General Notes

The level of measure for NWSS DCIPHER SARS-CoV-2 reporting:	Each SARS-CoV-2 PCR target ('pcr_target') that is measured should be each be reported on a separate row. Other fields that correspond to t "wide" with respect to most measurements made on a given sample,
Data types:	Fields are read in as strings; data type casting happens after file read i

Submission Requirements

Required fields:	These fields must be included in the data file; if they are omitted, file file even if all row values are [empty].
Non-required but non-empty fields:	Some fields are "not required" but also must have non-empty values, cause them to be flagged for quality control issues once uploaded.

Value Sets

Missing values:	Missing values should be left blank, denoted as [empty] in the Value S
Requesting additional values for categorical fields:	For categorical fields, restrict values to those listed in the Value Sets.
Case sensitivity:	Fields are not case sensitive.

Data Type Definitions

string	ASCII-encoded characters; do not use line breaks within a value
float	Floating-point (i.e., decimal) number
integer	Integer number
ZIP code	5-digit US ZIP code (#####)
date	yyyy-mm-dd
time	hh:mm (24-hr format in the local time zone)
list	Comma-separated strings
category	Categorical variable with a defined value set of strings
NPDES permit number	National Pollutant Discharge Elimination System (NPDES) permit num
EPA registry ID number	EPA Registry ID or Facility Registry Service (FRS) identifier (<########
time zone	Time zone, represented as a UTC time offset (UTC-[hh]:[mm], e.g., UT
jurisdiction id	String 20 characters or less, containing only numbers, English alphabe

Field Name Groups

Reporter

Collection Site

WWTP

Collection Method

Processing Method

SARSCoV2 Quantification Method

Sample

SARSCoV2 Quantification Results

Terminology

PCR:	Throughout this data dictionary, the term "PCR" (polymerase chain re transcriptase PCR)-based method for RNA targets, such as SARS-CoV- quantitative (real time) PCR or digital PCR.

Field Name Color Key	
🟫	Data that may be generated by the reporting jurisdiction public healt
🟧	Data likely generated by testing laboratories
🟦	Data likely generated by wastewater utilities
🟨	New fields or changes to existing fields

specified on a separate row in the CSV file. For example, if N1 and N2 are both measured for the same san
his sample, including 'sample_id', should be repeated across those rows. In general, this format can be tho
but "long" with respect to SARS-CoV-2 PCR targets.

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upload will be prohibited. For required fields that allow [empty] values, the field column header must be in

, conditional on the completion of another field. Omission of these fields will not interfere with upload of th

ets. Do not use other strings, such as "NA" or "[empty]", to denote missing values."

To request that values be added to the vocabulary, please contact NWSS staff.

ber (<2-letter abbreviation><#######>). Search engine to locate this identifier is available here: https://ech

####>). Search engine to locate this identifier is availble here: https://echo.epa.gov/facilities/facility-search

C-06:00); offsets can be found at https://www.timeanddate.com/time/zone/usa

tic characters, underscores, and hyphens (white space is not allowed); not case sensitive

action) is used as a shorthand for "PCR-based quantification methods", even when the method is an RT-PC
2. In addition, the term PCR does not refer to end-point PCR methods, but rather quantitative PCR methods

agency, possibly in collaboration with either wastewater utilities or testing laboratories

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cluded in the data

e data file, but will

o.epa.gov/facilities
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, such as

Field Name	Data Type
Reporter	
reporting_jurisdiction	category
Collection Site	
site_id	<#####-###-##-##-##>
county_names	list (comma-separated integers)
zipcode	ZIP code (#####)
population_served	integer
sewage_travel_time	float
sample_location	category
sample_location_specify	string
institution_type	category

WWTP

epaid	NPDES permit number (<2-letter abbreviation><#######>)
epa_registry_id	EPA Registry ID (<############>)
wwtp_name	string
wwtp_jurisdiction	category
capacity_mgd	float
industrial_input	float
stormwater_input	category
influent_equilibrated	category

Collection Method

sample_type	category
composite_freq	float
sample_matrix	category
collection_storage_time	float
collection_storage_temp	float
pretreatment	category
pretreatment_specify	string
Processing Method	
solids_separation	category
concentration_method	category
extraction_method	category
pre_conc_storage_time	float

pre_conc_storage_temp	float
pre_ext_storage_time	float
pre_ext_storage_temp	float
tot_conc_vol	float
ext_blank	category
rec_eff_target_name	category
rec_eff_spike_matrix	category
rec_eff_spike_conc	float
pasteurized	category
SARSCoV2 Quantification Method	
pcr_target	category
pcr_gene_target	category
pcr_gene_target_ref	string
pcr_type	category

lod_ref	string
hum_frac_target_mic	category
hum_frac_target_mic_ref	string
hum_frac_target_chem	category
hum_frac_target_chem_ref	string
other_norm_name	category
other_norm_ref	string
quant_stan_type	category
stan_ref	string
inhibition_method	string
num_no_target_control	category
Sample	
sample_collect_date	date ([yyyy]-[mm]-[dd])
sample_collect_time	time, 24-hr ([hh]:[mm])
time_zone	time zone (UTC-[hh]:[mm])

flow_rate	float
ph	float
conductivity	float
tss	float
collection_water_temp	float
equiv_sewage_amt	float
sample_id	jurisdiction id (a string 20 characters or less, containing only numbers, English alphabetic characters, underscores, and hyphens; white space is not allowed; not case sensitive)
lab_id	jurisdiction id (a string 20 characters or less, containing only numbers, English alphabetic characters, underscores, and hyphens; white space is not allowed; not case sensitive)

qc_ignore	category
dashboard_ignore	category
analysis_ignore	category

SARSCoV2 Quantification Results	
test_result_date	date ([yyyy]-[mm]-[dd])
pcr_target_units	category

