

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.

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

organism

<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'. 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_1_known_present	Name of persons or institute who collected the sample
collected_by	The reason the sample was collected
purpose_of_ww_sampling	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
purpose_of_ww_sequencing	The name of the agency that generated the sequence, e.g., Centers for Disease Control and Prevention
sequenced_by	The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., pepper mild mottle virus
ww_endog_control_1	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_conc	The protocol used to quantify 'ww_endog_control_1'. Specify a reference, website, or brief description.
ww_endog_control_1_protocol	

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 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 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	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.

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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
site_id	Nationally unique sampling site identifier assigned following NWSS format. <5 digit county FIPS code for WWTP address>-<3 digit facility code>-<2 digit interceptor and sewershed code>-<2 digit subsewershed code>-<2 digit site code>	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
zipcode	Zip code in which this sampling site is physically located (one 5-digit zip code)	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'. If 'upstream location' use the NPDES permit number for the wastewater treatment plant in which the water flows. If facility does not have an NPDES permit number, enter -1.	Yes
epa_registry_id	EPA registry ID for the wastewater treatment plant specified in 'wwtp_name'. If 'upstream location' use the registry ID number for the wastewater treatment plant in which the water flows. If the water does not flow to a treatment plant, enter -1.	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. If 'upstream location', use the design capacity for the wastewater treatment plant to which the water flows.	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

	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
composite_freq		
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. Do not specify pasteurization here; it should be specified in the 'pasteurized' field.	Yes
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?	Yes
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	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'). If 'hum_frac_mic_conc' has a non-empty value and it is not possible to measure flow rate at all, then this may have an empty value.	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 1CDP 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 1CDP 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 1CDP dashboard, this field will also prevent the sample from public data release.	No
analysis_ignore	Should 1CDP data analysis ignore this sample? If the value is "yes", then this sample will be excluded from 1CDP 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 1CDP data analysis.	No
validated_methods	Are the laboratory methods for the pcr_target validated within the jurisdiction? If lab methods are validated, the value will be "yes". If lab methods are unvalidated, the value will be "no". NWSS accepts both validated and unvalidated data.	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

	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. Only the technical or biological replicate concentrations for the same pcr_gene_target should be averaged. For example, if there are three replicates of a given PCR target, average those concentrations and report the average value only. Do not include the three individual concentrations. Different pcr_gene_target concentrations should not be averaged for this field (e.g., do not average concentrations for N1 and N2).	Yes
pcr_target_avg_conc		
	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_std_error		
	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_lo		
	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_cl_95_up		
	Was the concentration of the PCR target below the limit of detection?	No
pcr_target_below_lod		
	PCR target limit of detection back-calculated to unconcentrated sample basis	Yes
lod_sewage		
	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
ntc_amplify		

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

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.

major_lab_method

Yes

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"

major_lab_method_desc

Yes

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 'pcr_target' is not "sars-cov-2", "delta", "omicron", "hMPXV", "hMPXV Clade I", or "hMPXV Clade II" then this must be a type of digital PCR, i.e. "ddpcr", "qiagen dpcr", "fluidigm dpcr", "life technologies dpcr", "raindance dpcr", or "dpcr"

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'). If 'hum_frac_mic_conc' has a non-empty value and it is not possible to measure flow rate at all, then this may have an empty value.

If lab methods for the
pcr_target are unvalidated,
dashboard_ignore can be "yes"
for the entire validation
process time period.

The units should relate to the
PCR target indicated in
pcr_target

The concentration should
relate to the PCR target
indicated in pcr_target

The standard error should
relate to the PCR target
indicated in pcr_target

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

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

Whether the concentration
was below the LOD should be
based on the LOD of the PCR
target indicated in lod_sewage
The LOD should relate to the
PCR target indicated in
pcr_target

If 'inhibition_detect' is "yes",
then this must have a non-
empty value

If 'hum_frac_mic_unit' has a
non-empty value, then this
must have a non-empty value

If 'hum_frac_mic_conc' has a
non-empty value, then this
must have a non-empty value

