow-weighted composite"). A grab sample is defined as an individual sample collected without compositing or adding other samples, regardless of whether the sample matrix is liquid wastewater or sludge. | category | [See Valid Values](#sample_type) | [none] | YES |  |
| 04-02 | Collection Method | composite\_freq | Frequency of sub-sample collection (for composite samples only): for flow-weighted, the number of sub-samples collected per million gallons of flow; for time-weighted, the number of sub-samples per hour. Flow-weighted example: a value of 5 would indicate 5 sub-samples per million gallons, or 1 sub-sample per 200,000 gallons | float | [greater than or equal to 0]; [empty] | If flow-weighted composite: number per million gallons; if time-weighted or manual composite: number per hour | NO |  |
| 04-03 | Collection Method | sample\_matrix | Wastewater matrix from which the sample was collected | category | [See Valid Values](#sample_matrix) | [none] | YES |  |
| 04-04 | Collection Method | collection\_storage\_time | Duration of time the sample was stored after collection and prior to reaching the lab | float | [greater than or equal to 0]; [empty] | hours | NO |  |
| 04-05 | Collection Method | collection\_storage\_temp | Temperature at which the sample was stored after collection and prior to reaching the lab | float | [float]; [empty] | Celsius | NO |  |
| 04-06 | Collection Method | pretreatment | Was the sample treated with any chemicals prior to reaching the lab? These could include chemicals, such as stabilizers, added to the sample or chemicals, such as chlorine, added to the wastewater treatment train upstream of the sample collection point. Pasteurization should be specified in the 'pasteurized' field. | category | yes; no | [none] | NO | if "yes", then specify in **'pretreatment\_specify**' |
| 04-07 | Collection Method | pretreatment\_specify | If **'pretreatment'** is "yes", then specify the chemicals used | string | [string]; [empty] | [none] | NO |  |
|  |  |  |  |  |  |  |  |  |
| 05-01 | Processing Method | solids\_separation | Process used to separate solid and liquid phases of the sample, either prior to or in the absence of the concentration method specified in **'concentration\_method'** | category | [See Valid Values](#solids_separation) | [none] | NO |  |
| 05-02 | Processing Method | concentration\_method | Method used to concentrate the sample prior to analysis of the concentrate | category | [See Valid Values](#concentration_method) | [none] | YES |  |
| 05-03 | Processing Method | extraction\_method | Method used for nucleic acid extraction from the sample | category | [See Valid Values](#extraction_method) | [none] | YES |  |
| 05-04 | Processing Method | pre\_conc\_storage\_time | The approximate average duration of time between when samples reach the lab and when they are concentrated (if concentrated) | float | [greater than or equal to 0]; [empty] | hours | NO |  |
| 05-05 | Processing Method | pre\_conc\_storage\_temp | The storage temperature of samples after reaching the lab and prior to concentration (if concentrated) | float | [float]; [empty] | Celsius | NO |  |
| 05-06 | Processing Method | pre\_ext\_storage\_time | The approximate average duration of time between when samples are concentrated (if concentrated) and when they are extracted | float | [greater than or equal to 0]; [empty] | hours | NO |  |
| 05-07 | Processing Method | pre\_ext\_storage\_temp | The storage temperature of samples after concentration (if concentrated) and prior to extraction | float | [float]; [empty] | Celsius | NO |  |
| 05-08 | Processing Method | tot\_conc\_vol | Total volume of sample concentrated (if concentrated); this total volume is not necessarily assayed and is not necessarily equal to the value specified in **'equiv\_sewage\_amt**' | float | [greater than or equal to 0]; [empty] | mL | NO |  |
| 05-09 | Processing Method | ext\_blank | Are extraction blanks included in the extraction process? | category | yes; no | [none] | NO |  |
| 05-10 | Processing Method | rec\_eff\_target\_name | Name of the recovery efficiency control target that is spiked in | category | [See Valid Values](#rec_eff_target_name) | [none] | NO | If **'rec\_eff\_percent'** is equal to a value other than "-1", then this must have a non-empty value |
| 05-11 | Processing Method | rec\_eff\_spike\_matrix | Matrix into which the recovery efficiency control target is spiked | category | [See Valid Values](#rec_eff_spike_matrix) | [none] | NO | If **'rec\_eff\_target\_name'** has a non-empty value, then this must have a non-empty value |
| 05-12 | Processing Method | rec\_eff\_spike\_conc | Spike concentration, on average, of the recovery control on a per sample volume basis | float | [float]; [empty] | log10 copies/mL | YES | If **'rec\_eff\_target\_name'** has a non-empty value, then this must have a non-empty value |
| 05-13 | Processing Method | pasteurized | Was the sample pasteurized? | category | yes; no | [none] | NO |  |
|  |  |  |  |  |  |  |  |  |
| 06-01 | SARSCoV2 Quantification Method | pcr\_target | The target of the PCR quantification | category | sars-cov-2; delta; omicron | [none] | YES |  |