pcr_target_avg_conc	float
pcr_target_std_error	float
pcr_target_cl_95_lo	float
pcr_target_cl_95_up	float
pcr_target_below_lod	category
lod_sewage	float

ntc_amplify	category
rec_eff_percent	float
inhibition_detect	category
inhibition_adjust	category
hum_frac_mic_conc	float
hum_frac_mic_unit	category
hum_frac_chem_conc	float
hum_frac_chem_unit	category
other_norm_conc	float
other_norm_unit	category
quality_flag	category

major_lab_method	integer
major_lab_method_desc	string

Description	Value Set
The CDC Epidemiology and Laboratory Capacity (ELC) jurisdiction, most frequently a state, reporting these data (2-letter abbreviation)	[See Value Sets: vs_reporting_jurisdiction]
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>	
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.	[5-digit integers]
Zip code in which this sampling site is physically located (one 5-digit zip code)	[5-digit integers]
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)	[greater than or equal to 0]
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.	[greater than or equal to 0]; [empty]
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	[See Value Sets: vs_sample_location]
If 'sample_location' is "upstream", specify the collection location in the wastewater system; an arbitrary name may be used if you do not wish to disclose the real name.	[string, length less than or equal to 40 characters]; [empty]
If this sample represents wastewater from a single institution, facility, or building, specify the institution type; otherwise, specify "not institution specific"	[See Value Sets: vs_institution_type]

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.	[NPDES permit number]; -1 if not permitted
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.	[EPA Registry ID]; -1 if not registered with EPA
The name of the Wastewater Treatment Plant (WWTP) to which this wastewater flows. If this wastewater does not flow to a WWTP, specify an identifiable name for the septic or other treatment system to which this wastewater flows. An arbitrary name may be used if you do not wish to disclose the real name.	[string, length less than or equal to 40 characters]
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	[See Value Sets: vs_wwtp_jurisdiction]
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.	[greater than or equal to 0]
Approximate average percentage of wastewater from industrial sources that is received by the wastewater treatment plant specified in 'wwtp_name'	[0-100]; [empty]
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)?	[See Value Sets: vs_yne]
Is influent to the wastewater treatment plant specified in 'wwtp_name' ever stored prior to treatment to equilibrate or modulate the influent flow rate?	[See Value Sets: vs_yne]

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.	[See Value Sets: vs_sample_type]
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	[greater than or equal to 0]; [empty]
Wastewater matrix from which the sample was collected	[See Value Sets: vs_sample_matrix]
Duration of time from sample collection start time to time sample reached the lab.	[greater than or equal to 0]; [empty]
Temperature at which the sample was stored after collection and prior to reaching the lab	[float]; [empty]
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 be specify pasteurization here; it should be specified in the 'pasteurized' field.	[See Value Sets: vs_yn]
If 'pretreatment' is "yes", then specify the chemicals used	[string]; [empty]

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'	[See Value Sets: vs_solids_separation]
Method used to concentrate the sample prior to analysis of the concentrate	[See Value Sets: vs_concentration_method]
Method used for nucleic acid extraction from the sample	[See Value Sets: vs_extraction_method]
The approximate average duration of time between when samples reach the lab and when they are concentrated (if concentrated)	[greater than or equal to 0]; [empty]

The storage temperature of samples after reaching the lab and prior to concentration (if concentrated)	[float]; [empty]
The approximate average duration of time between when samples are concentrated (if concentrated) and when they are extracted	[greater than or equal to 0]; [empty]
The storage temperature of samples after concentration (if concentrated) and prior to extraction	[float]; [empty]
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'	[greater than or equal to 0]; [empty]
Are extraction blanks included in the extraction process?	[See Value Sets: vs_yne]
Name of the recovery efficiency control target that is spiked in	[See Value Sets: vs_rec_eff_target_name]
Matrix into which the recovery efficiency control target is spiked	[See Value Sets: vs_rec_eff_spike_matrix]
Spike concentration, on average, of the recovery control on a per sample volume basis	[float]; [empty]
Was the sample pasteurized?	[See Value Sets: vs_yn]
The target of the PCR quantification	[See Value Sets: vs_pcr_target]
The PCR gene used to quantify PCR target	[See Value Sets: vs_pcr_gene_target]
A publication, website, or brief description of the PCR gene target used	[string]
The type of PCR used to quantify the PCR target	[See Value Sets: vs_pcr_type]

A publication, website, or brief description of the method used to calculate the limit of detection	[string]
Name of microbial target used to estimate human fecal content	[See Value Sets: vs_hum_frac_target_mic]
A publication, website, or brief description of the microbial target specified in 'hum_frac_target_mic'	[string]; [empty]
Name of chemical compound used to estimate human fecal content	[See Value Sets: vs_hum_frac_target_chem]
A publication, website, or brief description of the chemical compound specified in 'hum_frac_target_chem'	[string]; [empty]
Name of a target or compound not specified in 'hum_frac_target_mic' or 'hum_frac_target_chem' used to estimate human fecal content	[See Value Sets: vs_other_norm_name]
A publication, website, or brief description of the target or compound specified in 'other_norm_name'	[string]; [empty]
The type of nucleic acid used as a standard for the PCR target quantification	[See Value Sets: vs_quant_stan_type]
A publication, website, or brief description of the quantitative standard material used	[string]
A publication, website, or brief description of the method used to evaluate molecular inhibition	[string]; none (if inhibition not tested)
Number of no-template controls (NTC) per instrument run	[See Value Sets: vs_num_no_target_control]
The date of sample collection; for composite samples, specify the date on which sample collection began	[date not after tomorrow's date]
The local time of sample collection; for composite samples, specify the time at which sample collection began	[time]
Current local time zone corresponding to the time specified in 'sample_collect_time', represented as a UTC time offset (e.g., UTC-06:00)	[time zone]

