

## NCBI field

## NCBI description

sample\_name  
sample\_title

Sample Name is a name that you choose for the sample. It can have any format, but we suggest that you make it concise, unique and consistent within your lab, and as informative as possible. Every Sample Name from a single Submitter must be unique.

Title of the sample.

bioproject\_accession

The accession number of the BioProject(s) to which the BioSample belongs. If the BioSample belongs to more than one BioProject, enter multiple bioproject\_accession columns. A valid BioProject accession has prefix PRJN, PRJE or PRJD, e.g., PRJNA12345.

organism

The most descriptive organism name for this sample (to the species, if possible). It is OK to submit an organism name that is not in our database. In the case of a new species, provide the desired organism name, and our taxonomists may assign a provisional taxID. In the case of unidentified species, choose the appropriate Genus and include 'sp.', e.g., "Escherichia sp.". When sequencing a genome from a non-metagenomic source, include a strain or isolate name too, e.g., "Pseudomonas sp. UK4". For more information about providing a valid organism, including new species, metagenomes (microbiomes) and metagenome-assembled genomes, see <https://www.ncbi.nlm.nih.gov/biosample/docs/organism/>.

|                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|--------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| collection_date    | <p>The date on which the sample was collected; date/time ranges are supported by providing two dates from among the supported value formats, delimited by a forward-slash character; collection times are supported by adding "T", then the hour and minute after the date, and must be in Coordinated Universal Time (UTC), otherwise known as "Zulu Time" (Z); supported formats include "DD-Mmm-YYYY", "Mmm-YYYY", "YYYY" or ISO 8601 standard "YYYY-mm-dd", "YYYY-mm", "YYYY-mm-ddThh:mm:ss"; e.g., 30-Oct-1990, Oct-1990, 1990, 1990-10-30, 1990-10, 21-Oct-1952/15-Feb-1953, 2015-10-11T17:53:03Z; valid non-ISO dates will be automatically transformed to ISO format</p> |
| geo_loc_name       | <p>Geographical origin of the sample; use the appropriate name from this list <a href="http://www.insdc.org/documents/country-qualifier-vocabulary">http://www.insdc.org/documents/country-qualifier-vocabulary</a>. Use a colon to separate the country or ocean from more detailed information about the location, eg "Canada: Vancouver" or "Germany: halfway down Zugspitze, Alps"</p>                                                                                                                                                                                                                                                                                       |
| isolation_source   | <p>Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| ww_population      | <p>Number of persons contributing wastewater to this sample collection site; if unknown, estimate to the nearest order of magnitude, e.g., 10000. If no estimate is available, input NA.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| ww_sample_duration | <p>Duration of composite sample collected, in units of hours, e.g., 24. Specify integer values. If the sample is not a composite sample, use 0.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ww_sample_matrix   | <p>The wastewater matrix that was sampled</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| ww_sample_type     | <p>Type of wastewater sample collected</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| ww_surv_target_1   | <p>Taxonomic name of the surveillance target. For the COVID-19 response, use 'SARS-CoV-2'.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

|                                |                                                                                                                                                                                                                                                              |
|--------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ww_surv_target_1_known_present | Is genetic material of the surveillance target(s) known to the submitter to be present in this wastewater sample? Presence defined as microbiological evidence of the target organism in the wastewater sample, such as genetic- or culture-based detection. |
| collected_by                   | Name of persons or institute who collected the sample                                                                                                                                                                                                        |
| purpose_of_ww_sampling         | The reason the sample was collected                                                                                                                                                                                                                          |
| purpose_of_ww_sequencing       | The reason the sample was sequenced, e.g., identification of mutations within a specific region, presence of clinically known mutations, or diversity of mutations across entire genome                                                                      |
| sequenced_by                   | The name of the agency that generated the sequence, e.g., Centers for Disease Control and Prevention                                                                                                                                                         |
| ww_endog_control_1             | The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., pepper mild mottle virus                                                                                                                                          |
| ww_endog_control_1_conc        | The concentration of the endogenous control specified in 'ww_endog_control_1' on a per wastewater unit basis, e.g., 700000000                                                                                                                                |
| ww_endog_control_1_protocol    | The protocol used to quantify 'ww_endog_control_1'. Specify a reference, website, or brief description.                                                                                                                                                      |
| ww_endog_control_1_units       | The units of the value specified in 'ww_endog_control_1_conc', e.g., copies/L wastewater                                                                                                                                                                     |
| ww_endog_control_2             | The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., crassphage                                                                                                                                                        |
| ww_endog_control_2_conc        | The concentration of the endogenous control specified in 'ww_endog_control_2' on a per wastewater unit basis, e.g., 140000000                                                                                                                                |
| ww_endog_control_2_protocol    | The protocol used to quantify 'ww_endog_control_2'. Specify a reference, website, or brief description.                                                                                                                                                      |
| ww_endog_control_2_units       | The units of the value specified in 'ww_endog_control_2_conc', e.g., copies/L wastewater                                                                                                                                                                     |

|                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|----------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ww_flow                          | Daily volumetric flow through collection site, in units of liters per day, e.g., 110000000.                                                                                                                                                                                                                                                                                                                                                |
| ww_industrial_effluent_percent   | Percentage of industrial effluents received by wastewater treatment plant, e.g., 10                                                                                                                                                                                                                                                                                                                                                        |
| ww_ph                            | pH measurement of the sample, or liquid portion of sample, or aqueous phase of the fluid, e.g., 7.2                                                                                                                                                                                                                                                                                                                                        |
| ww_population_source             | Source of value specified in 'ww_population', e.g., wastewater utility billing records, population of jurisdiction encompassing the wastewater service area, census blocks clipped to wastewater service area polygon                                                                                                                                                                                                                      |
| ww_pre_treatment                 | Describe any process of pre-treatment that removes materials that can be easily collected from the raw wastewater, e.g., flow equilibration basin promotes settling of some solids                                                                                                                                                                                                                                                         |
| ww_primary_sludge_retention_time | The time primary sludge remains in tank, in hours, e.g., 4.                                                                                                                                                                                                                                                                                                                                                                                |
| ww_processing_protocol           | The protocol used to process the wastewater sample. Processing includes laboratory procedures prior to and including nucleic acid purification (e.g., pasteurization, concentration, extraction, etc). Specify a reference, website, or brief description.                                                                                                                                                                                 |
| ww_sample_salinity               | Salinity is the total concentration of all dissolved salts in a liquid or solid (in the form of an extract obtained by centrifugation) sample or derived from the conductivity measurement (practical salinity) in milligrams per liter, e.g., 100.                                                                                                                                                                                        |
| ww_sample_site                   | The type of site where the wastewater sample was collected<br>Allowed values: correctional facility, long-term care facility, hospital, child day care, school, college or university, social services shelter, other residential building, ship, airplane, septic tank, other holding tank, wastewater treatment plant, wastewater lagoon, sewer pipeline, other, restricted access, not applicable, not collected, not provided, missing |