If 'hum_frac_chem_unit' has a
non-empty value, then this
must have a non-empty value

If 'hum_frac_chem_conc' has a
non-empty value, then this
must have a non-empty value

If 'other_norm_unit' has a non-
empty value, then this must
have a non-empty value

If 'other_norm_conc' has a
non-empty value, then this
must have a non-empty value

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

vs_concentration_method

Value Set

membrane filtration with addition of mgcl2
membrane filtration with sample acidification
membrane filtration with acidification and mgcl2
membrane filtration with no amendment
membrane filtration with addition of mgcl2, membrane recombined with separated solids
membrane filtration with sample acidification, membrane recombined with separated solids
membrane filtration with acidification and mgcl2, membrane recombined with separated solids
membrane filtration with no amendment, membrane recombined with separated solids
peg precipitation
aloh3 precipitation
ultracentrifugation
skimmed milk flocculation
beef extract flocculation
promega wastewater large volume tna capture kit
centricon ultrafiltration
amicon ultrafiltration
hollow fiber dead end ultrafiltration
innovaprep ultrafiltration
no liquid concentration, liquid recombined with separated solids
ceres nanotrap

zyzo environ water rna kit/ zyzo environ water rna kit (cat. r2042)
membrane filtration with addition of mgcl3
water concentrating buffer (R2042-1)
none

Description

vs_extraction_method

Value Set

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

zyzo environ water rna kit/ zyzo environ water rna kit (cat. r2042)
luminultra wastewater extraction kit
qiaamp viral rna kit
trizol and RNA purification kit
trizol, garnet bead beating, alcohol precipitation
zyzo quick-rna viral 96 kit #r1041
zyzo quick-rna viral kit #r1035
qiagen qiaamp dsp viral rna mini kit
monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zyzo)
exclusions based sample preparation (ESP)
sciencell viral rna isolation kit
thermo magmax viral/pathogen nucleic acid isolation kit
nucleomag (ref. 744220.4) using kingfisher automated instrument
dneasy powersoil pro kit
BOMB.bio protocol

vs_hum_frac_target_chem

Description	Value Set	Description
	caffeine	
	creatinine	
	sucralose	
	ibuprofen	
	[empty]	

vs_hum_frac_target_mic

Value Set	Description
pepper mild mottle virus	
crassphage	
hf183	
f+ rna coliphage	
f+ dna coliphage	
PMMoV (GT-Digital)	
[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

airport

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

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

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

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

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

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 wastewater

micrograms/g wet sludge

log10 micrograms/g wet sludge

micrograms/g dry sludge

log10 micrograms/g dry sludge

[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		vs_other_norm_name
Value Set	Description	Value Set
0		pepper mild mottle virus
1		crassphage
2		hf183
3		f+ rna coliphage
more than 3		f+ dna coliphage
		caffeine
		creatinine
		sucralose
		ibuprofen
		rnase p
		[empty]

Description	vs_pcr_target
	Value Set
	sars-cov-2
	delta
	omicron
	hMPXV
	hMPXV Clade I
	hMPXV Clade II
	caur
	NoV GI
	NoV GII
	FLUAV
	FLUBV
	NVO
	Cjejuni
	HAdV-F
	Col
	Gly
	Bla
	Integrase
	Tet
	RSV
	FLUAV A H5
	FLUAV A H1
	FLUAV A H3
	FLUAV A H7
	DENV-pan
	DENV-1
	DENV-2
	DENV-3
	DENV-4
	ev-d68
	OROV
	MeV_WT
	MeV_VA
	MeV
	RUBV
	MuV
	WNV

Description

<https://www.cdc.gov/mpox/outbreaks/2023/index.html>

Candida auris. Source: KEGG

Norovirus GI. Source: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3446575/> <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3446575/>

Norovirus GII. Source: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3446575/>

Influenza A. Source: Bacterial and Viral Bioinformatics Resource Center (BV-BRC)

Influenza B. Source: Bacterial and Viral Bioinformatics Resource Center (BV-BRC)