| 06-02 | SARSCoV2 Quantification Method | pcr\_gene\_target | The PCR gene used to quantify PCR target | category | [See Valid Values](#pcr_gene_target) | [none] | YES |  |
| 06-03 | SARSCoV2 Quantification Method | pcr\_gene\_target\_ref | A publication, website, or brief description of the PCR gene target used | string | [string] | [none] | YES |  |
| 06-04 | SARSCoV2 Quantification Method | pcr\_type | The type of PCR used to quantify the PCR target | category | [See Valid Values](#pcr_type) | [none] | YES |  |
| 06-05 | SARSCoV2 Quantification Method | lod\_ref | A publication, website, or brief description of the method used to calculate the limit of detection | string | [string] | [none] | YES |  |
| 06-06 | SARSCoV2 Quantification Method | hum\_frac\_target\_mic | Name of microbial target used to estimate human fecal content | category | pepper mild mottle virus; crassphage; hf183; f+ rna coliphage; f+ dna coliphage | [none] | NO | If **'hum\_frac\_mic\_conc'** has a non-empty value, then this must have a non-empty value |
| 06-07 | SARSCoV2 Quantification Method | hum\_frac\_target\_mic\_ref | A publication, website, or brief description of the microbial target specified in **'hum\_frac\_target\_mic'** | string | [string]; [empty] | [none] | NO | If **'hum\_frac\_mic\_conc'** has a non-empty value, then this must have a non-empty value |
| 06-08 | SARSCoV2 Quantification Method | hum\_frac\_target\_chem | Name of chemical compound used to estimate human fecal content | category | caffeine; ibuprofen; creatinine; sucralose; [empty] | [none] | NO | If '**hum\_frac\_chem\_conc'** has a non-empty value, then this must have a non-empty value |
| 06-09 | SARSCoV2 Quantification Method | hum\_frac\_target\_chem\_ref | A publication, website, or brief description of the chemical compound specified in **'hum\_frac\_target\_chem'** | string | [string]; [empty] | [none] | NO | If '**hum\_frac\_chem\_conc'** has a non-empty value, then this must have a non-empty value |
| 06-10 | SARSCoV2 Quantification Method | other\_norm\_name | Name of a target or compound not specified in **'hum\_frac\_target\_mic'** or **'hum\_frac\_target\_chem'** used to estimate human fecal content | category | [See Valid Values](#other_norm_name) | [none] | NO | If **'other\_norm\_conc'** has a non-empty value, then this must have a non-empty value |
| 06-11 | SARSCoV2 Quantification Method | other\_norm\_ref | A publication, website, or brief description of the target or compound specified in **'other\_norm\_name'** | string | [string]; [empty] | [none] | NO | If **'other\_norm\_conc'** has a non-empty value, then this must have a non-empty value |
| 06-12 | SARSCoV2 Quantification Method | quant\_stan\_type | The type of nucleic acid used as a standard for the PCR target quantification | category | dna; rna | [none] | YES |  |
| 06-13 | SARSCoV2 Quantification Method | stan\_ref | A publication, website, or brief description of the quantitative standard material used | string | [string] | [none] | YES |  |
| 06-14 | SARSCoV2 Quantification Method | inhibition\_method | A publication, website, or brief description of the method used to evaluate molecular inhibition | string | [string]; none (if inhibition not tested) | [none] | YES |  |
| 06-15 | SARSCoV2 Quantification Method | num\_no\_target\_control | Number of no-template controls (NTC) per instrument run | category | 0; 1; 2; 3; more than 3 | [none] | YES |  |
|  |  |  |  |  |  |  |  |  |
| 07-01 | Sample | sample\_collect\_date | The date of sample collection; for composite samples, specify the date on which sample collection began | date ([yyyy]-[mm]-[dd]) | [date not after tomorrow's date] | [none] | YES |  |
| 07-02 | Sample | sample\_collect\_time | The local time of sample collection; for composite samples, specify the time at which sample collection began | time, 24-hr ([hh]:[mm]) | [none] | [none] | YES |  |
| 07-03 | Sample | time\_zone | Current local time zone corresponding to the time specified in 's**ample\_collect\_time'**, represented as a UTC time offset (e.g., UTC-06:00) | time zone (UTC-[hh]:[mm]) | [time zone] | [none] | NO |  |
| 07-04 | Sample | flow\_rate | Wastewater volumetric flow rate at the sample collection location over the 24-hr period during which the sample was collected. If only an instantaneous flow measurement is available, it may be reported in units of million gallons per day. | float | [greater than or equal to 0]; [empty] | Million gallons per day (MGD) | YES | If **'pcr\_target\_units'** is on a per volume wastewater basis (e.g., copies/l wastewater), then this must have a non-empty value |
| 07-05 | Sample | ph | pH of wastewater sample (if sludge, pH of influent at time of collection) | float | [float]; [empty] | pH units | NO |  |
| 07-06 | Sample | conductivity | Specific conductivity of wastewater sample (if sludge, conductivity of influent at time of collection) | float | [greater than or equal to 0]; [empty] | microsiemens/cm | NO |  |
| 07-07 | Sample | tss | Total suspended solids of raw (or, if unavailable, post-grit removal) wastewater | float | [greater than or equal to 0]; [empty] | mg/L | NO |  |