|                               |                                                                                                                                                                                     |
|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ww_surv_jurisdiction          | A jurisdiction identifier that can be used to support linking the sample to a public health surveillance system, e.g., va                                                           |
| ww_surv_system_sample_id      | The sample ID used for submission to a public health surveillance system (e.g., CDC's National Wastewater Surveillance System), e.g., s123456                                       |
| ww_surv_target_1_conc         | The concentration of the wastewater surveillance target specified in 'ww_surv_target_1' on a per wastewater unit basis, e.g., 200000                                                |
| ww_surv_target_1_conc_unit    | The units of the value specified in 'ww_surv_target_1_conc', e.g., copies/L wastewater                                                                                              |
| ww_surv_target_1_extract      | Measured amount of surveillance target in the nucleic acid extract that was sequenced; on a per extract unit basis, rather than on a per wastewater sample unit basis, e.g., 100000 |
| ww_surv_target_1_extract_unit | The units of the value specified in 'ww_surv_target_1_extract', e.g., copies/microliter extract                                                                                     |
| ww_surv_target_1_gene         | The name of the gene quantified for the the surveillance target specified in 'ww_surv_target_1', e.g., N gene                                                                       |
| ww_surv_target_1_protocol     | The protocol used to quantify 'ww_surv_target_1'. Specify a reference, website, or brief description.                                                                               |
| ww_surv_target_2              | Taxonomic name of the surveillance target, eg, Norovirus                                                                                                                            |
| ww_surv_target_2_conc         | The concentration of the wastewater surveillance target specified in 'ww_surv_target_2' on a per wastewater unit basis, e.g., 24000                                                 |
| ww_surv_target_2_conc_unit    | The units of the value specified in 'ww_surv_target_2_conc', e.g., copies/L wastewater                                                                                              |
| ww_surv_target_2_extract      | Measured amount of surveillance target in the nucleic acid extract that was sequenced; on a per extract unit basis, rather than on a per wastewater sample unit basis, e.g., 12000  |

|                                          |                                                                                                                                                                                                                                                              |
|------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ww_surv_target_2_extract_unit            | The units of the value specified in 'ww_surv_target_2_extract', e.g., copies/microliter extract                                                                                                                                                              |
| ww_surv_target_2_gene                    | The name of the gene quantified for the the surveillance target specified in 'ww_surv_target_2', e.g., ORF1-ORF2 junction                                                                                                                                    |
| ww_surv_target_2_known_present           | Is genetic material of the surveillance target(s) known to the submitter to be present in this wastewater sample? Presence defined as microbiological evidence of the target organism in the wastewater sample, such as genetic- or culture-based detection. |
| ww_surv_target_2_protocol                | The protocol used to quantify 'ww_surv_target_2'. Specify a reference, website, or brief description.                                                                                                                                                        |
| ww_temperature                           | Temperature of the wastewater sample at the time of sampling in Celsius, e.g., 25.                                                                                                                                                                           |
| ww_total_suspended_solids<br>description | Total concentration of solids in raw wastewater influent sample including a wide variety of material, such as silt, decaying plant and animal matter in milligrams per liter, e.g., 500.<br>Description of the sample.                                       |

**NWSS field**

sample\_collect\_date

wwtp\_jurisdiction;  
county\_names;  
zipcode

sample\_location

population\_served

composite\_freq  
sample\_matrix  
sample\_type

pcr\_target



hum\_frac\_target\_mic;  
hum\_frac\_target\_chem;  
other\_norm\_name

hum\_frac\_mic\_conc;  
hum\_frac\_chem\_conc;  
other\_norm\_conc

hum\_frac\_target\_mic\_ref;  
hum\_frac\_target\_chem\_ref;  
other\_norm\_ref

hum\_frac\_mic\_unit;  
hum\_frac\_chem\_unit;  
other\_norm\_unit

hum\_frac\_target\_mic;  
hum\_frac\_target\_chem;  
other\_norm\_name

hum\_frac\_mic\_conc;  
hum\_frac\_chem\_conc;  
other\_norm\_conc

hum\_frac\_target\_mic\_ref;  
hum\_frac\_target\_chem\_ref;  
other\_norm\_ref

hum\_frac\_mic\_unit;  
hum\_frac\_chem\_unit;  
other\_norm\_unit

flow\_rate

industrial\_input

ph

if pretreatment == 'yes' then  
pretreatment\_specify

solids\_separation;  
concentration\_method;  
extraction\_method;  
pasteurized

derived from conductivity

institution\_type

wwtp\_jurisdiction

sample\_id

pcr\_target\_avg\_conc

pcr\_target\_units

pcr\_gene\_target

quant\_stan\_type;  
stan\_ref;  
inhibition\_method;  
num\_no\_target\_control;  
pcr\_gene\_target\_ref;  
pcr\_type

pcr\_target

pcr\_target\_avg\_conc

pcr\_target\_units

pcr\_gene\_target

quant\_stan\_type;  
stan\_ref;  
inhibition\_method;  
num\_no\_target\_control;  
pcr\_gene\_target\_ref;  
pcr\_type

collection\_water\_temp

tss

| NCBI field                  | NCBI description                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | NCBI required |
|-----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|
| sample_name<br>sample_title | <p>Sample Name is a name that you choose for the sample. It can have any format, but we suggest that you make it concise, unique and consistent within your lab, and as informative as possible. Every Sample Name from a single Submitter must be unique.</p> <p>Title of the sample.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Yes<br>No     |
| bioproject_accession        | <p>The accession number of the BioProject(s) to which the BioSample belongs. If the BioSample belongs to more than one BioProject, enter multiple bioproject_accession columns. A valid BioProject accession has prefix PRJN, PRJE or PRJD, e.g., PRJNA12345.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | No            |
| organism                    | <p>The most descriptive organism name for this sample (to the species, if possible). It is OK to submit an organism name that is not in our database. In the case of a new species, provide the desired organism name, and our taxonomists may assign a provisional taxID. In the case of unidentified species, choose the appropriate Genus and include 'sp.', e.g., "Escherichia sp.". When sequencing a genome from a non-metagenomic source, include a strain or isolate name too, e.g., "Pseudomonas sp. UK4". For more information about providing a valid organism, including new species, metagenomes (microbiomes) and metagenome-assembled genomes, see <a href="https://www.ncbi.nlm.nih.gov/biosample/docs/organism/">https://www.ncbi.nlm.nih.gov/biosample/docs/organism/</a>.</p> | Yes           |