Non-Variola Orthopoxvirus. Source: CDC <https://www.cdc.gov/mmwr/volumes/71/wr/mm7128e1.htm>

Campylobacter jejuni. Source: KEGG

Adenovirus Group F41. Source: PubChem Taxonomy

Colistin AMR

Vancomycin AMR

Beta-Lactamase AMR

Integrase AMR

Tetracycline AMR

Respiratory Syncytial Virus

Influenza A H5 targets (including H5, H5a, and H5b primers and probe sets). LOINC short name Guidance for Standards-Based Electronic Laboratory Reporting for Influenza <https://www.cdc.gov/flu/professionals/diagnosis/rtpcr-test-kits.htm>

Influenza A/ H1 targets (including H1, pdmH1, and H1pdm09). LOINC short name Guidance for Standards-Based Electronic Laboratory Reporting for Influenza <https://www.cdc.gov/flu/professionals/diagnosis/rtpcr-test-kits.htm>

Influenza A/ H3 targets. LOINC short name Guidance for Standards-Based Electronic Laboratory Reporting for Influenza <https://www.cdc.gov/flu/professionals/diagnosis/rtpcr-test-kits.htm>

Influenza A/ H7 targets. LOINC short name Guidance for Standards-Based Electronic Laboratory Reporting for Influenza <https://www.cdc.gov/flu/professionals/diagnosis/rtpcr-test-kits.htm>

Dengue viruses <https://www.cdc.gov/dengue/index.html>

dengue serotype 1 <https://www.cdc.gov/dengue/index.html>

dengue serotype 2 <https://www.cdc.gov/dengue/index.html>

dengue serotype 3 <https://www.cdc.gov/dengue/index.html>

dengue serotype 4 <https://www.cdc.gov/dengue/index.html>

Enterovirus D68 target. <https://www.cdc.gov/non-polio-enterovirus/about/about-enterovirus-d68.html>

Oropouche virus: <https://www.cdc.gov/oropouche/about/index.html>

Wild-type Measles Virus

Vaccine-associated Measles Virus

Pan-Measles, that does not distinguish vaccine-associated and wild-type measles virus

Rubella Virus

Mumps Virus

West Nile Virus

vs_pcr_gene_target

Value Set

	n
	n1
	n2
	n3
	e_sarbeco
	n_sarbeco
	rdrp_sarsr
6575/	niid_2019-ncov_n
	rdrp gene / ncov_ip2
	rdrp gene / ncov_ip4
	taqpath n
	taqpath s
	orf1b
	orf1ab
	n1 and n2 combined
	s
	orf1a
	ddcov_n
	ddcov_e
	ip2 and ip4 combined

CDC N1 (GT-Digital)

Reporting for Influenza CDC N2 (GT-Digital)

dc.gov/flu/professionals

dc.gov/flu/professionals

	a1306s
	p2046l
	p2287s
	t3646a
	v2930l
	g662s
	p100l
	a1918v
	t19r
	e156g
	del 157/158
	l452r
	p681r
	d950n
	i82t
	d63g
	r203m
	g215c
	d377y
	wt214
	del156-157
	k856r
	s2083i
	del2084/2084

a2710t
p3395h
del3674/3676
i3758v
i1566v
a67v
del69/70
a67v/del69/del70
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
ins214epe
del142-144
del31-33
l24s
lppa24s
p13L
E9L-NVAR
G2R_G
G2R_WA
C3L
B6R
gtmol_hMPXV
MCR-1.1
VanA-A
blaNDM
blaKPC
blaOXA-48
blaVIM
blaCTX-M-1

blaCMY
blaTEM
Class I Integrase
blaSHV
TetW
blaIMP
caur
NoV GI
NoV GII
InfA1
InfA2