| 07-08 | Sample | collection\_water\_temp | Sample temperature at time of collection | float | [greater than or equal to 0]; [empty] | Celsius | NO |  |
| 07-09 | Sample | equiv\_sewage\_amt | Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction | float | [greater than or equal to 0]; [empty] | mL wastewater or g sludge | NO |  |
| 07-10 | Sample | sample\_id | An ID assigned to a wastewater sample. It must be a string 20 characters or less, containing only numbers, English alphabetic characters, underscores, and hyphens; white space is not allowed; not case sensitive). It must be unique for this NWSS reporting jurisdiction. Wastewater samples that are split and measured by different labs should have the same sample ID but different lab IDs. Wastewater samples for which multiple PCR targets are measured should also have the same sample ID. Note: do not include PII in this field. | string | [sample id] | [none] | YES |  |
| 07-11 | Sample | lab\_id | An ID assigned to a testing lab. It must be a string 20 characters or less, containing only numbers, English alphabetic characters, underscores, and hyphens; white space is not allowed; not case sensitive). It must be unique across labs used for this NWSS reporting jurisdiction's testing. If the same lab is used across multiple NWSS reporting jurisdictions, each NWSS reporting jurisdiction may assign that lab a different lab ID. Note: including PII in this field is discouraged. | string | [lab id] | [none] | YES |  |
| 07-12 | Sample | qc\_ignore | Should the DCIPHER QC report ignore this sample? The purpose of this field is to allow for removal of samples from the QC report so that samples with unresolvable QC issues do not clutter the report. | category | yes; no | [none] | NO |  |
| 07-13 | Sample | dashboard\_ignore | Should the DCIPHER dashboard ignore this sample? | category | yes; no | [none] | NO |  |
| 07-14 | Sample | analysis\_ignore | Should DCIPHER data analysis ignore this sample? | category | yes; no | [none] | NO |  |
|  |  |  |  |  |  |  |  |  |
| 08-01 | SARSCoV2 Quantification Results | test\_result\_date | The date on which this PCR target measurement was made | date ([yyyy]-[mm]-[dd]) | [date not after tomorrow's date and not before **'sample\_collect\_date'**] | [none] | YES |  |
| 08-02 | SARSCoV2 Quantification Results | pcr\_target\_units | Units of PCR target sample concentration | category | [See Valid Values](#mic_chem_units) | [none] | YES | The units should relate to the PCR target indicated in **‘pcr\_target’** |
| 08-03 | SARSCoV2 Quantification Results | pcr\_target\_avg\_conc | Concentration of the PCR target back-calculated to unconcentrated sample basis; enter "0" if no amplification occurred, using the definition of amplification described in 'ntc\_amplify'; otherwise, enter the estimated concentration; do not adjust for matrix recovery efficiency | float | [any float other than 0]; 0 (if no amplification observed) | [units specified in **'pcr\_target\_units'**] | YES | The concentration should relate to the PCR target indicated in **‘pcr\_target’** |
| 08-04 | SARSCoV2 Quantification Results | pcr\_target\_std\_error | Standard error (SE) of the PCR target in wastewater sample, or best estimate that is consistently available. If sample replicates are always performed, use SE of sample replicates; else, if processing replicates are always performed, use SE of processing replicates; else, if qPCR is performed, use SE of PCR replicates; else, if digital PCR is performed, use error from multiple replicates if available, and Poisson error if not | float | [greater than or equal to 0]; -1 (if cannot be calculated, such as when no amplification observed); [empty] | [units specified in **'pcr\_target\_units'**] | NO | The standard error should relate to the PCR target indicated in **‘pcr\_target’** |
| 08-05 | SARSCoV2 Quantification Results | pcr\_target\_cl\_95\_lo | Lower bound of 95% confidence interval of the PCR target in wastewater sample, or best estimate that is consistently available. | float | [any float other than -1]; -1 (if cannot be calculated, such as when no amplification observed); [empty] | [units specified in **'pcr\_target\_units'**] | NO | The lower bound of the 95% confidence interval should relate to the PCR target indicated in **‘pcr\_target’** |
| 08-06 | SARSCoV2 Quantification Results | pcr\_target\_cl\_95\_up | Upper bound of 95% confidence interval of the PCR target in wastewater sample, or best estimate that is consistently available. | float | [any float other than -1]; -1 (if cannot be calculated, such as when no amplification observed); [empty] | [units specified in **'pcr\_target\_units'**] | NO | The upper bound of the 95% confidence interval should relate to the PCR target indicated in **‘pcr\_target’** |
| 08-07 | SARSCoV2 Quantification Results | pcr\_target\_below\_lod | Was the concentration of the PCR target below the limit of detection? | category | yes; no | [none] | YES | Whether the concentration was below the LOD should be based on the LOD of the PCR target indicated in ‘**lod\_sewage**’ |