|                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |     |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| collection_date    | The date on which the sample was collected; date/time ranges are supported by providing two dates from among the supported value formats, delimited by a forward-slash character; collection times are supported by adding "T", then the hour and minute after the date, and must be in Coordinated Universal Time (UTC), otherwise known as "Zulu Time" (Z); supported formats include "DD-Mmm-YYYY", "Mmm-YYYY", "YYYY" or ISO 8601 standard "YYYY-mm-dd", "YYYY-mm", "YYYY-mm-ddThh:mm:ss"; e.g., 30-Oct-1990, Oct-1990, 1990, 1990-10-30, 1990-10, 21-Oct-1952/15-Feb-1953, 2015-10-11T17:53:03Z; valid non-ISO dates will be automatically transformed to ISO format | Yes |
| geo_loc_name       | Geographical origin of the sample; use the appropriate name from this list <a href="http://www.insdc.org/documents/country-qualifier-vocabulary">http://www.insdc.org/documents/country-qualifier-vocabulary</a> . Use a colon to separate the country or ocean from more detailed information about the location, eg "Canada: Vancouver" or "Germany: halfway down Zugspitze, Alps"                                                                                                                                                                                                                                                                                      | Yes |
| isolation_source   | Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Yes |
| ww_population      | Number of persons contributing wastewater to this sample collection site; if unknown, estimate to the nearest order of magnitude, e.g., 10000. If no estimate is available, input NA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Yes |
| ww_sample_duration | Duration of composite sample collected, in units of hours, e.g., 24. Specify integer values. If the sample is not a composite sample, use 0.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Yes |

|                                |                                                                                                                                                                                                                                                              |     |
|--------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| ww_sample_matrix               | The wastewater matrix that was sampled                                                                                                                                                                                                                       | Yes |
| ww_sample_type                 | Type of wastewater sample collected                                                                                                                                                                                                                          | Yes |
| ww_surv_target_1               | Taxonomic name of the surveillance target. For the COVID-19 response, use 'SARS-CoV-2'.                                                                                                                                                                      | Yes |
| ww_surv_target_1_known_present | Is genetic material of the surveillance target(s) known to the submitter to be present in this wastewater sample? Presence defined as microbiological evidence of the target organism in the wastewater sample, such as genetic- or culture-based detection. | Yes |
| collected_by                   | Name of persons or institute who collected the sample                                                                                                                                                                                                        | No  |
| purpose_of_ww_sampling         | The reason the sample was collected                                                                                                                                                                                                                          | No  |
| purpose_of_ww_sequencing       | The reason the sample was sequenced, e.g., identification of mutations within a specific region, presence of clinically known mutations, or diversity of mutations across entire genome                                                                      | No  |
| sequenced_by                   | The name of the agency that generated the sequence, e.g., Centers for Disease Control and Prevention                                                                                                                                                         | No  |
| ww_endog_control_1             | The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., pepper mild mottle virus                                                                                                                                          | No  |
| ww_endog_control_1_conc        | The concentration of the endogenous control specified in 'ww_endog_control_1' on a per wastewater unit basis, e.g., 700000000                                                                                                                                | No  |

|                                  |                                                                                                                                                                                                                       |    |
|----------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| ww_endog_control_1_protocol      | The protocol used to quantify 'ww_endog_control_1'. Specify a reference, website, or brief description.                                                                                                               | No |
| ww_endog_control_1_units         | The units of the value specified in 'ww_endog_control_1_conc', e.g., copies/L wastewater                                                                                                                              | No |
| ww_endog_control_2               | The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., crassphage                                                                                                                 | No |
| ww_endog_control_2_conc          | The concentration of the endogenous control specified in 'ww_endog_control_2' on a per wastewater unit basis, e.g., 140000000                                                                                         | No |
| ww_endog_control_2_protocol      | The protocol used to quantify 'ww_endog_control_2'. Specify a reference, website, or brief description.                                                                                                               | No |
| ww_endog_control_2_units         | The units of the value specified in 'ww_endog_control_2_conc', e.g., copies/L wastewater                                                                                                                              | No |
| ww_flow                          | Daily volumetric flow through collection site, in units of liters per day, e.g., 110000000.                                                                                                                           | No |
| ww_industrial_effluent_percent   | Percentage of industrial effluents received by wastewater treatment plant, e.g., 10                                                                                                                                   | No |
| ww_ph                            | pH measurement of the sample, or liquid portion of sample, or aqueous phase of the fluid, e.g., 7.2                                                                                                                   | No |
| ww_population_source             | Source of value specified in 'ww_population', e.g., wastewater utility billing records, population of jurisdiction encompassing the wastewater service area, census blocks clipped to wastewater service area polygon | No |
| ww_pre_treatment                 | Describe any process of pre-treatment that removes materials that can be easily collected from the raw wastewater, e.g., flow equilibration basin promotes settling of some solids                                    | No |
| ww_primary_sludge_retention_time | The time primary sludge remains in tank, in hours, e.g., 4.                                                                                                                                                           | No |



|                            |                                                                                                                                                                                                                                                                                                                                                                                                                                            |    |
|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| ww_processing_protocol     | The protocol used to process the wastewater sample. Processing includes laboratory procedures prior to and including nucleic acid purification (e.g., pasteurization, concentration, extraction, etc). Specify a reference, website, or brief description.                                                                                                                                                                                 | No |
| ww_sample_salinity         | Salinity is the total concentration of all dissolved salts in a liquid or solid (in the form of an extract obtained by centrifugation) sample or derived from the conductivity measurement (practical salinity) in milligrams per liter, e.g., 100.                                                                                                                                                                                        | No |
| ww_sample_site             | The type of site where the wastewater sample was collected<br>Allowed values: correctional facility, long-term care facility, hospital, child day care, school, college or university, social services shelter, other residential building, ship, airplane, septic tank, other holding tank, wastewater treatment plant, wastewater lagoon, sewer pipeline, other, restricted access, not applicable, not collected, not provided, missing | No |
| ww_surv_jurisdiction       | A jurisdiction identifier that can be used to support linking the sample to a public health surveillance system, e.g., va                                                                                                                                                                                                                                                                                                                  | No |
| ww_surv_system_sample_id   | The sample ID used for submission to a public health surveillance system (e.g., CDC's National Wastewater Surveillance System), e.g., s123456                                                                                                                                                                                                                                                                                              | No |
| ww_surv_target_1_conc      | The concentration of the wastewater surveillance target specified in 'ww_surv_target_1' on a per wastewater unit basis, e.g., 200000                                                                                                                                                                                                                                                                                                       | No |
| ww_surv_target_1_conc_unit | The units of the value specified in 'ww_surv_target_1_conc', e.g., copies/L wastewater                                                                                                                                                                                                                                                                                                                                                     | No |
| ww_surv_target_1_extract   | Measured amount of surveillance target in the nucleic acid extract that was sequenced; on a per extract unit basis, rather than on a per wastewater sample unit basis, e.g., 100000                                                                                                                                                                                                                                                        | No |

