

General Notes

The level of measure for NWSS 1CDP 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 the "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 i 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:	
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-2 quantitative (real time) PCR or digital PCR.

Field Name Color Key	
	Data that may be generated by the reporting jurisdiction public health
	Data likely generated by testing laboratories
	Data likely generated by wastewater utilities
	New fields or changes to existing fields
Document Tabs	
Metadata	This tab contains a comprehensive line list of all approved NWSS varia name, description, data type, units, submission requirements, and de
Value Sets	Provides standardized, approved value sets for variables listed in the l along with their corresponding descriptions.
Change Log	This tab maintains a chronological record of all modifications made to changes made to each new version.
Associated PCR and Gene Targets	This tab maps each approved pcr_target to its corresponding pcr_gen

specified on a separate row in the CSV file. For example, if N1 and N2 are both measured for the same sample, including 'sample_id', should be repeated across those rows. In general, this format can be thought of as "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 included, conditional on the completion of another field. Omission of these fields will not interfere with upload of the file.

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

number (<2-letter abbreviation><#####>). Search engine to locate this identifier is available here: <https://echo.epa.gov/facilities/facility-search>. Search engine to locate this identifier is available here: <https://echo.epa.gov/facilities/facility-search>. Offsets can be found at <https://www.timeanddate.com/time/zone/usa>. Alphanumeric 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-PCR. 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

ables used within the dataset. For each variable, the following information is provided: variable dependencies.

Metadata tab. Values are grouped by their associated variable and include permissible values

the data dictionary. Each entry includes a new file name, version, and a brief description of the

e_targets, forming a relational reference between the two variables.

[REDACTED]

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[REDACTED]

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re data file, but will

[REDACTED]

[REDACTED]

no.epa.gov/facilities
r?mediaSelected=cwa

[REDACTED]

[REDACTED]

R (reverse
i, 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	
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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 24 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
validated_methods	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
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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 <u>not</u> 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_me]
Method used for nucleic acid extraction from the sample	[See Value Sets: vs_extraction_metho]
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_na]
Matrix into which the recovery efficiency control target is spiked	[See Value Sets: vs_rec_eff_spike_ma]
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]
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]
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_c]

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. [sample id]

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.

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 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'.

[\[See Value Sets: vs_yne\]](#)

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.

[\[See Value Sets: vs_yne\]](#)

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.

[\[See Value Sets: vs_yne\]](#)

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.

[\[See Value Sets: vs_yne\]](#)

The date on which this PCR target measurement was made

[date greater than sample collect date and less than 1CDP 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]
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]
Concentration of target specified in 'other_norm_name'	[float]; [empty]
Concentration units of target specified in 'other_norm_name'	[See Value Sets: vs_mic_chem_units]
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]
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]

Units

[Submission Requirement](#)

[none]

Required

Required

[none]

Required

[none]

Required

[none]

Required

Hours

Not required

[none]

Required

[none]

Required

[none]

Required

[none] Required

[none] Not required

[none] Required

[none] Required

Million gallons per day (MGD) Required

percent Not required

[none] Not required

[none] Not required

[none] Required

If flow-weighted composite:
number per million gallons; if time-
weighted or manual composite:
number per hour

Not required

[none]

Required

Hours

Not required

Celsius

Not required

[none]

Required

[none]

Not required

[none]

Not required

[none]

Required

[none]

Required

Hours

Not required

Celsius

Not required

Hours

Not required

Celsius

Not required

mL

Not required

[none]	Not required
[none]	Required
[none]	Required
log10 copies/mL	Required
[none]	Required
[none]	Required
[none]	Required
[none]	Required
[none]	Required
[none]	Required
[none]	Not required
[none]	Not required
[none]	Not required
[none]	Not required
[none]	Not required
[none]	Not required
[none]	Required
[none]	Required
[none]	Required
[none]	Required

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

[none]

Not required

[none]

Not required

[none]

Not required

[none]

Not required

[none]

Required

[none]

Required

[units specified in
'pcr_target_units']

Required

[units specified in
'pcr_target_units']

Not required

[units specified in
'pcr_target_units']

Not required

[units specified in
'pcr_target_units']

Not required

[none]

Not required

[units specified in
'pcr_target_units']
[none]

Required

Required

percent

Required

[none]

Required

[none]	Required
[units specified in 'hum_frac_mic_unit']	Not required
[none]	Not required
[units specified in 'hum_frac_chem_unit']	Not required
[none]	Not required
[units specified in 'other_norm_conc']	Not required
[none]	Not required
[none]	Not required
[none]	Required