| 08-08 | SARSCoV2 Quantification Results | lod\_sewage | PCR target limit of detection back-calculated to unconcentrated sample basis | float | [float] | [units specified in **'pcr\_target\_units'**] | YES | The LOD should relate to the PCR target indicated in ‘**pcr\_target’** |
| 08-09 | SARSCoV2 Quantification Results | ntc\_amplify | For qPCR, did any no-template controls on this instrument run have a Ct value less than 40? For ddPCR, did any no-template controls on this instrument run have 3 or more positive droplets? | category | yes; no | [none] | YES |  |
| 08-10 | SARSCoV2 Quantification Results | rec\_eff\_percent | Percent of spiked recovery control, specified in **'rec\_eff\_target\_name'**, that was recovered | float | [greater than or equal to 0]; -1 (if not tested) | percent | YES |  |
| 08-11 | SARSCoV2 Quantification Results | inhibition\_detect | Was molecular inhibition detected? | category | yes; no; not tested | [none] | YES |  |
| 08-12 | SARSCoV2 Quantification Results | inhibition\_adjust | Was inhibition incorporated into the PCR target concentration calculation? | category | yes; no | [none] | YES |  |
| 08-13 | SARSCoV2 Quantification Results | hum\_frac\_mic\_conc | Concentration of microbial target specified in **'hum\_frac\_target\_mic';** follow the same guidelines outlined for **'pcr\_target\_avg\_conc'** | float | [float]; [empty] | [units specified in '**hum\_frac\_mic\_unit'**] | NO | If **'hum\_frac\_mic\_unit'** has a non-empty value, then this must have a non-empty value |
| 08-14 | SARSCoV2 Quantification Results | hum\_frac\_mic\_unit | Concentration units of microbial target specified in **'hum\_frac\_target\_mic'** | category | [See Valid Values](#mic_chem_units) | [none] | NO | If **'hum\_frac\_mic\_conc'** has a non-empty value, then this must have a non-empty value |
| 08-15 | SARSCoV2 Quantification Results | hum\_frac\_chem\_conc | Concentration of chemical target specified in **'hum\_frac\_target\_chem'** | float | [float]; [empty] | [units specified in **'hum\_frac\_chem\_unit'**] | NO | If **'hum\_frac\_chem\_unit'** has a non-empty value, then this must have a non-empty value |
| 08-16 | SARSCoV2 Quantification Results | hum\_frac\_chem\_unit | Concentration units of chemical target specified in **'hum\_frac\_target\_chem'** | category | [See Valid Values](#mic_chem_units) | [none] | NO | If **'hum\_frac\_chem\_conc'** has a non-empty value, then this must have a non-empty value |
| 08-17 | SARSCoV2 Quantification Results | other\_norm\_name | Concentration of target specified in **'other\_norm\_name'** | float | [float]; [empty] | [units specified in **'other\_norm\_conc'**] | NO | If '**other\_norm\_unit'** has a non-empty value, then this must have a non-empty value |
| 08-18 | SARSCoV2 Quantification Results | other\_norm\_unit | Concentration units of target specified in **'other\_norm\_name'** | category | [See Valid Values](#mic_chem_units) | [none] | NO | If '**other\_norm\_conc'** has a non-empty value, then this must have a non-empty value |
| 08-19 | SARSCoV2 Quantification Results | quality\_flag | Does this observation have quality control issues? | category | yes; no | [none] | NO |  |
| 08-20 | SARSCoV2 Quantification Results | major\_lab\_method | A number used to distinguish major lab methods at the reporting jurisdiction level | integer | [greater than or equal to 0]; [empty] | [none] | NO |  |
| 08-21 | SARSCoV2 Quantification Results | major\_lab\_method\_desc | Brief description of the basis for assigning a ‘**major\_lab\_method’** | string | [string]; [empty] | [none] | NO |  |
|  |  |  |  |  |  |  |  |  |
| 09-01 | Additional CA Data | Sample Location Longitude | The longitude of the sample location | float | [none] | Decimal Degrees | YES |  |
| 09-02 | Additional CA Data | Sample Location Latitude | The latitude of the sample location | float | [none] | Decimal Degrees | YES |  |
| 09-03 | Additional CA Data | Laboratory Doing the Analysis | Name of the laboratory performing the analysis | string | [none] | [none] | YES |  |
| 09-04 | Additional CA Data | Contact Person | Name and affiliation of the person(s) submitting and responsible for the data | string | [none] | [none] | YES |  |
| 09-05 | Additional CA Data | Email of Data Steward | Email address of the person(s) submitting data | string | [none] | [none] | YES |  |
| 09-06 | Additional CA Data | Date Data Submitted | Date and time data submitted | date | [none] | [none] | YES |  |
| 09-07 | Additional CA Data | Phone Number of Contact Name | Phone number of the person(s) submitting and responsible for the data | string | [none] | [none] | YES |  |
| 09-08 | Additional CA Data | Elevation | Elevation of sample location | float | [none] | Feet | NO |  |
| 09-09 | Additional CA Data | Bottle Type | Type of sample bottle used to collect sample | string | [none] | [none] | NO |  |
| 09-10 | Additional CA Data | Sample Volume Collected | Volume of sample bottle used to collect sample | float | [none] | [none] | NO |  |
| 09-11 | Additional CA Data | Facility Name | Facility Name as described in permit and stored in CIWQS | string | [none] | [none] | NO |  |