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.	[greater than or equal to 0]; [empty]
pH of wastewater sample (if sludge, pH of influent at time of collection)	[float]; [empty]
Specific conductivity of wastewater sample (if sludge, conductivity of influent at time of collection)	[greater than or equal to 0]; [empty]
Total suspended solids of raw (or, if unavailable, post-grit removal) wastewater	[greater than or equal to 0]; [empty]
Sample temperature at time of collection	[greater than or equal to 0]; [empty]
Equivalent unconcentrated volume of wastewater or mass of sludge in PCR reaction	[greater than or equal to 0]; [empty]
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.	[sample 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.	[lab id]

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’.	[See Value Sets: vs_yne]
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.	[See Value Sets: vs_yne]
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.	[See Value Sets: vs_yne]
The date on which this PCR target measurement was made	[date greater than sample collect date and less than DCIPHER upload date]
Units of PCR target sample concentration	[See Value Sets: vs_mic_chem_units]

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).	[any float other than 0]; 0 (if no amplification observed)
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	[greater than or equal to 0]; -1 (if cannot be calculated, such as when no amplification observed)
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)	[any float other than -1]; -1 (if cannot be calculated, such as when no amplification observed)
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)	[any float other than -1]; -1 (if cannot be calculated, such as when no amplification observed)
Was the concentration of the PCR target below the limit of detection?	[See Value Sets: vs_yne]
PCR target limit of detection back-calculated to unconcentrated sample basis	[float]

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?	[See Value Sets: vs_yn]
Percent of spiked recovery control, specified in 'rec_eff_target_name', that was recovered	[greater than or equal to 0.0]; -1 (if not tested)
Was molecular inhibition detected?	[See Value Sets: vs_ynn]
Was inhibition incorporated into the PCR target concentration calculation?	[See Value Sets: vs_yne]
Concentration of microbial target specified in 'hum_frac_target_mic'; follow the same guidelines outlined for 'pcr_target_avg_conc'	[float]; [empty]
Concentration units of microbial target specified in 'hum_frac_target_mic'	[See Value Sets: vs_mic_chem_units_e]
Concentration of chemical target specified in 'hum_frac_target_chem'	[float]; [empty]
Concentration units of chemical target specified in 'hum_frac_target_chem'	[See Value Sets: vs_mic_chem_units_e]
Concentration of target spcified in 'other_norm_name'	[float]; [empty]
Concentration units of target spcified in 'other_norm_name'	[See Value Sets: vs_mic_chem_units_e]
Does this observation have quality control issues?	[See Value Sets: vs_yne]

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.	[greater than or equal to 0]; [empty]
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"	[string]; [empty]

Units	Submission Requirement	Dependent Fields
[none]	Required	None
	Required	None
[none]	Required	None
[none]	Required	None
[none]	Required	None
Hours	Not required	None
[none]	Required	If 'sample_location' is "upstream", specify in 'sample_location_specify'
[none]	Required	If sample_location is "upstream", then this must have a non-empty value
[none]	Required	None

[none]	Required	None
[none]	Not required	None
[none]	Required	None
[none]	Required	None
Million gallons per day (MGD)	Required	None
percent	Not required	None
[none]	Not required	None
[none]	Not required	None

[none]	Required	None
If flow-weighted composite: number per million gallons; if time-weighted or manual composite: number per hour	Not required	None
[none]	Required	None
Hours	Not required	None
Celsius	Not required	None
[none]	Required	if 'pretreatment' is "yes", then specify in 'pretreatment_specify'
[none]	Not required	if 'pretreatment' is "yes", then 'pretreatment_specify' must have a non-empty field
[none]	Not required	None
[none]	Required	None
[none]	Required	None
Hours	Not required	None

Celsius	Not required	None
Hours	Not required	None
Celsius	Not required	None
mL	Not required	None
[none]	Not required	None
[none]	Required	If 'rec_eff_percent' is equal to a value other than "-1", then this must have a non-empty value
[none]	Required	If 'rec_eff_target_name' has a non-empty value, then this must have a non-empty value
log10 copies/mL	Required	If 'rec_eff_target_name' has a non-empty value, then this must have a non-empty value
[none]	Required	None
[none]	Required	None
[none]	Required	The value selected for pcr_gene_target should align with the value selected for pcr_target
[none]	Required	None
[none]	Required	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"

[none]	Required	None
[none]	Not required	If 'hum_frac_mic_conc' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'hum_frac_mic_conc' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'hum_frac_chem_conc' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'hum_frac_chem_conc' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'other_norm_conc' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'other_norm_conc' has a non-empty value, then this must have a non-empty value
[none]	Required	None
[none]	Required	None
[none]	Required	None
[none]	Required	None
[none]	Required	None
[none]	Required	None
[none]	Not required	None

Million gallons per day (MGD)	Required.	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.
pH units	Not required	None
microsiemens/cm	Not required	None
mg/L	Not required	None
Celsius	Not required	None
mL wastewater or g sludge	Not required	None
[none]	Required	None
[none]	Required	None

[none]	Not required	None
[none]	Not required	None
[none]	Not required	None
[none]	Required	None
[none]	Required	The units should relate to the PCR target indicated in pcr_target

[units specified in 'pcr_target_units']	Required	The concentration should relate to the PCR target indicated in pcr_target
[units specified in 'pcr_target_units']	Not required	The standard error should relate to the PCR target indicated in pcr_target
[units specified in 'pcr_target_units']	Not required	The lower bound of the 95% confidence interval should relate to the PCR target indicated in pcr_target
[units specified in 'pcr_target_units']	Not required	The upper bound of the 95% confidence interval should relate to the PCR target indicated in pcr_target
[none]	Not required	Whether the concentration was below the LOD should be based on the LOD of the PCR target indicated in lod_sewage
[units specified in 'pcr_target_units']	Required	The LOD should relate to the PCR target indicated in pcr_target