|                                |                                                                                                                                                                                                                                                              |    |
|--------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| ww_surv_target_1_extract_unit  | The units of the value specified in 'ww_surv_target_1_extract', e.g., copies/microliter extract                                                                                                                                                              | No |
| ww_surv_target_1_gene          | The name of the gene quantified for the the surveillance target specified in 'ww_surv_target_1', e.g., N gene                                                                                                                                                | No |
| ww_surv_target_1_protocol      | The protocol used to quantify 'ww_surv_target_1'. Specify a reference, website, or brief description.                                                                                                                                                        | No |
| ww_surv_target_2               | Taxonomic name of the surveillance target, eg, Norovirus                                                                                                                                                                                                     | No |
| ww_surv_target_2_conc          | The concentration of the wastewater surveillance target specified in 'ww_surv_target_2' on a per wastewater unit basis, e.g., 24000                                                                                                                          | No |
| ww_surv_target_2_conc_unit     | The units of the value specified in 'ww_surv_target_2_conc', e.g., copies/L wastewater                                                                                                                                                                       | No |
| ww_surv_target_2_extract       | Measured amount of surveillance target in the nucleic acid extract that was sequenced; on a per extract unit basis, rather than on a per wastewater sample unit basis, e.g., 12000                                                                           | No |
| ww_surv_target_2_extract_unit  | The units of the value specified in 'ww_surv_target_2_extract', e.g., copies/microliter extract                                                                                                                                                              | No |
| ww_surv_target_2_gene          | The name of the gene quantified for the the surveillance target specified in 'ww_surv_target_2', e.g., ORF1-ORF2 junction                                                                                                                                    | No |
| ww_surv_target_2_known_present | Is genetic material of the surveillance target(s) known to the submitter to be present in this wastewater sample? Presence defined as microbiological evidence of the target organism in the wastewater sample, such as genetic- or culture-based detection. | No |
| ww_surv_target_2_protocol      | The protocol used to quantify 'ww_surv_target_2'. Specify a reference, website, or brief description.                                                                                                                                                        | No |
| ww_temperature                 | Temperature of the wastewater sample at the time of sampling in Celsius, e.g., 25.                                                                                                                                                                           | No |

|                                          |                                                                                                                                                                                                                                 |          |
|------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|
| ww_total_suspended_solids<br>description | Total concentration of solids in raw wastewater<br>influent sample including a wide variety of<br>material, such as silt, decaying plant and animal<br>matter in milligrams per liter, e.g., 500.<br>Description of the sample. | No<br>No |
|------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------|

## Notes

If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

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If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

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If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

If information is unavailable for any mandatory field, please enter 'not collected', 'not applicable' or 'missing' as appropriate.

| NWSS field              | NWSS description                                                                                                                                                                                                                                                                                                                                                                  | NWSS required |
|-------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|
| reporting_jurisdiction  | The CDC Epidemiology and Laboratory Capacity (ELC) jurisdiction, most frequently a state, reporting these data (2-letter abbreviation)                                                                                                                                                                                                                                            | Yes           |
| county_names            | 5-digit numeric FIPS codes of all counties and county equivalents served by this sampling site (i.e., served by this wastewater treatment plant or, if 'sample_location' is "upstream", then by this upstream location). Note that most jurisdictions are covered by counties, but some are covered by county equivalents, such as independent cities, parishes, or census areas. | Yes           |
| other_jurisdiction      | This field has been deprecated. Specify FIPS codes for counties and county equivalents in 'county_names'.                                                                                                                                                                                                                                                                         | No            |
| zipcode                 | ZIP code in which this sampling site is located                                                                                                                                                                                                                                                                                                                                   | Yes           |
| population_served       | Estimated number of persons served by this sampling site (i.e., served by this wastewater treatment plant or, if 'sample_location' is "upstream", then by this upstream location)                                                                                                                                                                                                 | Yes           |
| sewage_travel_time      | What is the approximate sewage travel time, on average, from sewage source to this sampling site (i.e., this wastewater treatment plant or, if 'sample_location' is "upstream", then this upstream location)? This should be specified as a duration in hours, not a time of day.                                                                                                 | No            |
| 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                                                                                                                                                              | Yes           |
| 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.                                                                                                                                                                                                         | Yes           |

|                       |                                                                                                                                                                                                                                                                                                                                                                                     |     |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| institution_type      | If this sample represents wastewater from a single institution, facility, or building, specify the institution type; otherwise, specify "not institution specific"                                                                                                                                                                                                                  | Yes |
| epaid                 | NPDES permit number for the wastewater treatment plant specified in 'wwtp_name'                                                                                                                                                                                                                                                                                                     | No  |
| 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.                                                                     | Yes |
| wwtp_jurisdiction     | State, DC, US territory, or Freely Associated State jurisdiction name (2-letter abbreviation) in which the wastewater treatment plant provided in 'wwtp_name' is located                                                                                                                                                                                                            | Yes |
| capacity_mgd          | Wastewater treatment plant design capacity. This should be the capacity for which the plant is permitted.                                                                                                                                                                                                                                                                           | Yes |
| industrial_input      | Approximate average percentage of wastewater from industrial sources that is received by the wastewater treatment plant specified in 'wwtp_name'                                                                                                                                                                                                                                    | No  |
| 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)?                                                                                                                                                                                                              | No  |
| 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?                                                                                                                                                                                                                            | No  |
| 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. | Yes |



|                         |                                                                                                                                                                                                                                                                                                                                       |     |
|-------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| 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 | No  |
| sample_matrix           | Wastewater matrix from which the sample was collected                                                                                                                                                                                                                                                                                 | Yes |
| collection_storage_time | Duration of time the sample was stored after collection and prior to reaching the lab                                                                                                                                                                                                                                                 | No  |
| collection_storage_temp | Temperature at which the sample was stored after collection and prior to reaching the lab                                                                                                                                                                                                                                             | No  |
| 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.          | No  |
| pretreatment_specify    | If 'pretreatment' is "yes", then specify the chemicals used                                                                                                                                                                                                                                                                           | No  |
| 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'                                                                                                                                                                     | No  |
| concentration_method    | Method used to concentrate the sample prior to analysis of the concentrate                                                                                                                                                                                                                                                            | Yes |
| extraction_method       | Method used for nucleic acid extraction from the sample                                                                                                                                                                                                                                                                               | Yes |
| pre_conc_storage_time   | The approximate average duration of time between when samples reach the lab and when they are concentrated (if concentrated)                                                                                                                                                                                                          | No  |
| pre_conc_storage_temp   | The storage temperature of samples after reaching the lab and prior to concentration (if concentrated)                                                                                                                                                                                                                                | No  |

|                      |                                                                                                                                                                               |     |
|----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| pre_ext_storage_time | The approximate average duration of time between when samples are concentrated (if concentrated) and when they are extracted                                                  | No  |
| pre_ext_storage_temp | The storage temperature of samples after concentration (if concentrated) and prior to extraction                                                                              | No  |
| 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' | No  |
| ext_blank            | Are extraction blanks included in the extraction process?                                                                                                                     | No  |
| rec_eff_target_name  | Name of the recovery efficiency control target that is spiked in                                                                                                              | Yes |
| rec_eff_spike_matrix | Matrix into which the recovery efficiency control target is spiked                                                                                                            | Yes |
| rec_eff_spike_conc   | Spike concentration, on average, of the recovery control on a per sample volume basis                                                                                         | Yes |
| pasteurized          | Was the sample pasteurized?                                                                                                                                                   | No  |
| pcr_target           | The target of the PCR quantification                                                                                                                                          | Yes |
| pcr_gene_target      | The PCR gene used to quantify PCR target                                                                                                                                      | Yes |
| pcr_gene_target_ref  | A publication, website, or brief description of the PCR gene target used                                                                                                      | Yes |
| pcr_type             | The type of PCR used to quantify the PCR target                                                                                                                               | Yes |
| lod_ref              | A publication, website, or brief description of the method used to calculate the limit of detection                                                                           | Yes |
| hum_frac_target_mic  | Name of microbial target used to estimate human fecal content                                                                                                                 | No  |