**Data Type Definitions**

|  |  |
| --- | --- |
| **string** | ASCII-encoded characters; do not use line breaks within a value |
| **float** | Floating-point (i.e., decimal) number |
| **integer** | Integer number |
| **ZIP code** | 5-digit US ZIP code (#####) |
| **date** | yyyy-mm-dd |
| **time** | hh:mm (24-hr format in the local time zone) |
| **list** | Comma-separated strings |
| **category** | Categorical variable with a defined value set of strings |
| **NPDES permit number** | National Pollutant Discharge Elimination System (NPDES) permit number (<2-letter abbreviation><#######>) |
| **time zone** | Time zone, represented as a UTC time offset (UTC-[hh]:[mm], e.g., UTC-06:00); offsets can be found at https://www.timeanddate.com/time/zone/usa |
| **jurisdiction id** | String 20 characters or less, containing only numbers, English alphabetic characters, underscores, and hyphens (white space is not allowed); not case sensitive |

**mic\_chem\_units**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| copies/L wastewater |  |
| log10 copies/L wastewater |  |
| copies/g wet sludge | Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven |
| log10 copies/g wet sludge | Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven |
| copies/g dry sludge | Dry sludge mass is based on the mass of solids after drying in a drying oven |
| log10 copies/g dry sludge | Dry sludge mass is based on the mass of solids after drying in a drying oven |
| micrograms/L wastewater |
| log10 micrograms/L wastewater |
| micrograms/g wet sludge | Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven |
| log10 micrograms/g wet sludge | Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven |
| micrograms/g dry sludge | Dry sludge mass is based on the mass of solids after drying in a drying oven |
| log10 micrograms/g dry sludge | Dry sludge mass is based on the mass of solids after drying in a drying oven |
| [empty] |  |