[none]	Required	None
percent	Required	None
[none]	Required	None
[none]	Required	If 'inhibition_detect' is "yes", then this must have a non-empty value
[units specified in 'hum_frac_mic_unit']	Not required	If 'hum_frac_mic_unit' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'hum_frac_mic_conc' has a non-empty value, then this must have a non-empty value
[units specified in 'hum_frac_chem_unit']	Not required	If 'hum_frac_chem_unit' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'hum_frac_chem_conc' has a non-empty value, then this must have a non-empty value
[units specified in 'other_norm_conc']	Not required	If 'other_norm_unit' has a non-empty value, then this must have a non-empty value
[none]	Not required	If 'other_norm_conc' has a non-empty value, then this must have a non-empty value
[none]	Not required	None

[none]	Required	None
[none]	Required	None

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
membrane filtration with addition of mgcl2
membrane filtration with sample acidification
membrane filtration with acidification and mgcl2
membrane filtration with no amendment
membrane filtration with addition of mgcl2, membrane recombined with separated solids
membrane filtration with sample acidification, membrane recombined with separated solids
membrane filtration with acidification and mgcl2, membrane recombined with separated solids
membrane filtration with no amendment, membrane recombined with separated solids
peg precipitation
aloh3 precipitation
ultracentrifugation
skimmed milk flocculation
beef extract flocculation
promega wastewater large volume tna capture kit
centricon ultrafiltration
amicon ultrafiltration
hollow fiber dead end ultrafiltration
innovaprep ultrafiltration
no liquid concentration, liquid recombined with separated solids
ceres nanotrap
zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)
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
zymo quick-rna fungal/bacterial miniprep #r2014
thermo magmax microbiome ultra nucleic acid isolation kit
zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)
luminultra wastewater extraction kit
qiaamp viral rna kit
trizol and RNA purification kit
trizol, garnet bead beating, alcohol precipitation
zymo quick-rna viral 96 kit #r1041
zymo 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 (zymo)
exclusions based sample preparation (ESP)
sciencell viral rna isolation kit
thermo magmax viral/pathogen nucleic acid isolation kit

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

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 licensed
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 facilities
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

Value Set	Description
sars-cov-2	
delta	
omicron	
hMPXV	
hMPXV Clade I	
hMPXV Clade II	
caur	Candida auris. Source: KEGG
NoV GI	Norovirus GI. Source: https://www.ncbi.nlm.nih.gov/pm
NoV GII	Norovirus GII. Source: https://www.ncbi.nlm.nih.gov/pm
FLUAV	Influenza A. Source: Bacterial and Viral Bioinformatics R
FLUBV	Influenza B. Source: Bacterial and Viral Bioinformatics R
NVO	Non-Variolla Orthopoxvirus. Source: CDC https://ww
Cjejuni	Campylobacter jejuni. Source: KEGG
HAdV-F	Adenovirus Group F41. Source: PubChem Taxonomy
Col	Colistin AMR
Gly	Vancomycin AMR
Bla	Beta-Lactamase AMR
Integrase	Integrase AMR
Tet	Tetracycline AMR
RSV	Respiratory Syncytial Virus
Fluor	Fluoroquinolone AMR
Macro	Macrolide AMR
Shigella	Shigella spp.
STEC	Shiga-toxin producing or intimin-producing E. coli or othe
cycloc	Cyclospora cayetanensis
Other Bacteria	Other bacteria not listed
Other Virus	Other virus not listed
Other Parasite	Other parasite not listed
Other Fungus or Ye	Other fungus or yeast not listed
Other Eukaryote	Other eukaryote not listed
Other Archaea	Other archaea not listed

vs_pcr_gene_target

Value Set
n1
n2
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
CDC N1 (GT-Digital)
CDC N2 (GT-Digital)
N2 (PREvalence)
E (PREvalence)
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
E9L-OPX3
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 combi
InfB
Cjejuni
HAdV-F
RSVL1
ipaH
18S rRNA
mph(A)
stx1
stx2
eae
RSV
fluor
Other

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
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sars-cov-2 gene target; Detection of N1 and N2 targets was performed on a single fluorescence channel, such that distinct me
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hMPXV gene target. orthopoxvirus DNA polymerase. CDC Assay all hMPXV and non-variola Orthopoxvirus. https://doi.org/10.
hMPXV gene target. G2R_G primers and probe: detects all MPXV strains . https://doi.org/10.1016/j.jviromet.2010.07.012
hMPXV Clade II gene target. hMPXV G2R_WA primers and probe: detects Clade II viruses.CDC https://doi:10.1016/j.jviromet.2
hMPXV Clade I gene target. hMPXV C3L primers and probe: detects Clade I viruses . CDC https://doi:10.1016/j.jviromet.2010.0
hMPXV gene target. CDC https://doi.org/10.4269/ajtmh.2010.09-0716
hMPXV gene target. Envelope protien gene CDC Assay; selective for MPXV. CDC https://doi.org/10.1016/j.jcv.2006.03.012