InfA1 and InfA2 combined

InfB
Cjejuni
HAdV-F
RSV-A and RSV-B combined
INFA_H5 (Verily)
INFA_H5 (CDC)
INFA_H5 (GT-Digital)
FLUAV A H1_Cv1
FLUAV A H1_Cv2
FLUAV A H3_Cv1
FLUAV A H7_Cv1
DENV-1-NS5
DENV-2-E gene
DENV-3-prM
DENV-4-prM
DENV-pan1
INFA_H5Nx (WHO)
INFA_clade 2.3.4.4x (WHO)
vp1
OROV_S
OROV_Cv1
OROV_Cv2
E3L 393
dD14-16
INFA_H1pdm09 (CDC)
INFA_H3 (CDC)

hMPXV_Clade_I OPG210 (GT-Digital)

MeV_WT (GT-Digital)

MeV_M_Gene_WT_Combined

MeV_M_Gene_VA

FLUAV A H3_Cv2

MeV_N_Gene_N3 (CDC)

RUBV_gp1_gene

MuV_N_gene_v2 (CDC)

MeV_M_Gene_WT1

MeV_M_Gene_WT2

MeV_N_Gene_WT (WWScan)

hMPXV_Clade_II (GT-Digital)

RSV (Wadsworth)

INFA_H1pdm09 (Wadsworth)

WNV (GT-Digital)

WNV (Qiagen)

WNV_WNENV (CDC)

FLUAV A H1_Cv3

Description

CDC validated SARS-CoV-2 assay. CDC IFU Source: Qiagen QIAcuity® Digital PCR (dPCR) Duplex Assay for De

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, si

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

delta gene target

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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

[illegible]

Cephamycin Beta-Lactamase AMR gene target. Source: ARG-ANNOT

Beta-Lactamase AMR gene target. Source: ARG-ANNOT

Integrase AMR gene target.

Beta-Lactamase AMR gene target. Source: ARG-ANNOT

Tetracycline AMR gene target. Source: ARG-ANNOT

Imipenemase (IMP) Beta-Lactamase AMR gene target. Source: ARG-ANNOT

Candida auris gene target. Source: <https://www.cdc.gov/fungal/candida-auris/pdf/Real-time-PCR-based-Ic>

Norovirus GI ORF1-ORF2 junction gene target. Source: <https://wwwnc.cdc.gov/eid/article/17/8/10-1837-t>

Norovirus GII ORF1-ORF2 junction gene target. Source: <https://wwwnc.cdc.gov/eid/article/17/8/10-1837-t>

THIS ENTRY SHOULD ONLY BE CHOSEN AFTER CONSULTATION WITH THE NWSS PROGRAM. THIS PRIMER S

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Influenza A gene target; Detection of InfA1 and InfA2 targets is performed in a single fluorescence channel, such that distinct measurements for InfA1 and InfA2 do not exist. Sources: Multiplex Real-Time Reverse Transcription PCR for Influenza A Virus, Influenza B Virus, and Severe Acute Respiratory Syndrome Coronavirus 2, https://wwwnc.cdc.gov/eid/article/27/7/21-0462_article; and Singleplex Digital PCR Testing of Influenza A, H1pdm09, H3, and H5 from Wastewater (Version 1) IFU for wastewater testing; Also includes commercial kits that use the CDC infA assay scheme, such as the GT-Digital Influenza and SARS-CoV-2 Wastewater Surveillance Multiplex Assay Kit for the QIAcuity™ Digital PCR System.

Influenza B gene target. Source: <https://www.cdc.gov/flu/php/laboratories/influenza-sars-cov-2-multiple>;

Campylobacter jejuni gene target. Source: <https://www.sciencedirect.com/science/article/pii/S088240101>

Adenovirus Group F41 Fiber gene target. Source: <https://www.sciencedirect.com/science/article/pii/S002>

CDC validated RSV assay, including primer sets for both RSV-A and RSV-B viruses. Separate probes for RSV: Verily and WastewaterSCAN <https://doi.org/10.1021/acs.estlett.4c00331>

CDC Human Influenza A H5 virus assay; Sources: CDC Human Influenza Virus Real-Time RT-PCR Diagnostic GT-Molecular Influenza A H5 assay, for example: <https://www.gtmolecular.com/product/gt-digital-h5-was>

Verily NWSS commercial contract

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dengue serotype 1 gene target from <https://pubmed.ncbi.nlm.nih.gov/23875046/>

dengue serotype 2 gene target from <https://pubmed.ncbi.nlm.nih.gov/23875046/>

dengue serotype 3 gene target from <https://pubmed.ncbi.nlm.nih.gov/23875046/>

dengue serotype 4 gene target from <https://pubmed.ncbi.nlm.nih.gov/23875046/>

Pan dengue gene target from <https://pubmed.ncbi.nlm.nih.gov/23875046/>

Protocol 2: Real-time RT-PCR for Influenza A(H5) HA gene <https://cdn.who.int/media/docs/default-source>.