[none]	Required
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Dependent Fields

None

None

None

None

None

None

If 'sample_location' is "upstream", specify in
'sample_location_specify'

If sample_location is "upstream", then this must
have a non-empty value

None

None

None

None

None

None

None

None

None



None

None

None

None

None

if 'pretreatment' is "yes", then specify in
'pretreatment_specify'

if 'pretreatment' is "yes", then
'pretreatment_specify' must have a non-empty
field



None

None

None

None

None

None

None

None

None

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

None



None

The value selected for pcr_gene_target should align with the value selected for pcr_target

None

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

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

None

None

None

None



None

None

None

If 'pcr_target_units' is on a per volume wastewater basis (e.g., copies/l wastewater), and 'hum_frac_mic_conc' is empty, then 'flow_rate' is required and must be greater than zero. If a value for 'hum_frac_mic_conc' is provided, 'flow_rate' may be empty (i.e., measurements of wastewater solids are permitted empty values for 'flow_rate').

None

None

None

None

None

None

None

None

None

None

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

None

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
None

None

None

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

None

None

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_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

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

Invitroge Dynabeads Intact Virus Enrichment (Cat 10700D/10701D)

Description

<https://www.thermofisher.com/order/catalog/p>

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
Applied Biosystems MagMax Wastewater Ultra Nucleic Acid Isolation Kit
Zymo Quick-RNA Fecal/Soil Microbe Microprep Kit (Cat R2040)

vs_hum_frac_target_chem		
Description	Value Set	Description
	caffeine	
	creatinine	
	sucralose	
	ibuprofen	
	[empty]	

<https://www.thermofisher.com/order/catalog/product/A52606?SID=srch-srp-A52606>

<https://www.zymoresearch.com/products/quick-rna-fecal-soil-microbe-micropr>

vs_hum_frac_target_mic

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

ep-kit

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 officials

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

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

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

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

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

Solely higher education dormitory buildings

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

Other type of social services shelter

Individual residential buildings or institutions not captured in other categories

Any commercial facility not captured in other commercial facility categories

vs_mic_chem_units

Value Set

copies/L wastewater

log10 copies/L wastewater

copies/g wet sludge

log10 copies/g wet sludge

copies/g dry sludge

log10 copies/g dry sludge

micrograms/L wastewater

log10 micrograms/L wastewater

micrograms/g wet sludge

log10 micrograms/g wet sludge

micrograms/g dry sludge

log10 micrograms/g dry sludge

Description

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

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

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

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

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

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

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

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

vs_mic_chem_units_e

Value Set

copies/L wastewater

log10 copies/L wastewater

copies/g wet sludge

log10 copies/g wet sludge

copies/g dry sludge

log10 copies/g dry sludge

micrograms/L wastewater

log10 micrograms/L wastew:

micrograms/g wet sludge

log10 micrograms/g wet sluc

micrograms/g dry sludge

log10 micrograms/g dry slud

[empty]

Description

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

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

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

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

ater

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

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

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

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

vs_num_no_target_control

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

0	
1	
2	
3	
more than 3	

vs_other_norm_name

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

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

vs_pcr_targetValue 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

Name

Alum

Aduo

Ttri

Sste

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

Necator americanus

Ascaris lumbricoide

Ancylostoma duodenale

Trichuris trichiura

Strongyloides stercoralis

vs_pcr_gene_target

Value Set

n
n1
n2
n3
e_sarbeco
n_sarbeco
rdrrp_sarsr
6575/
niid_2019-ncov_n
rdrrp gene / ncov_ip2
rdrrp 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

MeV_N_Gene_N1 (CDC)

MeV_N_Gene_WT_v2 (WWScan)

Name_ITS-2 (GT-Digital)

Alum_Sat-DNA (GT-Digital)

Aduo_ITS-2 (GT-Digital)

Ttri_ITS-1 (GT-Digital)

Sste_18S-rRNA (GT-Digital)

caur_5.8S (GT-Digital)

InfA_M_Gene (MO)

InfA_H1_M2_Gene (MO)

InfA_H3_NP_Gene (MO)

InfB_M2_Gene (MO)

Description

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

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, si

sars-cov-2 gene target

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hMPXV gene target. orthopoxvirus DNA polymerase. CDC Assay all hMPXV and non-variola Orthopoxvirus.