hMPXV gene target. hMPXV gene target proprietary GT Molecular
Colistin AMR gene target. Source: ARG-ANNOT
Vancomycin AMR gene target. Source: ARG-ANNOT
New-Delhi Metallo- (NDM) Beta-Lactamase AMR gene target. Source: ARG-ANNOT
Klebsiella pneumoniae Carbapenam (KPC) Beta-Lactamase AMR gene target. Source: ARG-ANNOT
OXA-type Beta-Lactamase AMR gene target. Source: ARG-ANNOT
Verone Integron-Encoded Metallo- (VIM) Beta-Lactamase AMR gene target. Source: ARG-ANNOT
CTX-M Beta-Lactamase AMR gene target. Source: ARG-ANNOT
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
Impenemase (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-Id-C-auris-508.pdf
Norovirus GI ORF1-ORF2 junction gene target. Source: https://wwwnc.cdc.gov/eid/article/17/8/10-1837-t2#r27
Norovirus GII ORF1-ORF2 junction gene target. Source: https://wwwnc.cdc.gov/eid/article/17/8/10-1837-t2#r27
Influenza A 1 gene target. Source: https://www.cdc.gov/coronavirus/2019-ncov/lab/multiplex.html?CDC_AA_refVal=https%3
Influenza A 2 gene target. Source: https://www.cdc.gov/coronavirus/2019-ncov/lab/multiplex.html?CDC_AA_refVal=https%3
Influenza A gene target; Detection of InfA1 and InfA2 targets was performed on a single fluorescence channel, such that distin
Influenza B gene target. Source: https://www.cdc.gov/coronavirus/2019-ncov/lab/multiplex.html?CDC_AA_refVal=https%3A
Campylobacter jejuni gene target. Source: https://www.sciencedirect.com/science/article/pii/S0882401017303728?via%3Dih
Adenovirus Group F41 Fiber gene target. Source: https://www.sciencedirect.com/science/article/pii/S0022347608006744?via
RSV-A and RSV-B gene tartget. Primer sets are reactive to both viruses. Two separate probes for RSV-A and RSV-B. https://cd
Shigella gene target
Eukaryotic gene target (e.g., Cyclospora)
Macrolide resistance target
STEC gene target
STEC gene target
STEC gene target
RSV gene target
Fluoroquinolone gene target
Please contact NWSS staff to submit data using the "Other" category, or to request that values be added to the vocabulary.

	vs_pcr_type Value Set
	qpcr
	ddpcr
	qiagen dpcr
	fluidigm dpcr
	life technologies dpcr
	raindance dpcr
	dpcr

9-ncov%2Flab%2Fmultiplex-primer-probes

9-ncov%2Flab%2Fmultiplex-primer-probes

xist. An example is the GT-Digital Influenza

-ncov%2Flab%2Fmultiplex-primer-probes.

/rsv-surveillance/who-rsv-surveillance-stra

Description
Real-time PCR, also called 'quantitative' PCR
Used to refer specifically to BioRad digital droplet emulsification technology
Generic digital PCR

s.html
s.html
and SARS-CoV-2 Wastewater Surveillance Multiplex Assay Kits.
html

ategy-phase-26mar2021.-final.pdf?sfvrsn=d8b1c36a_9;%20https://journals.plos.org/plosone/articl

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]	

e?id=10.1371/journal.pone.0015098

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	

vs_reporting_jurisdiction

Value Set	Description
AL	Alabama
AK	Alaska
AS	American Samoa
AZ	Arizona
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

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_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
27-hr flow-weighted composite
26-hr flow-weighted composite
25-hr flow-weighted composite
24-hr flow-weighted composite
23-hr flow-weighted composite
22-hr flow-weighted composite
21-hr flow-weighted composite
20-hr flow-weighted composite
19-hr flow-weighted composite
18-hr flow-weighted composite
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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
72-hr time-weighted composite
48-hr time-weighted composite
47-hr time-weighted composite
46-hr time-weighted composite
45-hr time-weighted composite
44-hr time-weighted composite
43-hr time-weighted composite
42-hr time-weighted composite
41-hr time-weighted composite
40-hr time-weighted composite
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6-hr time-weighted composite
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3-hr time-weighted composite
2-hr time-weighted composite
1-hr time-weighted composite
48-hr manual composite
47-hr manual composite
46-hr manual composite
45-hr manual composite

44-hr manual composite
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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
35-hr passive sample
34-hr passive sample
33-hr passive sample
32-hr passive sample
31-hr passive sample
30-hr passive sample
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14-hr passive sample
13-hr passive sample
12-hr passive sample

11-hr passive sample
10-hr passive sample
9-hr passive sample
8-hr passive sample
7-hr passive sample
6-hr passive sample
5-hr passive sample
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
E.g., Moore swabs
E.g., Moore swabs
E.g., Moore swabs
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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
oncentration 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	

Use of semantic versioning began with v2.0.0. A description follows; see https://semv
Major changes (indicated by X in version X.Y.Z): not backwards compatible. In the con
Minor changes (indicated by Y in version X.Y.Z): backwards compatible functionality a
Patches (indicated by Z in version X.Y.Z): backwards compatible bug fixes. In the conte

Date of change	**New file name**
20200923	NWSS_DCIPHERForm_DataDictionary_Sent-to-states_9.23.20
20201020	NWSS_DCIPHERForm_DataDictionary_20201020
20201021	NWSS_DCIPHERForm_DataDictionary_20201021
20201103	NWSS_DCIPHERForm_DataDictionary_20201103
20201105	NWSS_DCIPHERForm_DataDictionary_20201104
20201201	NWSS_DCIPHERForm_DataDictionary_20201201
20201204	NWSS_DCIPHERForm_DataDictionary_20201204
20201215	NWSS_DCIPHERForm_DataDictionary_20201215
20201218	NWSS_DCIPHERForm_DataDictionary_20201218
20210111	NWSS_DCIPHERForm_DataDictionary_20210111
202101222	NWSS_DCIPHERForm_DataDictionary_20210122