|                          |                                                                                                                                          |     |
|--------------------------|------------------------------------------------------------------------------------------------------------------------------------------|-----|
| hum_frac_target_mic_ref  | A publication, website, or brief description of the microbial target specified in 'hum_frac_target_mic'                                  | No  |
| hum_frac_target_chem     | Name of chemical compound used to estimate human fecal content                                                                           | No  |
| hum_frac_target_chem_ref | A publication, website, or brief description of the chemical compound specified in 'hum_frac_target_chem'                                | No  |
| 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       | No  |
| other_norm_ref           | A publication, website, or brief description of the target or compound specified in 'other_norm_name'                                    | No  |
| quant_stan_type          | The type of nucleic acid used as a standard for the PCR target quantification                                                            | Yes |
| stan_ref                 | A publication, website, or brief description of the quantitative standard material used                                                  | Yes |
| inhibition_method        | A publication, website, or brief description of the method used to evaluate molecular inhibition                                         | Yes |
| num_no_target_control    | Number of no-template controls (NTC) per instrument run                                                                                  | Yes |
| sample_collect_date      | The date of sample collection; for composite samples, specify the date on which sample collection began                                  | Yes |
| sample_collect_time      | The local time of sample collection; for composite samples, specify the time at which sample collection began                            | Yes |
| time_zone                | Current local time zone corresponding to the time specified in 'sample_collect_time', represented as a UTC time offset (e.g., UTC-06:00) | No  |

|                       |                                                                                                                                                                                                                                                                                                                                                                   |     |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| 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.                                                                                                                    | Yes |
| ph                    | pH of wastewater sample (if sludge, pH of influent at time of collection)                                                                                                                                                                                                                                                                                         | No  |
| conductivity          | Specific conductivity of wastewater sample (if sludge, conductivity of influent at time of collection)                                                                                                                                                                                                                                                            | No  |
| tss                   | Total suspended solids of raw (or, if unavailable, post-grit removal) wastewater                                                                                                                                                                                                                                                                                  | No  |
| collection_water_temp | Sample temperature at time of collection                                                                                                                                                                                                                                                                                                                          | No  |
| equiv_sewage_amt      | Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction                                                                                                                                                                                                                                                                                  | No  |
| sample_id             | An ID assigned to a wastewater sample. 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. | Yes |
| lab_id                | An ID assigned to a testing lab. 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.                                              | Yes |

|           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |    |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| qc_ignore | <p>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. This field only affects whether samples are shown in the QC report, not how they are otherwise processed or analyzed. If the value is "yes", then this sample will be excluded from the QC report. If the value is "no" or [empty], then this sample will be included in the QC report for up to 90 days. Samples will only be included in the QC report for up to 90 days, regardless of the value specified in 'qc_ignore'.</p> | No |
|-----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|

|                  |                                                                                                                                                                                                                                                                                                                                                                    |    |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| dashboard_ignore | <p>Should the DCIPHER dashboard ignore this sample? If the value is "yes", then this sample will be excluded from the dashboard. If the value is "no" or [empty], then this sample will be included in the dashboard.</p> <p>In addition to excluding the sample from the DCIPHER dashboard, this field will also prevent the sample from public data release.</p> | No |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|

|                 |                                                                                                                                                                                                                                                                                                       |    |
|-----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|
| analysis_ignore | <p>Should DCIPHER data analysis ignore this sample? If the value is "yes", then this sample will be excluded from DCIPHER data analysis, which will also cause it to be excluded from the dashboard. If the value is "no" or [empty], then this sample will be included in DCIPHER data analysis.</p> | No |
|-----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|

|                  |                                                               |     |
|------------------|---------------------------------------------------------------|-----|
| test_result_date | <p>The date on which this PCR target measurement was made</p> | Yes |
|------------------|---------------------------------------------------------------|-----|

|                  |                                                 |     |
|------------------|-------------------------------------------------|-----|
| pcr_target_units | <p>Units of PCR target sample concentration</p> | Yes |
|------------------|-------------------------------------------------|-----|

|                     |                                                                                                                                                                                                                                                                                             |     |
|---------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| pcr_target_avg_conc | <p>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</p> | Yes |
|---------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|

|                      |                                                                                                                                                                                                                                                                                                                                                                                                                                               |     |
|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| 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 | No  |
| 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. Follow the same hierarchy as described for standard error. (Note: 'cl' stands for confidence limit)                                                                                                                                                                                                           | No  |
| 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. Follow the same hierarchy as described for standard error. (Note: 'cl' stands for confidence limit)                                                                                                                                                                                                           | No  |
| pcr_target_below_lod | Was the concentration of the PCR target below the limit of detection?                                                                                                                                                                                                                                                                                                                                                                         | No  |
| lod_sewage           | PCR target limit of detection back-calculated to unconcentrated sample basis                                                                                                                                                                                                                                                                                                                                                                  | Yes |
| 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?                                                                                                                                                                                                                                                  | Yes |
| rec_eff_percent      | Percent of spiked recovery control, specified in 'rec_eff_target_name', that was recovered                                                                                                                                                                                                                                                                                                                                                    | Yes |
| inhibition_detect    | Was molecular inhibition detected?                                                                                                                                                                                                                                                                                                                                                                                                            | Yes |
| inhibition_adjust    | Was inhibition incorporated into the PCR target concentration calculation?                                                                                                                                                                                                                                                                                                                                                                    | Yes |

|                    |                                                                                                                                     |    |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------|----|
| hum_frac_mic_conc  | Concentration of microbial target specified in 'hum_frac_target_mic'; follow the same guidelines outlined for 'pcr_target_avg_conc' | No |
| hum_frac_mic_unit  | Concentration units of microbial target specified in 'hum_frac_target_mic'                                                          | No |
| hum_frac_chem_conc | Concentration of chemical target specified in 'hum_frac_target_chem'                                                                | No |
| hum_frac_chem_unit | Concentration units of chemical target specified in 'hum_frac_target_chem'                                                          | No |
| other_norm_conc    | Concentration of target specified in 'other_norm_name'                                                                              | No |
| other_norm_unit    | Concentration units of target specified in 'other_norm_name'                                                                        | No |
| quality_flag       | Does this observation have quality control issues?                                                                                  | No |

major\_lab\_method

A number used to distinguish major lab methods at the reporting jurisdiction level. Differences in lab methods may limit the comparability of PCR target concentrations. Reporting jurisdictions should use this field to indicate that lab methods are sufficiently different that caution should be used when comparing PCR target concentrations across them. These differences may result from any lab processing or quantification steps, including different PCR gene targets. Note that 'major\_lab\_method' may be the same for different laboratories if the reporting jurisdiction believes concentrations measured by those laboratories are comparable; conversely, 'major\_lab\_method' may be different for the same laboratory if changes made to the laboratory protocol rendered concentrations not comparable.