**institution\_types**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| not institution specific | This sample does not represent wastewater from a single institution, facility, or building |
| correctional | A prison, penitentiary, penal facility, jail, detention unit, or other facility in which persons are incarcerated by government officials |
| long term care - nursing home | A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. Generally licensed by CMS. |
| long term care - assisted living | A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. May be licensed as healthcare facility based on state regulations. |
| other long term care | Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities or assisted living facilities. An example of this is a state-licensed intermediate care facility. |
| short stay acute care hospital | |
| long term acute care hospital | Acute care hospitals that provide care for patients with average length of stay longer than 25 days. LTACH patients are often transferred from intensive care units of ACH. |
| child day care |  |
| k12 | A school serving students in the kindergarten to 12th grade range |
| higher ed dorm | Solely higher education dormitory buildings |
| higher ed other | Higher education buildings or facilities that do not include dorms or that include dorms and other buildings |
| social services shelter | Other type of social services shelter |
| other residential building | Individual residential buildings or institutions not captured in other categories |
| ship |  |
| airplane |  |

**sample\_type**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| grab | An individual sample collected without compositing or adding other samples |
| 48-hr flow-weighted composite |
| 47-hr flow-weighted composite |
| 46-hr flow-weighted composite |
| 45-hr flow-weighted composite |
| 44-hr flow-weighted composite |
| 43-hr flow-weighted composite |
| 42-hr flow-weighted composite |
| 41-hr flow-weighted composite |
| 40-hr flow-weighted composite |
| 39-hr flow-weighted composite |
| 38-hr flow-weighted composite |
| 37-hr flow-weighted composite |
| 36-hr flow-weighted composite |
| 35-hr flow-weighted composite |
| 34-hr flow-weighted composite |
| 33-hr flow-weighted composite |
| 32-hr flow-weighted composite |
| 31-hr flow-weighted composite |
| 30-hr flow-weighted composite |
| 29-hr flow-weighted composite |
| 28-hr flow-weighted composite |
| 27-hr flow-weighted composite |
| 26-hr flow-weighted composite |
| 25-hr flow-weighted composite |
| 24-hr flow-weighted composite |
| 23-hr flow-weighted composite |
| 22-hr flow-weighted composite |
| 21-hr flow-weighted composite |
| 20-hr flow-weighted composite |
| 19-hr flow-weighted composite |
| 18-hr flow-weighted composite |
| 17-hr flow-weighted composite |
| 16-hr flow-weighted composite |
| 15-hr flow-weighted composite |
| 14-hr flow-weighted composite |
| 13-hr flow-weighted composite |
| 12-hr flow-weighted composite |
| 11-hr flow-weighted composite |
| 10-hr flow-weighted composite |
| 9-hr flow-weighted composite |
| 8-hr flow-weighted composite |
| 7-hr flow-weighted composite |
| 6-hr flow-weighted composite |
| 5-hr flow-weighted composite |
| 4-hr flow-weighted composite |
| 3-hr flow-weighted composite |
| 2-hr flow-weighted composite |
| 1-hr flow-weighted composite |
| 48-hr time-weighted composite |
| 47-hr time-weighted composite |
| 46-hr time-weighted composite |
| 45-hr time-weighted composite |
| 44-hr time-weighted composite |
| 43-hr time-weighted composite |
| 42-hr time-weighted composite |
| 41-hr time-weighted composite |
| 40-hr time-weighted composite |
| 39-hr time-weighted composite |
| 38-hr time-weighted composite |
| 37-hr time-weighted composite |
| 36-hr time-weighted composite |
| 35-hr time-weighted composite |
| 34-hr time-weighted composite |
| 33-hr time-weighted composite |
| 32-hr time-weighted composite |
| 31-hr time-weighted composite |
| 30-hr time-weighted composite |
| 29-hr time-weighted composite |
| 28-hr time-weighted composite |
| 27-hr time-weighted composite |
| 26-hr time-weighted composite |
| 25-hr time-weighted composite |
| 24-hr time-weighted composite |
| 23-hr time-weighted composite |
| 22-hr time-weighted composite |
| 21-hr time-weighted composite |
| 20-hr time-weighted composite |
| 19-hr time-weighted composite |
| 18-hr time-weighted composite |
| 17-hr time-weighted composite |
| 16-hr time-weighted composite |
| 15-hr time-weighted composite |
| 14-hr time-weighted composite |
| 13-hr time-weighted composite |
| 12-hr time-weighted composite |
| 11-hr time-weighted composite |
| 10-hr time-weighted composite |
| 9-hr time-weighted composite |
| 8-hr time-weighted composite |
| 7-hr time-weighted composite |
| 6-hr time-weighted composite |
| 5-hr time-weighted composite |
| 4-hr time-weighted composite |
| 3-hr time-weighted composite |
| 2-hr time-weighted composite |
| 1-hr time-weighted composite |
| 48-hr manual composite |
| 47-hr manual composite |
| 46-hr manual composite |
| 45-hr manual composite |
| 44-hr manual composite |
| 43-hr manual composite |
| 42-hr manual composite |
| 41-hr manual composite |
| 40-hr manual composite |
| 39-hr manual composite |
| 38-hr manual composite |
| 37-hr manual composite |
| 36-hr manual composite |
| 35-hr manual composite |
| 34-hr manual composite |
| 33-hr manual composite |
| 32-hr manual composite |
| 31-hr manual composite |
| 30-hr manual composite |
| 29-hr manual composite |
| 28-hr manual composite |
| 27-hr manual composite |
| 26-hr manual composite |
| 25-hr manual composite |
| 24-hr manual composite |
| 23-hr manual composite |
| 22-hr manual composite |
| 21-hr manual composite |
| 20-hr manual composite |
| 19-hr manual composite |
| 18-hr manual composite |
| 17-hr manual composite |
| 16-hr manual composite |
| 15-hr manual composite |
| 14-hr manual composite |
| 13-hr manual composite |
| 12-hr manual composite |
| 11-hr manual composite |
| 10-hr manual composite |
| 9-hr manual composite |
| 8-hr manual composite |
| 7-hr manual composite |
| 6-hr manual composite |
| 5-hr manual composite |
| 4-hr manual composite |
| 3-hr manual composite |
| 2-hr manual composite |
| 1-hr manual composite |