Protocol 2: Real-time RT-PCR for Influenza A(H5) HA gene <https://cdn.who.int/media/docs/default-source>.

Human enterovirus D68 gene target VP1 <https://doi.org/10.3201/eid3003.231223>

Oropouche virus S segment from <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC165340/>

Oropouche virus Verily NWSS commercial contract <https://doi.org/10.1016/j.diagmicrobio.2019.114894>

Oropouche virus WHO/PAHO/Naveca assay <https://doi.org/10.1590/0074-02760160062>

hMPXV Clade I gene target. Verily NWSS commercial contract mpox pan clade I

hMPXV Clade I gene target. <https://doi.org/10.2807/1560-7917.ES.2024.29.32.2400486>

Singleplex Digital PCR Testing of Influenza A, H1pdm09, H3, and H5 from Wastewater IFU for wastewater t

Singleplex Digital PCR Testing of Influenza A, H1pdm09, H3, and H5 from Wastewater IFU for wastewater testing.

GT-Molecular Digital Mpox Clade I OPG210 assay, for example: <https://www.gtmolecular.com/product/gt-digital-mpox-clade-i-opg210-rox-add-on-assay-qiacuity/>;

<https://www.gtmolecular.com/product/gt-digital-mpox-clade-i-opg210-rox-add-on-assay-v1-0-for-the-bio-rad-qx600-digital-pcr-system-copy/>

GT-Molecular Digital MeV (measles virus) WT (wild type) assay, for example:
<https://www.gtmolecular.com/product/gt-digital-mev-wt-wastewater-surveillance-assay-v1-0-for-the-qiacuity-digital-pcr-system/>
Measles virus M gene WT1 (wild type 1) AND WT2 (wild type 2) assay target probes in the same detection channel. From <https://pubs.acs.org/doi/10.1021/acs.est.4c05344>

Measles virus M gene vaccine strain assay (VA). From <https://pubs.acs.org/doi/10.1021/acs.est.4c05344>
Verily NWSS commercial contract H3 v2

Measles virus N gene assay target (N3). From <https://pubmed.ncbi.nlm.nih.gov/16274752/>

Rubella virus RUBVgp1 gene assay target. From <https://pubs.acs.org/doi/10.1021/acs.est.4c05344>

Mumps virus N gene assay target. From <https://www.cdc.gov/mumps/downloads/simple-protocol-MuV-r1>

Measles virus M gene WT1 (wild type 1) assay probe and target. From <https://pubs.acs.org/doi/10.1021/a>

Measles virus M gene WT2 (wild type 2) assay probe and target. From <https://pubs.acs.org/doi/10.1021/a>

Measles virus N Gene WT (wild type) assay target. Modified from: <https://pmc.ncbi.nlm.nih.gov/articles/P>

GT-Molecular Digital Mpox Clade II assay, for example: <https://www.gtmolecular.com/product/dpcr-nvompox-assay-kit-for-the-bio-rad-qx200-v1-1-beta/?>

`_gl=1*1rzwljf*_gcl_au*MjA5MzMzMtAzMi4xNzQ1NDI4MTA5*_ga*MTI4MjM1MDg0My4xNzQ1NDI4MTA5*_ga_N4HPZP2900*czE3NTI0OTg2MjkkbzE4JGcxJHQxNzUyNDk4Njc2JGoxMyRsMCRoMA..;`
<https://www.gtmolecular.com/product/gt-digital-nvompox-assay-kit-for-the-qiacuity-v1-1-beta/?>

`_gl=1*11d4h9i*_gcl_au*MjA5MzMzMtAzMi4xNzQ1NDI4MTA5*_ga*MTI4MjM1MDg0My4xNzQ1NDI4MTA5*_ga_N4HPZP2900*czE3NTI0OTg2MjkkbzE4JGcxJHQxNzUyNDk4OTlyJGoxMyRsMCRoMA..`

Respiratory Syncytial Virus matrix gene target. NYS Wadsworth Center modified from:

<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0015098>

Influenza A H1pdm09 gene target. NYS Wadsworth Center unpublished.