No

major\_lab\_method\_desc

Brief description of the basis for assigning a 'major\_lab\_method', e.g., "this lab uses a lab method distinct from other labs in this reporting jurisdiction", "this lab changed lab methods - new concentration method" or "lab method is same as other labs in this reporting jurisdiction but performance differs"

No



## Notes

If 'sample\_location' is  
"upstream", specify in  
'sample\_location\_specify'

If sample\_location is  
"upstream", then this must  
have a non-empty value

if 'pretreatment' is "yes", then  
specify in  
'pretreatment\_specify'

if 'pretreatment' is "yes", then  
specify in  
'pretreatment\_specify'

If 'rec\_eff\_percent' is equal to a value other than "-1", then this must have a non-empty value

If 'rec\_eff\_target\_name' has a non-empty value, then this must have a non-empty value

If 'rec\_eff\_target\_name' has a non-empty value, then this must have a non-empty value

The value selected for pcr\_gene\_target should align with the value selected for pcr\_target

If 'hum\_frac\_mic\_conc' has a non-empty value, then this must have a non-empty value

If 'hum\_frac\_mic\_conc' has a non-empty value, then this must have a non-empty value

If 'hum\_frac\_chem\_conc' has a non-empty value, then this must have a non-empty value

If 'hum\_frac\_chem\_conc' has a non-empty value, then this must have a non-empty value

If 'other\_norm\_conc' has a non-empty value, then this must have a non-empty value

If 'other\_norm\_conc' has a non-empty value, then this must have a non-empty value

If 'sars\_cov2\_units' is on a per volume wastewater basis (e.g., copies/l wastewater), then this must have a non-empty value (i.e., measurements of wastewater solids are permitted empty values for 'flow\_rate')

The units should relate to the  
PCR target indicated in  
pcr\_target

The concentration should  
relate to the PCR target  
indicated in pcr\_target

The standard error should relate to the PCR target indicated in pcr\_target

The lower bound of the 95% confidence interval should relate to the PCR target indicated in pcr\_target

The upper bound of the 95% confidence interval should relate to the PCR target indicated in pcr\_target

Whether the concentration was below the LOD should be based on the LOD of the PCR target indicated in lod\_sewage

The LOD should relate to the PCR target indicated in pcr\_target

If 'inhibition\_detect' is "yes", then this must have a non-empty value

If 'hum\_frac\_mic\_unit' has a non-empty value, then this must have a non-empty value

If 'hum\_frac\_mic\_conc' has a non-empty value, then this must have a non-empty value

If 'hum\_frac\_chem\_unit' has a non-empty value, then this must have a non-empty value

If 'hum\_frac\_chem\_conc' has a non-empty value, then this must have a non-empty value

If 'other\_norm\_unit' has a non-empty value, then this must have a non-empty value

If 'other\_norm\_conc' has a non-empty value, then this must have a non-empty value



| Field                  | Value Set Name            | Value Set Name: |
|------------------------|---------------------------|-----------------|
| concentration_method   | vs_concentration_method   |                 |
| extraction_method      | vs_extraction_method      |                 |
| hum_frac_target_chem   | vs_hum_frac_target_chem   |                 |
| hum_frac_target_mic    | vs_hum_frac_target_mic    |                 |
| institution_type       | vs_institution_type       |                 |
| sars_cov2_units        | vs_mic_chem_units         |                 |
| hum_frac_chem_unit     | vs_mic_chem_units_e       |                 |
| other_norm_units       | vs_mic_chem_units_e       |                 |
| hum_frac_mic_unit      | vs_mic_chem_units_e       |                 |
| num_no_target_control  | vs_num_no_target_control  |                 |
| other_norm_name        | vs_other_norm_name        |                 |
| pcr_target             | vs_pcr_target             |                 |
| pcr_gene_target        | vs_pcr_gene_target        |                 |
| pcr_type               | vs_pcr_type               |                 |
| quant_stan_type        | vs_quant_stan_type        |                 |
| rec_eff_spike_matrix   | vs_rec_eff_spike_matrix   |                 |
| rec_eff_target_name    | vs_rec_eff_target_name    |                 |
| reporting_jurisdiction | vs_reporting_jurisdiction |                 |
| sample_location        | vs_sample_location        |                 |
| sample_matrix          | vs_sample_matrix          |                 |
| sample_type            | vs_sample_type            |                 |
| solids_separation      | vs_solids_separation      |                 |
| wwtp_jurisdiction      | vs_wwtp_jurisdiction      |                 |
| sars_cov2_below_lod    | vs_yn                     |                 |
| ntc_amplify            | vs_yn                     |                 |
| stormwater_input       | vs_yn                     |                 |
| influent_equilibrated  | vs_yn                     |                 |
| pretreatment           | vs_yn                     |                 |
| ext_blank              | vs_yn                     |                 |
| pasteurized            | vs_yn                     |                 |
| inhibition_adjust      | vs_yn                     |                 |
| quality_flag           | vs_yn                     |                 |
| inhibition_detect      | vs_ynn                    |                 |

## vs\_concentration\_method

| Value Set                                                                        | Description |
|----------------------------------------------------------------------------------|-------------|
| 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 s |             |
| membrane filtration with sample acidification, membrane recombined with separate |             |
| membrane filtration with acidification and mgcl2, membrane recombined with separ |             |
| membrane filtration with no amendment, membrane recombined with separated sol    |             |
| 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                                                                             |             |

| <b>vs_extraction_method</b>                                                                                                                                                                                     |             | <b>vs_hum_frac_target_chem</b> |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------|--------------------------------|
| Value Set                                                                                                                                                                                                       | Description | Value Set                      |
| qiagen allprep powerviral dna/rna kit                                                                                                                                                                           |             | caffeine                       |
| qiagen allprep powerfecal dna/rna kit                                                                                                                                                                           |             | creatinine                     |
| qiagen allprep dna/rna kit                                                                                                                                                                                      |             | sucralose                      |
| qiagen rneasy powermicrobiome kit                                                                                                                                                                               |             | ibuprofen                      |
| qiagen powerwater kit                                                                                                                                                                                           |             | [empty]                        |
| 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 ( <a href="https://www.protocols.io/view/v-4-direct-wastewater-rna-capture-and-purification-bpdfmi3n">https://www.protocols.io/view/v-4-direct-wastewater-rna-capture-and-purification-bpdfmi3n</a> ) |             |                                |
| qiagen qiaamp buffers with epoch columns                                                                                                                                                                        |             |                                |
| zyzo quick-rna fungal/bacterial miniprep #r2014                                                                                                                                                                 |             |                                |
| thermo magmax microbiome ultra nucleic acid isolation kit                                                                                                                                                       |             |                                |
| zyzo environ water rna kit/ zyzo environ water rna kit (cat. r204)                                                                                                                                              |             |                                |