**sample\_matrix**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| raw wastewater | Wastewater without any form of treatment applied to it |
| post grit removal | Wastewater after removal of large solids at a treatment plant but prior to a primary clarifier |
| primary sludge | Sludge from the primary clarifier |
| primary effluent | Effluent from the primary clarifier |
| secondary sludge | Sludge from the secondary clarifier |
| secondary effluent | Efluent from the secondary clarifier |
| septage | Wastewater sampled from within a septic tank |
| holding tank | Wastewater sampled from a holding tank, such as from an airplane or ship |

**solids\_separation**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| filtration | Filtration to remove solids from a wastewater sample prior to further concentration or analysis of the liquid filtrate |
| centrifugation | Centrifugation prior to or in the absence of a concentration step; centrifugation as part of a flocculation or precipitation process, or part of a filtration-based concentration process, is considered part of a concentration method; centrifugation to dewater sludge samples is considered a solids separation process, not a concentration process |
| gravity settling | Solids separated from liquid by allowing solids to settle by gravity |
| none |  |
| [empty] |  |

**concentration\_method**

|  |
| --- |
| **Value Set** |
| membrane filtration with addition of mgcl2 |
| membrane filtration with sample acidification |
| membrane filtration with acidification and mgcl2 |
| membrane filtration with no amendment |
| membrane filtration with addition of mgcl2, membrane recombined with separated solids |
| membrane filtration with sample acidification, membrane recombined with separated solids |
| membrane filtration with acidification and mgcl2, membrane recombined with separated solids |
| membrane filtration with no amendment, membrane recombined with separated solids |
| peg precipitation |
| aloh3 precipitation |
| ultracentrifugation |
| skimmed milk flocculation |
| beef extract flocculation |
| promega wastewater large volume tna capture kit |
| centricon ultrafiltration |
| amicon ultrafiltration |
| hollow fiber dead end ultrafiltration |
| innovaprep ultrafiltration |
| no liquid concentration, liquid recombined with separated solids |
| ceres nanotrap |
| zymo environ water rna kit/ zymo environ water rna kit (cat. r2042) |
| none |

**extraction\_method**

|  |
| --- |
| **Value Set** |
| qiagen allprep powerviral dna/rna kit |
| qiagen allprep powerfecal dna/rna kit |
| qiagen allprep dna/rna kit |
| qiagen rneasy powermicrobiome kit |
| qiagen powerwater kit |
| qiagen rneasy kit |
| qiagen ez1 virus mini kit v2.0 |
| promega ht tna kit |
| promega automated tna kit |
| promega manual tna kit |
| promega wastewater large volume tna capture kit |
| nuclisens automated magnetic bead extraction kit |
| nuclisens manual magnetic bead extraction kit |
| phenol chloroform |
| chemagic viral dna/rna 300 kit |
| trizol, zymo mag beads w/ zymo clean and concentrator |
| 4s method (https://www.protocols.io/view/v-4-direct-wastewater-rna-capture-and-purification-bpdfmi3n) |
| qiagen qiaamp buffers with epoch columns |
| zymo quick-rna fungal/bacterial miniprep #r2014 |
| thermo magmax microbiome ultra nucleic acid isolation kit |
| zymo environ water rna kit/ zymo environ water rna kit (cat. r2042) |