GT-Molecular Digital West Nile Virus Assay. Source: <https://www.gtmolecular.com/product/gt-digital-west-nile-virus-wastewater-surveillance-assay-v1-0-for-the-qia-gen-qiacuity-digital-pcr-system/>

Qiagen West Nile virus Polyprotein gene target. Source: <https://geneglobe.qiagen.com/us/product-groups/dpcr-microbial-dna-detection-assays/DMA00455>

West Nile virus envelope gene target. From: <https://pmc.ncbi.nlm.nih.gov/articles/PMC87542/>

Verily NWSS commercial contract

vs_pcr_type

Value Set

etection and Quantqpcr

ddpcr

qiagen dpcr

fluidigm dpcr

life technologies dpcr

raindance dpcr

dpcr

uch that distinct measurements for N1 and

. <https://doi.org/10.1016/j.jcv.2006.03.012>
et.2010.07.012
10.1016/j.jviromet.2010.07.012
16/j.jviromet.2010.07.012
jcv.2006.03.012

d-C-auris-508.pdf

2#r27

t2#r27

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x-assay.html

L7303728?via%3Dhub

2347608006744?via%3Dhub

-A and RSV-B on a single fluorescence char

Panel (Influenza A/H5 Subtyping Kit) <https://www.qiagen.com/us/products/60102/influenza-a-h5-subtyping-kit>

ewater-surveillance-assay-kit-for-the-qia

/influenza/molecular-detection-of-influenza

/influenza/molecular-detection-of-influenza

testing.

RT-PCR.pdf

cs.est.4c05344

cs.est.4c05344

MC5328441/

Description

Real-time PCR, also called 'quantitative' PCR

Used to refer specifically to BioRad digital droplet emulsification technology

Generic digital PCR

1 N2 do not exist

† THE INFA2 PRIMER SET IN THE COMPLETE INFA ASSAY. Influenza A 1 gene target. Source: <https://www.cdc.gov/flu/php/laboratories/nucleic-acid-detection.html>; and Singleplex Digital PCR Testin
† THE INFA1 PRIMER SET IN THE COMPLETE INFA ASSAY. Influenza A 2 gene target. Source: <https://www.cdc.gov/flu/php/laboratories/nucleic-acid-detection.html>; and Singleplex Digital PCR Testin

anel (note that distinct measurements for RSV-A and RSV-B do not exist). CDC IFU Source: Qiagen Q
://www.cdc.gov/flu/php/laboratories/nucleic-acid-detection.html; and Singleplex Digital PCR Testin
gen-qiacuity-digital-pcr-system-copy/.

za-viruses/protocols_influenza_virus_detection_feb_2021.pdf?sfvrsn=df7d268a_5
za-viruses/protocols_influenza_virus_detection_feb_2021.pdf?sfvrsn=df7d268a_5

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]	

[/www.cdc.gov/flu/php/laboratories/influenza-sars-cov-2-multiplex-assay.html](https://www.cdc.gov/flu/php/laboratories/influenza-sars-cov-2-multiplex-assay.html)
www.cdc.gov/flu/php/laboratories/influenza-sars-cov-2-multiplex-assay.html

IAcuity® Digital PCR (dPCR) Duplex Assay for Detection and Quantification of SARS-CoV-2 and Respiratory Syncytial Virus (RSV) from Wastewater IFU for wastewater testing.