202101225	NWSS_DCIPHERForm_DataDictionary_20210125
20210127	NWSS_DCIPHERForm_DataDictionary_20210127
202102110	NWSS_DCIPHERForm_DataDictionary_20210210
20210319	NWSS_DCIPHER_Data_Dictionary_v2.0.0_20210323

20210416	NWSS_DCIPHER_Data_Dictionary_v2.0.1_20210416
20210512	NWSS_DCIPHER_Data_Dictionary_v2.0.2_20210512

20210621	NWSS_DCIPHER_Data_Dictionary_v2.0.3_20210621
20210818	NWSS_DCIPHER_Data_Dictionary_v2.1.0_20210818

20211028	NWSS_DCIPHER_Data_Dictionary_v2.1.1_20211028
2021202	NWSS_DCIPHER_Data_Dictionary_v3.0.0_2021202
20211208	NWSS_DCIPHER_Data_Dictionary_v3.1.0_20211208

20220524	NWSS_DCIPHER_Data_Dictionary_v3.1.1_20220524
20220906	NWSS Data Dictionary_v3_1_3_20220906
20221018	NWSS Data Dictionary_v3_1_4_20221018
20221122	NWSS Data Dictionary_v3_1_5_20221122

20230322	NWSS Data Dictionary_v4.0.0_20230322
20230606	NWSS Data Dictionary_v5.0.0_20230606

ver.org/ for further details.
ntext of NWSS DCIPHER data submission, these are changes that w
dded. In the context of NWSS DCIPHER data submission, these ma
ext of NWSS DCIPHER data submission, these may be clarifications

Version
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3.1.0

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3.1.3

3.1.4

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5.0.0

ould cause submission (see note on Submission Requirements) of a
y be additions of non-required fields, name changes to non-requirec
of field descriptions, additions to value sets, or reorganization of the

Major changes

NA

None

Replaced Pascal Case variable names with snake case variable names to align with bulk upload template variables

None

None

Changed "Required Field" value for the 'state' variable in the "Wastewater Treatment Plant" table from blank to "Required"

None

None

None

None

None

None

None

None

1. New required fields (3): 'institution_type', 'sample_id', 'lab_id';
2. Name changes to required fields (2): 'state' changed to 'wwtp_jurisdiction', 'reporting_state' changed to 'reporting_jurisdiction';

None

None

None

None

None

1. Addition of a new required field 'pcr_gene_target' which should contain the information previously captured in 'pcr_target'.
2. Renaming of fields:
'sars_cov2_units' renamed to 'pcr_target_units'
'sars_cov2_avg_conc' renamed to 'pcr_target_avg_conc'
'sars_cov2_std_error' renamed to 'pcr_target_std_error'
'sars_cov2_cl_95_lo' renamed to 'pcr_target_cl_95_lo'
'sars_cov2_cl_95_up' renamed to 'pcr_target_cl_95_up'
'sars_cov2_below_lod' renamed to 'pcr_target_below_lod'

1. Renaming of fields:
'pcr_target_ref' renamed to 'pcr_gene_target_ref'

None

none

none

none

none

1. Changing existing fields to required (5): 'epaid', 'pretreatment', 'pasteurized', 'major_lab_method', 'major_lab_method_desc'

1. Add new required field: 'site_id'

data file, if unaltered, to fail upload. These may include addition of r
d fields, or changes to value sets, which will not prohibit upload but v
e metadata.

Minor changes

NA

1. Changed to allow for sampling location not associated with treatment plant;
2. EPAID no longer required

None

None

A number of changes were made to reflect the shift from form-based data submission, which had built-in validation prior to submission, to CSV file submission to DCIPHER:
1. Recharacterized "Pre-populated value set" values as "Allowed values";
2. Added variable type column

Changed 'composite_freq' from "Required" (if composite) to "Not required"

None

None

None

None

None

None

None

1. Important description change relevant for upstream sites for 3 fields: 'county_names', 'other_jurisdiction', and 'sewage_travel_time' (these previously pertained to the treatment plant but have been changed to pertain to the sampling site, which is more relevant);
2. Removal and addition of values in value sets (>2 fields): 'sample_location' ("primary influent" and "primary sludge" changed to "wwtp"), 'rec_eff_target_name' ("bovine coronavirus" changed to "bcov vaccine"), other fields where similar values with the same meaning were submitted have been consolidated into one value, and will be indicated in QC checks;
3. Addition of non-required fields (3): 'pasteurized', 'time_zone', 'solids_separation'
4. Name changes to non-required fields (4): 'hum_frac_target_phys' changed to 'other_norm_name', 'hum_frac_target_phys_ref' changed to 'other_norm_ref', 'hum_frac_phys_conc' changed to 'other_norm_conc', 'hum_frac_phys_unit' changed to 'other_norm_unit'

None

None

None

1. Addition of non-required fields:
'qc_ignore' has been added to allow samples to be intentionally excluded from the DCIPHER QC report;
'analysis_ignore' has been added to allow samples to be intentionally excluded from DCIPHER data analysis;
'dashboard_ignore' has been added to allow samples to be intentionally excluded from the DCIPHER dashboard;
'major_lab_method' has been added to allow reporting jurisdictions to identify major lab methods in their data, which may be useful for determining groups of SARS-CoV-2 results that can be reasonably compared;
'major_lab_method_desc' has been added to allow a brief description of the rationale for assigning a 'major_lab_method'.

None

1. Repurposing of existing fields:
'pcr_target' will be repurposed from the field where PCR gene target information is submitted to now capturing what the overall PCR target was. For example, 'n1' was previously submitted to indicate the target gene for total SARS-CoV-2 was n1. Now that information will be captured in 'pcr_gene_target' and 'pcr_target' will be 'sars-cov-2'. For variants, you would put the variant target gene in 'pcr_gene_target' and 'pcr_target' would be the variant name (currently 'delta' or 'omicron').

