NCBI field	NCBI description
sample_name	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.
sample_title	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 http://www.insdc.org/documents/country-qualifier-vocabulary. 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 identifer 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	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	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 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.	Yes
sample_title	Title of the sample.	No
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.	No
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/.	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 http://www.insdc.org/documents/country-qualifier-vocabulary. 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 identifer 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	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.	No
description	Description of the sample.	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.

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.

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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	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’.	No
dashboard_ignore	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. In addition to excluding the sample from the DCIPHER dashboard, this field will also prevent the sample from public data release.	No
analysis_ignore	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.	No
test_result_date	The date on which this PCR target measurement was made	Yes
pcr_target_units	Units of PCR target sample concentration	Yes
pcr_target_avg_conc	Concentration of the PCR target back-calculated to unconcentrated sample basis; enter "0" if no amplification occurred, using the definition of amplification described in 'ntc_amplify'; otherwise, enter the estimated concentration; do not adjust for matrix recovery efficiency	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 spcified in 'other_norm_name'	No
other_norm_unit	Concentration units of target spcified 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	
zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)	
none	

vs_extraction_method

Value Set	Description
qiagen allprep powerviral dna/rna kit	
qiagen allprep powerfecal dna/rna kit	
qiagen allprep dna/rna kit	
qiagen rneasy powermicrobiome kit	
qiagen powerwater kit	
qiagen rneasy kit	
qiagen ez1 virus mini kit v2.0	
promega ht tna kit	
promega automated tna kit	
promega manual tna kit	
promega wastewater large volume tna capture kit	
nuclisens automated magnetic bead extraction kit	
nuclisens manual magnetic bead extraction kit	
phenol chloroform	
chemagic viral dna/rna 300 kit	
trizol, zymo mag beads w/ zymo clean and concentrator	
4s method (https://www.protocols.io/view/v-4-direct-wastewater-rna-capture-and-purification-bpdfmi3n)	
qiagen qiaamp buffers with epoch columns	
zymo quick-rna fungal/bacterial miniprep #r2014	
thermo magmax microbiome ultra nucleic acid isolation kit	
zymo environ water rna kit/ zymo environ water rna kit (cat. r204	

vs_hum_frac_target_chem

Value Set
caffeine
creatinine
sucralose
ibuprofen
[empty]

	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 offi
A residential healthcare facility that provides 24-medical care. These are also called skilled nursing facilities. Generally license
A residential facility that provides assistance with daily care but generally does not provide skilled nursing care. May be licens
Other residential facilities that provide daily and/or medical care, but are not defined as nursing home/skilled nursing facilitie
Acute care hospitals that provide care for patients with average length of stay longer than 25 days. LTACH patients are often t
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 wastewa
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]	

vs_pcr_target		**vs_pcr_gene_target**
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
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omicron gene target
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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]	

vs_rec_eff_target_name

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

vs_reporting_jurisdiction

Value Set
AL
AK
AS
AZ
AR
CA
CI
CO
MP
CT
DE
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

	vs_sample_location
Description	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
Efluent 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
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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
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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
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32-hr manual composite
31-hr manual composite
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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 proce
Solids separated from liquid by allowing solids to settle by gravity

vs_wwtp_jurisdiction

	Value Set	Description
	AL	Alabama
ncentration proce	AK	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_yne

Value Set	Description
yes	
no	
[empty]	

vs_ynn

Value Set	Description
yes	
no	
not tested	