**vs\_hum\_frac\_target\_mic**

Description

Value Set

Description

---

pepper mild mottle virus

crassphage

hf183

f+ rna coliphage

f+ dna coliphage

[empty]

## **vs\_institution\_type**

Value Set

---

not institution specific

correctional

long term care - nursing home

long term care - assisted living

other long term care

short stay acute care hospital

long term acute care hospital

child day care

k12

higher ed dorm

higher ed other

social services shelter

other residential building

ship

airplane

other worksite

## Description

---

This sample does not represent wastewater from a single institution, facility, or building

A prison, penitentiary, penal facility, jail, detention unit, or other facility in which persons are incarcerated by government officials

A residential healthcare facility that provides 24-hour medical care. These are also called skilled nursing facilities. Generally licensed

A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. May be licensed

Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilities

Acute care hospitals that provide care for patients with average length of stay longer than 25 days. LTACH patients are often treated

A school serving students in the kindergarten to 12th grade range

Solely higher education dormitory buildings

Higher education buildings or facilities that do not include dorms or that include dorms and other buildings

Other type of social services shelter

Individual residential buildings or institutions not captured in other categories

Any commercial facility not captured in other commercial facility categories

## vs\_mic\_chem\_units

Value Set

---

copies/L wastewater

log10 copies/L wastewater

copies/g wet sludge

log10 copies/g wet sludge

copies/g dry sludge

log10 copies/g dry sludge

micrograms/L wastewater

log10 micrograms/L wastewater

micrograms/g wet sludge

log10 micrograms/g wet sludge

micrograms/g dry sludge

log10 micrograms/g dry sludge

## Description

---

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven



**vs\_mic\_chem\_units\_e**

Value Set

---

copies/L wastewater

log10 copies/L wastewater

copies/g wet sludge

log10 copies/g wet sludge

copies/g dry sludge

log10 copies/g dry sludge

micrograms/L wastewater

log10 micrograms/L wastew:

micrograms/g wet sludge

log10 micrograms/g wet sluc

micrograms/g dry sludge

log10 micrograms/g dry slud

[empty]

## Description

---

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

ater

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Wet sludge mass is based on the mass of sludge without drying the solids in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

Dry sludge mass is based on the mass of solids after drying in a drying oven

**vs\_num\_no\_target\_control**

| Value Set | Description |
|-----------|-------------|
|-----------|-------------|

|             |  |
|-------------|--|
| 0           |  |
| 1           |  |
| 2           |  |
| 3           |  |
| more than 3 |  |

**vs\_other\_norm\_name**

| Value Set | Description |
|-----------|-------------|
|-----------|-------------|

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

| <b>vs_pcr_target</b> |             | <b>vs_pcr_gene_target</b> |
|----------------------|-------------|---------------------------|
| Value Set            | Description | Value Set                 |
| sars-cov-2           |             | n1                        |
| delta                |             | n2                        |
| omicron              |             | n3                        |
|                      |             | e_sarbeco                 |
|                      |             | n_sarbeco                 |
|                      |             | rdrp_sarsr                |
|                      |             | niid_2019-ncov_n          |
|                      |             | rdrp gene / ncov_ip2      |
|                      |             | rdrp gene / ncov_ip4      |
|                      |             | taqpath n                 |
|                      |             | taqpath s                 |
|                      |             | orf1b                     |
|                      |             | orf1ab                    |
|                      |             | n1 and n2 combined        |
|                      |             | n                         |
|                      |             | s                         |
|                      |             | orf1a                     |
|                      |             | ddcov_n                   |
|                      |             | ddcov_e                   |
|                      |             | ip2 and ip4 combined      |
|                      |             | a1306s                    |
|                      |             | p2046l                    |
|                      |             | p2287s                    |
|                      |             | t3646a                    |
|                      |             | v2930l                    |
|                      |             | g662s                     |
|                      |             | p100l                     |
|                      |             | a1918v                    |
|                      |             | t19r                      |
|                      |             | e156g                     |
|                      |             | del 157/158               |
|                      |             | l452r                     |
|                      |             | p681r                     |
|                      |             | d950n                     |
|                      |             | i82t                      |
|                      |             | d63g                      |
|                      |             | r203m                     |
|                      |             | g215c                     |
|                      |             | d377y                     |
|                      |             | k856r                     |
|                      |             | s2083i                    |
|                      |             | del2084/2084              |
|                      |             | a2710t                    |

p3395h  
del3674/3676  
i3758v  
i1566v  
a67v  
del69/70  
del143/145  
n211i  
del212/212  
g339d  
s371l  
s373p  
s375f  
s477n  
e484a  
q493r  
g496s  
q498r  
y505h  
t547k  
n679k  
d796y  
n856k  
q954h  
n969k  
l981f  
t9i  
d3g  
q19e  
a63t

## Description

---

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target; Detection of N1 and N2 targets was performed on a single fluorescence channel, such that distinct me

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

sars-cov-2 gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

delta gene target

omicron gene target

omicron gene target

omicron gene target

omicron gene target



**vs\_pcr\_type**

Value Set

---

qpcr

ddpcr

qiagen dpcr

fluidigm dpcr

life technologies dpcr

raindance dpcr



## Description

---

Real-time PCR, also called 'quantitative' PCR

Used to refer specifically to BioRad digital droplet emulsification technology

**vs\_quant\_stan\_type**

| Value Set | Description |
|-----------|-------------|
|-----------|-------------|

|     |  |
|-----|--|
| dna |  |
|-----|--|

|     |  |
|-----|--|
| rna |  |
|-----|--|

**vs\_rec\_eff\_spike\_matrix**

| Value Set | Description |
|-----------|-------------|
|-----------|-------------|

|            |  |
|------------|--|
| raw sample |  |
|------------|--|

|                                |  |
|--------------------------------|--|
| raw sample post pasteurization |  |
|--------------------------------|--|

|                  |  |
|------------------|--|
| clarified sample |  |
|------------------|--|

|                    |  |
|--------------------|--|
| sample concentrate |  |
|--------------------|--|

|              |  |
|--------------|--|
| lysis buffer |  |
|--------------|--|

|                  |  |
|------------------|--|
| dewatered solids |  |
|------------------|--|

|         |  |
|---------|--|
| [empty] |  |
|---------|--|

| <b>vs_rec_eff_target_name</b>     |             | <b>vs_reporting_jurisdiction</b> |
|-----------------------------------|-------------|----------------------------------|
| Value Set                         | Description | Value Set                        |
| bcov vaccine                      |             | AL                               |
| bcov culture                      |             | AK                               |
| brsv vaccine                      |             | AS                               |
| brsv culture                      |             | AZ                               |
| murine coronavirus                |             | AR                               |
| oc43                              |             | CA                               |
| phi6                              |             | CI                               |
| puro                              |             | CO                               |
| ms2 coliphage                     |             | MP                               |
| hep g armored rna                 |             | CT                               |
| heat inactivated sars-cov-2 virus |             | DE                               |
| [empty]                           |             | DC                               |
|                                   |             | FM                               |
|                                   |             | FL                               |
|                                   |             | GA                               |
|                                   |             | GU                               |
|                                   |             | HI                               |
|                                   |             | HO                               |
|                                   |             | ID                               |
|                                   |             | IL                               |
|                                   |             | IN                               |
|                                   |             | IA                               |
|                                   |             | KS                               |
|                                   |             | KY                               |
|                                   |             | LC                               |
|                                   |             | LA                               |
|                                   |             | ME                               |
|                                   |             | MD                               |
|                                   |             | MA                               |
|                                   |             | MI                               |
|                                   |             | MN                               |
|                                   |             | MS                               |
|                                   |             | MO                               |
|                                   |             | MT                               |
|                                   |             | NE                               |
|                                   |             | NV                               |
|                                   |             | NH                               |
|                                   |             | NJ                               |
|                                   |             | NM                               |
|                                   |             | NY                               |
|                                   |             | NZ                               |
|                                   |             | NC                               |
|                                   |             | ND                               |