None

None

none

none

none

none

1. Changes to value sets: 'pcr_target' now allows 'caur', 'NoV GI', 'NoVGII', 'FLUAV', 'FLUBV', 'NVO', 'Cjejuni', 'HAdV-F', 'Col', 'Gly', 'Bla', 'Integrase', 'Tet'. 'pcr_gene_target' now allows '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', 'InfB', 'Cjejuni', 'HAdv-F'. 'sample_type' now allows '72-hr time-weighted composite'. 'pasteurized' no longer allows [empty]. 'pretreatment' no longer allows [empty]. 'extraction_method' now allows 'exclusions based sample preparation (ESP)'
2. Changes to dependencies of existing field: 'pcr_type' must be a type of dpcr if 'pcr_target' is <u>not</u> 'sars-covs-2', 'delta', 'omicron', '
3. Added 'epa_registry_id' field

1. Changes to value sets: 'extraction method' now allows 'sciencell viral rna isolation kit', 'thermo magmax viral/pathogen nucleic acid isolation kit'.

equired fields or name changes to required fields.

will be flagged in on-platform QC checks.

Patches

NA

Description of treatment plant changed to be 'identifiable name'

Added red to data source color scheme to denote DCIPHER generated variables.

Clarified that state variable response for WWTP should be 2-letter abbreviation.

A number of changes were made to reflect the shift from form-based data submission, which had built-in validation prior to submission, to CSV file submission:
1. Changed "Forced column" to "Required Field";
2. Changed possible responses for "Required Field" to "Not required" and "Required";
3. Changed "DCIPHER Form Format", "DCIPHER Form Pre-populated Value Set", and "DCIPHER Form Data Validation" column names to denote Internal-Use only;
4. Made all values lower case (not a major change because all values are cast to lower during file parsing);

Changed 'pcr_target_ref' description to "A publication, website, or description of the PCR gene target used"

Changed "Allowed values" from "[any]" to "0-100" for 'industrial_input' to clarify percentage units

Changed "Tooltip / descriptive text" for standard error and confidence interval fields so that '-1' is only entered when these values cannot be calculated

Changed "Tooltip / descriptive text" for 'ntc_amplify' field to be more specific: "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?" This definition aligns with the definition of positivity given on the NWSS webpage for Data Reporting and Analytics, and aligns with guidance provided by a ddPCR instrument manufacturer.

Added clarification to "Tooltip / descriptive text" for 'population_served' field to consider population estimates for upstream sampling locations: "if the sampling location is upstream of a treatment plant (i.e., sample_location = "upstream"), please use the estimated population served by the corresponding service area"

Added additional text and example to "Tooltip / descriptive text" for 'composite_freq' to clarify definition

1. Removed "Internal Use" columns;
2. Updated "Allowed values" column to make 'suggested' values more explicit (e.g., for fields that do not have a finite value set but have values that are commonly used) and to indicate where '-1' should be used to indicate unavailable data for required numeric fields;
3. Added "Notes" column to provide additional guidance, such as where appropriate to leave blank;
4. Clarified "Tooltip / descriptive text" for 'sars_cov2_std_error' and 'tss';
5. Changed "Display Variable Name" for 'population_served' for clarity

1. Additions to Value Sets:
'sample_type' now allows composite sample values for any integer duration from 1 to 30 hrs;
'flow_rate' now allows empty values to accommodate a 'sample_matrix' that is not a flowing liquid, such as "primary sludge" or "holding tank";
'concentration_method' now allows values that capture when solids and liquid are separated but both are tested, e.g., "membrane filtration with addition of mgcl2, membrane recombined with separated solids";
'pcr_target' now allows these additional values: "n", "s," "orf1a";
'rec_eff_spike_matrix' now allows [empty] values;
'hum_frac_target_chem' now allows [empty] values;
'hum_frac_target_mic' now allows [empty] values;
'other_norm_name' now allows [empty] values;
'hum_frac_mic_unit' now allows [empty] values;
'hum_frac_chem_unit' now allows [empty] values;
'other_norm_unit' now allows [empty] values;
2. Description clarification:
'other_jurisdiction' has been further clarified to indicate that this refers to locations that exist outside of county boundaries;
'sample_id' has been clarified to indicate that PII must not be included in this field;
'lab_id' has been clarified to indicate that PII is discouraged from being included in this field;
the 'jurisdiction id' data type description has been modified to explicitly state that is is not case sensitive, which was previously and is still described in the note on all data types in the Read Me tab

1. Additions to Value Sets:
'extraction_method' now allows "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)";
'pcr_target' now allows "ddcov_n" and "ddcov_e"

1. Additions to Value Sets:
'rec_eff_spike_matrix' now allows "dewatered solids";
'flow_rate' now allows empty values when SARS-CoV-2 units are provided on a per mass sludge basis;
'concentration_method' now allows "innovaprep ultrafiltration";
'extraction_method' now allows "qiagen qiaamp buffers with epoch columns";
'hum_frac_target_mic' and 'other_norm_name' both now allow "f+ rna coliphage" and "f+ dna coliphage";
2. Description clarification:
'pretreatment' has been clarified to indicate that this field pertains to both chemicals added to the sample and chemicals added as part of the treatment train upstream of the sample collection point, but that pasteurization should be specified in the 'pasteurized' field