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

murine hepatitis virus

MHV (PREvalence)

BCoV (GT-Digital)

[empty]

parapoxvirus

ory Syncytial Virus (RSV) in Wastewater

vs_reporting_jurisdiction

Value Set	Description
AL	Alabama
AK	Alaska
AS	American Samoa
AZ	Arizona
AZMC	Maricopa County, AZ
AR	Arkansas
CA	California
CI	Chicago, IL
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
HO	Houston, TX
ID	Idaho
IL	Illinois
IN	Indiana
IA	Iowa
KS	Kansas
KY	Kentucky
LC	Los Angeles County, CA
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
NZ	New York City, NY
NC	North Carolina
ND	North Dakota
OH	Ohio
OK	Oklahoma
OR	Oregon
PA	Pennsylvania

PH	Philadelphia, PA
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
AP	Acoma Pueblo
CN	Catawba Nation
CVBPI	Coyote Valley Band of Pomo Indians
EBCI	Eastern Band of Cherokee Indians
GTBI	Grand Traverse Band of Ottawa and Chippewa Indians
MAT	Mescalero Apache Tribe
NPT	Nez Perce Tribe
OMT	Otoe-Missouria Tribe
SBT	The Shoshone Bannock Tribes
TRIT	Tule River Indian Tribe
ZP	Zuni Pueblo
PBCI	Poarch Band of Creek Indians
TMBCI	Turtle Mountain Band of Chippewa Indians

vs_sample_location

Value Set
wwtp
upstream

Description

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

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
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6-hr flow-weighted composite
5-hr flow-weighted composite
4-hr flow-weighted composite
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2-hr flow-weighted composite

1-hr flow-weighted composite
96-hr time-weighted composite
72-hr time-weighted composite
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1-hr time-weighted composite

96-hr manual composite
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4-hr manual composite

3-hr manual composite

2-hr manual composite

1-hr manual composite

72-hr passive sample

48-hr passive sample

47-hr passive sample

46-hr passive sample

45-hr passive sample

44-hr passive sample

43-hr passive sample

42-hr passive sample

41-hr passive sample

40-hr passive sample

39-hr passive sample

38-hr passive sample

37-hr passive sample

36-hr passive sample

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6-hr passive sample
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4-hr passive sample
3-hr passive sample
2-hr passive sample
1-hr passive sample
120-hr passive sample

Description

An individual sample collected without compositing or adding other samples

E.g., Moore swabs

E.g., Moore swabs

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E.g., Moore swabs

[illegible]

vs_solids_separation

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

filtration	Filtration to remove solids from a wastewater sample prior to
------------	---

centrifugation	Centrifugation prior to or in the absence of a concentration st
----------------	---

gravity settling	Solids separated from liquid by allowing solids to settle by gra
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none	
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[empty]	
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vs_wwtp_jurisdiction

Value Set

AL

AK

AS

AZ

AR

CA

CO

MP

CT

DE

DC

FM

FL

GA

GU

HI

ID

IL

IN

IA

KS

KY

LA

ME

MD

MA

MI

MN

MS

MO

MT

NE

NV

NH

NJ

NM

NY

NC

ND

OH

OK

OR

PA

PR

MH

PW

RI

SC

SD
TN
TX
VI
UT
VT
VA
WA
WV
WI
WY

vs_yn	
Description	Value Set Description
Alabama	yes
Alaska	no
American Samoa	
Arizona	
Arkansas	
California	
Colorado	
Commonwealth of Northern Mariana Islands	
Connecticut	
Delaware	
District of Columbia	
Federated States of Micronesia	
Florida	
Georgia	
Guam	
Hawaii	
Idaho	
Illinois	
Indiana	
Iowa	
Kansas	
Kentucky	
Louisiana	
Maine	
Maryland	
Massachusetts	
Michigan	
Minnesota	
Mississippi	
Missouri	
Montana	
Nebraska	
Nevada	
New Hampshire	
New Jersey	
New Mexico	
New York	
North Carolina	
North Dakota	
Ohio	
Oklahoma	
Oregon	
Pennsylvania	
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

vs_yne

Value Set	Description
yes	
no	
[empty]	

vs_ynn

Value Set	Description
yes	
no	
not tested	