OH  
OK  
OR  
PA  
PH  
PR  
MH  
PW  
RI  
SC  
SD  
TN  
TX  
VI  
UT  
VT  
VA  
WA  
WV  
WI  
WY

| Description                              | vs_sample_location<br>Value Set |
|------------------------------------------|---------------------------------|
| Alabama                                  | wwtp                            |
| Alaska                                   | upstream                        |
| American Samoa                           |                                 |
| Arizona                                  |                                 |
| Arkansas                                 |                                 |
| California                               |                                 |
| Chicago, IL                              |                                 |
| Colorado                                 |                                 |
| Commonwealth of Northern Mariana Islands |                                 |
| Connecticut                              |                                 |
| Delaware                                 |                                 |
| District of Columbia                     |                                 |
| Federated States of Micronesia           |                                 |
| Florida                                  |                                 |
| Georgia                                  |                                 |
| Guam                                     |                                 |
| Hawaii                                   |                                 |
| Houston, TX                              |                                 |
| Idaho                                    |                                 |
| Illinois                                 |                                 |
| Indiana                                  |                                 |
| Iowa                                     |                                 |
| Kansas                                   |                                 |
| Kentucky                                 |                                 |
| Los Angeles County, CA                   |                                 |
| Louisiana                                |                                 |
| Maine                                    |                                 |
| Maryland                                 |                                 |
| Massachusetts                            |                                 |
| Michigan                                 |                                 |
| Minnesota                                |                                 |
| Mississippi                              |                                 |
| Missouri                                 |                                 |
| Montana                                  |                                 |
| Nebraska                                 |                                 |
| Nevada                                   |                                 |
| New Hampshire                            |                                 |
| New Jersey                               |                                 |
| New Mexico                               |                                 |
| New York                                 |                                 |
| New York City, NY                        |                                 |
| North Carolina                           |                                 |
| North Dakota                             |                                 |

Ohio  
Oklahoma  
Oregon  
Pennsylvania  
Philadelphia, PA  
Puerto Rico  
Republic of the Marshall Islands  
Republic of Palau  
Rhode Island  
South Carolina  
South Dakota  
Tennessee  
Texas  
U.S. Virgin Islands  
Utah  
Vermont  
Virginia  
Washington  
West Virginia  
Wisconsin  
Wyoming

Description

---

A sampling location at a wastewater treatment plant or other community-scale treatment infrastructure specified in 'wwtp\_n

A sampling location other than "wwtp"

**vs\_sample\_matrix**

Value Set

---

raw wastewater

post grit removal

primary sludge

primary effluent

secondary sludge

secondary effluent

septage

holding tank



## Description

---

Wastewater without any form of treatment applied to it

Wastewater after removal of large solids at a treatment plant but prior to a primary clarifier

Sludge from the primary clarifier

Effluent from the primary clarifier

Sludge from the secondary clarifier

Effluent from the secondary clarifier

Wastewater sampled from within a septic tank

Wastewater sampled from a holding tank, such as from an airplane or ship

## vs\_sample\_type

Value Set

---

grab

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  
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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  
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23-hr manual composite  
22-hr manual composite  
21-hr manual composite  
20-hr manual composite  
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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

Description

---

An individual sample collected without compositing or adding other samples

## **vs\_solids\_separation**

Value Set

---

filtration

centrifugation

gravity settling

none

[empty]

## Description

---

Filtration to remove solids from a wastewater sample prior to further concentration or analysis of the liquid filtrate

Centrifugation prior to or in the absence of a concentration step; centrifugation as part of a flocculation or precipitation process

Solids separated from liquid by allowing solids to settle by gravity



**vs\_wwtp\_jurisdiction**

| Value Set             | Description                              |
|-----------------------|------------------------------------------|
| AL                    | Alabama                                  |
| concentration proceAK | Alaska                                   |
| AS                    | American Samoa                           |
| AZ                    | Arizona                                  |
| AR                    | Arkansas                                 |
| CA                    | California                               |
| CO                    | Colorado                                 |
| MP                    | Commonwealth of Northern Mariana Islands |
| CT                    | Connecticut                              |
| DE                    | Delaware                                 |
| DC                    | District of Columbia                     |
| FM                    | Federated States of Micronesia           |
| FL                    | Florida                                  |
| GA                    | Georgia                                  |
| GU                    | Guam                                     |
| HI                    | Hawaii                                   |
| ID                    | Idaho                                    |
| IL                    | Illinois                                 |
| IN                    | Indiana                                  |
| IA                    | Iowa                                     |
| KS                    | Kansas                                   |
| KY                    | Kentucky                                 |
| LA                    | Louisiana                                |
| ME                    | Maine                                    |
| MD                    | Maryland                                 |
| MA                    | Massachusetts                            |
| MI                    | Michigan                                 |
| MN                    | Minnesota                                |
| MS                    | Mississippi                              |
| MO                    | Missouri                                 |
| MT                    | Montana                                  |
| NE                    | Nebraska                                 |
| NV                    | Nevada                                   |
| NH                    | New Hampshire                            |
| NJ                    | New Jersey                               |
| NM                    | New Mexico                               |
| NY                    | New York                                 |
| NC                    | North Carolina                           |
| ND                    | North Dakota                             |
| OH                    | Ohio                                     |
| OK                    | Oklahoma                                 |
| OR                    | Oregon                                   |
| PA                    | Pennsylvania                             |

|    |                                  |
|----|----------------------------------|
| PR | Puerto Rico                      |
| MH | Republic of the Marshall Islands |
| PW | Republic of Palau                |
| RI | Rhode Island                     |
| SC | South Carolina                   |
| SD | South Dakota                     |
| TN | Tennessee                        |
| TX | Texas                            |
| VI | U.S. Virgin Islands              |
| UT | Utah                             |
| VT | Vermont                          |
| VA | Virginia                         |
| WA | Washington                       |
| WV | West Virginia                    |
| WI | Wisconsin                        |
| WY | Wyoming                          |

**vs\_yn**

Value Set Description

yes

no

**vs\_yn**

Value Set Description

yes

no

[empty]

**vs\_ynn**

Value Set Description

yes

no

not tested