1. Additions to Value Sets:
'extraction_method' now allows "zymo quick-rna fungal/bacterial miniprep #r2014";
'pcr_target' now allows "ip2 and ip4 combined";
'sars_cov2_below_lod' now allows [empty] values;
'concentration_method' now allows "ceres nanotrap";
2. Corrections to Value Sets (value yet to be used):
'reporting_jurisdiction' value for Arkansas has been corrected to "AR";
'extraction_method' value "qiange allprep dna/rna kit" has been corrected to "qiagen allprep dna/rna kit";
3. Dependent Fields clarification:
Dependent Fields for 'flow_rate' has been clarified to indicate that 'flow_rate' can have an [empty] value when SARS-CoV-2 RNA is measured on a per unit wastewater solids basis, rather than a per volume wastewater basis;
4. Dependent Fields change:
All uncertainty fields now allow [empty] values, regardless of the values submitted for the other uncertainty fields. In other words, the three fields 'sars_cov2_std_error', 'sars_cov2_cl_95_lo', and 'sars_cov2_cl_95_up' are now all allowed to be [empty];
5. Requirement dropped:
'sars_cov2_std_error', 'sars_cov2_cl_95_lo', 'sars_cov2_cl_95_up', and 'sars_cov2_below_lod' are no longer required.

1. Additions to Value Sets:
'concentration_method' now allows "aloh3 precipitation";
'rec_eff_target_name' now allows "heat inactivated sars-cov-2 virus";
'extraction_method' now allows "qiagen ez1 virus mini kit v2.0" and "thermo magmax microbiome ultra nucleic acid isolation kit";
'sample_type' now allows composite sample values for any integer duration from 1 to 48 hrs;
'vs_rec_eff_target_name' now allows "bcov culture" and "brsv culture";
'extraction_method' now allows "zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)";
'concentration_method' now allows "zymo environ water rna kit/ zymo environ water rna kit (cat. r2042)";
2. Description clarification:
'capacity_mgd' has been clarified to indicate that this should be the capacity for which the plant is permitted;
3. Description change:
'county_names' has been changed to ask for FIPS codes rather than names; it also now takes values for both counties and county equivalents;
'other_jurisdiction' has been deprecated, since all jurisdictions previously specified in this field should now be specified in the 'county_names' field. Submitting this field will not interfere with data upload, but this field will no longer be used;
4. Requirement dropped:
'other_jurisdiction' is no longer required;

1. Additions to Value Sets:
'vs_other_norm_name' now allows "rnase p";
'vs_institution_type' now allows 'other_worksite'
'vs_pcr_gene_target' now allows 'delta' and 'omicron' genes targets. See 'vs_pcr_gene_target' for the updated valueset options
'vs_pcr_target' now **<u>only</u>** allows 'sars-cov-2', 'delta', and 'omicron'
2. Field description modifications:
Many PCR fields have been modified to reflect the new PCR targets now able to be submitted using the dynamic 'pcr_target' fields as opposed to the total SARS-CoV-2 specific descriptions.

None

1.Additions to Value Sets:
'vs_concentration_method' now allows 'membrane filtration with addition of mgcl3'
'vs_extraction_method' now allows 'luminultra wastewater extraction kit', 'qiaamp viral rna kit', 'trizol and RNA purificaton kit', 'trizol, garnet bead beating, alcohol precipitation', 'zymo quick-rna viral 96 kit #r1041', 'zymo quick-rna viral kit #r1035', 'qiagen qiaamp dsp viral rna mini kit'
'vs_pcr_gene_target' now allows 'wt214', 'ins214epe', 'del142-144', 'del156-157', 'del31-33'
'vs_pcr_type' now allows 'qiagen dpcr', 'fluidigm dpcr', 'life technologies dpcr', 'raindance dpcr', 'dpcr'
'vs_rec_eff_target_name' now allows 'murine hepatitis virus'
'vs_reporting_jurisdiction' now allows 'AP', 'CN', 'CVBPI', 'EBCI', 'GTBI', 'MAT', 'NPT', 'OMT', 'SBT', 'TRIT', 'ZP'
'vs_sample_type' now allows '120-hr passive sample', from '48-hr passive sample' to '1-hr passive sample' in one hour increments
2. Field description modified:
'pcr_gene_target' description modified to clarify different gene target concentrations should not be averaged

1. Additons to Value Sets: 'pcr_gene_target' now allows 'CDC N1 (GT-Digital)', 'CDC N2 (GT-Digital)', 'N2 (PREvalence)', 'E (PREvalence)'. 'rec_eff_target_name' now allows: 'MHV (PREvalence)', 'BCoV (GT-Digital)'. 'hum_frac_target_mic' now allows: 'PMMoV (GT-Digital)'

1. Additions to Value Sets: 'pcr_target' now allows: 'hMPXV', 'hMPXV Clade I', and 'hMPXV Clade II'. 'rec_eff_target_name' now allows: parapoxvirus'. 'pcr_gene_target' now allows: 'E9L-NVAR', 'G2R_G', 'G2R_WA', 'C3L', 'E9L-OPX3', 'B6R', 'B2R', and 'gtmol_hMPXV'

1. Additions to Value Sets: 'pcr_gene_target' now allows 'a67v/del69/del70'. Reporting_jurisdiction now allows: 'PBCI'.

1. Addition to Value Sets:'concentration_methods' now allows: 'water concentrating buffer (R2042-1)'; 'extraction_method' now allows 'monarch total RNA miniprep kit (new england biolabs) + onestep PCR inhibitor removal kit (zymo)'; 'pcr_gene_target' now includes 'p13L'; 'sample_type' now includes '72-hr time-weighted composite'.

1. Clarifications of field or value set descriptions (2): 'zipcode', 'capacity_mdg', 'test_result_date', 'pcr_target_avg_conc', 'pcr_target_std_error', 'pcr_target_cl_95_lo', 'pcr_target_cl_95_up'
2. Added website to look-up NPDES ID and EPA Registry ID to 'Read Me' and to description in 'Metadata' tabs.
3. Removed space from "other long term care" value for 'institution type'