

**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	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
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"
isolation_source	Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived.
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.
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.
ww_sample_matrix	The wastewater matrix that was sampled
ww_sample_type	Type of wastewater sample collected
ww_surv_target_1	Taxonomic name of the surveillance target. For the COVID-19 response, use 'SARS-CoV-2'.

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 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 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. 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 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 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 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 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. Description of the sample.	No No
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## Notes

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

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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_yne	
influent_equilibrated	vs_yne	
pretreatment	vs_yne	
ext_blank	vs_yne	
pasteurized	vs_yne	
inhibition_adjust	vs_yne	
quality_flag	vs_yne	
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	
zyzo 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/ zymo 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 by the state.

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

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 in these facilities.

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 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  
39-hr time-weighted composite  
38-hr time-weighted composite  
37-hr time-weighted composite  
36-hr time-weighted composite  
35-hr time-weighted composite  
34-hr time-weighted composite  
33-hr time-weighted composite  
32-hr time-weighted composite  
31-hr time-weighted composite  
30-hr time-weighted composite  
29-hr time-weighted composite  
28-hr time-weighted composite  
27-hr time-weighted composite  
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24-hr time-weighted composite  
23-hr time-weighted composite  
22-hr time-weighted composite  
21-hr time-weighted composite  
20-hr time-weighted composite  
19-hr time-weighted composite  
18-hr time-weighted composite  
17-hr time-weighted composite  
16-hr time-weighted composite  
15-hr time-weighted composite  
14-hr time-weighted composite  
13-hr time-weighted composite  
12-hr time-weighted composite  
11-hr time-weighted composite  
10-hr time-weighted composite

9-hr time-weighted composite  
8-hr time-weighted composite  
7-hr time-weighted composite  
6-hr time-weighted composite  
5-hr time-weighted composite  
4-hr time-weighted composite  
3-hr time-weighted composite  
2-hr time-weighted composite  
1-hr time-weighted composite  
48-hr manual composite  
47-hr manual composite  
46-hr manual composite  
45-hr manual composite  
44-hr manual composite  
43-hr manual composite  
42-hr manual composite  
41-hr manual composite  
40-hr manual composite  
39-hr manual composite  
38-hr manual composite  
37-hr manual composite  
36-hr manual composite  
35-hr manual composite  
34-hr manual composite  
33-hr manual composite  
32-hr manual composite  
31-hr manual composite  
30-hr manual composite  
29-hr manual composite  
28-hr manual composite  
27-hr manual composite  
26-hr manual composite  
25-hr manual composite  
24-hr manual composite  
23-hr manual composite  
22-hr manual composite  
21-hr manual composite  
20-hr manual composite  
19-hr manual composite  
18-hr manual composite  
17-hr manual composite  
16-hr manual composite  
15-hr manual composite  
14-hr manual composite  
13-hr manual composite

12-hr manual composite  
11-hr manual composite  
10-hr manual composite  
9-hr manual composite  
8-hr manual composite  
7-hr manual composite  
6-hr manual composite  
5-hr manual composite  
4-hr manual composite  
3-hr manual composite  
2-hr manual composite  
1-hr manual composite

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