**rec\_eff\_target\_name**

|  |
| --- |
| **Value Set** |
| bcov vaccine |
| bcov culture |
| brsv vaccine |
| brsv culture |
| murine coronavirus |
| oc43 |
| phi6 |
| puro |
| ms2 coliphage |
| hep g armored rna |
| heat inactivated sars-cov-2 virus |
| [empty] |

**rec\_eff\_spike\_matrix**

|  |
| --- |
| **Value Set** |
| raw sample |
| raw sample post pasteurization |
| clarified sample |
| sample concentrate |
| lysis buffer |
| dewatered solids |
| [empty] |

**pcr\_gene\_target**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| n1 | sars-cov-2 gene target |
| n2 | sars-cov-2 gene target |
| n3 | sars-cov-2 gene target |
| e\_sarbeco | sars-cov-2 gene target |
| n\_sarbeco | sars-cov-2 gene target |
| rdrp\_sarsr | sars-cov-2 gene target |
| niid\_2019-ncov\_n | sars-cov-2 gene target |
| rdrp gene / ncov\_ip2 | sars-cov-2 gene target |
| rdrp gene / ncov\_ip4 | sars-cov-2 gene target |
| taqpath n | sars-cov-2 gene target |
| taqpath s | sars-cov-2 gene target |
| orf1b | sars-cov-2 gene target |
| orf1ab | sars-cov-2 gene target |
| n1 and n2 combined | sars-cov-2 gene target; Detection of N1 and N2 targets was performed on a single fluorescence channel, such that distinct measurements for N1 and N2 do not exist |
| n | sars-cov-2 gene target |
| s | sars-cov-2 gene target |
| orf1a | sars-cov-2 gene target |
| ddcov\_n | sars-cov-2 gene target |
| ddcov\_e | sars-cov-2 gene target |
| ip2 and ip4 combined | sars-cov-2 gene target |
| a1306s | delta gene target |
| p2046l | delta gene target |
| p2287s | delta gene target |
| t3646a | delta gene target |
| v2930l | delta gene target |
| g662s | delta gene target |
| p100l | delta gene target |
| a1918v | delta gene target |
| t19r | delta gene target |
| e156g | delta gene target |
| del 157/158 | delta gene target |
| l452r | delta gene target |
| p681r | delta gene target |
| d950n | delta gene target |
| i82t | delta gene target |
| d63g | delta gene target |
| r203m | delta gene target |
| g215c | delta gene target |
| d377y | delta gene target |
| k856r | omicron gene target |
| s2083i | omicron gene target |
| del2084/2084 | omicron gene target |
| a2710t | omicron gene target |
| p3395h | omicron gene target |
| del3674/3676 | omicron gene target |
| i3758v | omicron gene target |
| i1566v | omicron gene target |
| a67v | omicron gene target |
| del69/70 | omicron gene target |
| del143/145 | omicron gene target |
| n211i | omicron gene target |
| del212/212 | omicron gene target |
| g339d | omicron gene target |
| s371l | omicron gene target |
| s373p | omicron gene target |
| s375f | omicron gene target |
| s477n | omicron gene target |
| e484a | omicron gene target |
| q493r | omicron gene target |
| g496s | omicron gene target |
| q498r | omicron gene target |
| y505h | omicron gene target |
| t547k | omicron gene target |
| n679k | omicron gene target |
| d796y | omicron gene target |
| n856k | omicron gene target |
| q954h | omicron gene target |
| n969k | omicron gene target |
| l981f | omicron gene target |
| t9i | omicron gene target |
| d3g | omicron gene target |
| q19e | omicron gene target |
| a63t | omicron gene target |

**other\_norm\_name**

|  |
| --- |
| **Value Set** |
| pepper mild mottle virus |
| crassphage |
| hf183 |
| f+ rna coliphage |
| f+ dna coliphage |
| caffeine |
| creatinine |
| sucralose |
| ibuprofen |
| rnase p |
| [empty] |

**pcr\_type**

|  |  |
| --- | --- |
| **Value Set** | **Description** |
| qpcr | Real-time PCR, also called 'quantitative' PCR |
| ddpcr | Used to refer specifically to BioRad digital droplet emulsification technology |
| qiagen dpcr |  |
| fluidigm dpcr |  |
| life technologies dpcr |  |
| raindance dpcr |  |