hMPXV gene target. G2R_G primers and probe: detects all MPXV strains . <https://doi.org/10.1016/j.jvirom>

hMPXV Clade II gene target. hMPXV G2R_WA primers and probe: detects Clade II viruses.CDC <https://doi.org/10.1016/j.jvirom.2019.104622>

hMPXV Clade I gene target. hMPXV C3L primers and probe: detects Clade I viruses . CDC <https://doi.org/10.1016/j.jvirom.2019.104622>

hMPXV gene target. Envelope protein gene CDC Assay; selective for MPXV. CDC <https://doi.org/10.1016/j.jvirom.2019.104622>

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 Carbapenem (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

Cepharmycin 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-lc>

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

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

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

Verily NWSS commercial contract

Verily NWSS commercial contract

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
Singleplex Digital PCR Testing of Influenza A, H1pdm09, H3, and H5 from Wastewater IFU for wastewater testing.
GT-Molecular Digital Mpx Clade I OPG210 assay, for example:
<https://www.gtmolecular.com/product/gt-digital-mpox-clade-i-opg210-rox-add-on-assay-qiacyuity/>;
<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-qiacyuity-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
THIS ENTRY SHOULD ONLY BE CHOSEN AFTER CONSULTATION WITH THE NWSS PROGRAM. Measles virus
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-rl>
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 Mpx Clade II assay, for example: https://www.gtmolecular.com/product/dpcr-nvompox-assay-kit-for-the-bio-rad-qx200-v1-1-beta/?_gl=1*1rzwjlf*_gcl_au*MjA5MzMzMtAzMi4xNzQ1NDI4MTA5*_ga*MTI4MjM1MDg0My4xNzQ1NDI4MTE5*_ga_N4HPZP2900*czE3NTI0OTg2MjkkkbzE4JGcxJHJHxNzUyNDk4Njc2JGoxMyRsMCRoMA..
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-qiagen-qiacyuity-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

THIS ENTRY SHOULD ONLY BE CHOSEN AFTER CONSULTATION WITH THE NWSS PROGRAM. Measles virus | Measles virus N Gene WT (wild type) assay target version 2. Modified from: <https://pmc.ncbi.nlm.nih.gov/>

GT-Molecular Digital *Necator*

americanus (NecA) ITS-2 Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: <https://www.gtmolecular.com/product/gt-digital-soil-transmitted-helminths-wastewater-panel-bio-rad-qx600/>

GT-Molecular Digital *Ascaris lumbricoides* (AscL) Satellite DNA Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: <https://www.gtmolecular.com/product/gt-digital-soil-transmitted-helminths-wastewater-panel-bio-rad-qx600/>

GT-Molecular Digital *Ancylostoma duodenale* (AnsD) ITS-2 Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: <https://www.gtmolecular.com/product/gt-digital-soil-transmitted-helminths-wastewater-panel-bio-rad-qx600/>

GT-Molecular Digital *Trichuris trichiura* (TriT) ITS-1 Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: <https://www.gtmolecular.com/product/gt-digital-soil-transmitted-helminths-wastewater-panel-bio-rad-qx600/>

GT-Molecular Digital *Strongyloides stercoralis* (StrS) 18S rRNA Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: <https://www.gtmolecular.com/product/gt-digital-soil-transmitted-helminths-wastewater-panel-bio-rad-qx600/>

GT-Molecular Digital *C. auris* assay, for example: <https://www.gtmolecular.com/product/gt-digital-c-auris-wastewater-surveillance-assay-kit-for-the-qiacuity-digital-pcr-system-v2-0/>

Influenza A M gene target developed by University of Missouri

Influenza A H1 M2 gene target developed by University of Missouri

Influenza A H3 NP gene target developed by University of Missouri

Influenza B M2 gene target developed by University of Missouri

vs_pcr_type

Value Set

detection and Quantqpcr

ddpcr

qiagen dpcr

fluidigm dpcr

life technologies dpcr

raindance dpcr

dpcr

uch that distinct measurements for N1 and

et.2010.07.012
10.1016/j.jviromet.2010.07.012
16/j.jviromet.2010.07.012
jcv.2006.03.012

l-C-auris-508.pdf
2#r27
t2#r27
ET IS INTENDED FOR USE TOGETHER WITH
ET IS INTENDED FOR USE TOGETHER WITH

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
tewater-surveillance-assay-kit-for-the-qia

/influenza/molecular-detection-of-influenza
/influenza/molecular-detection-of-influenza

testing.

N gene assay target (N3). From <https://pubmed.ncbi.nlm.nih.gov/1654441/>

RT-PCR.pdf
cs.est.4c05344
cs.est.4c05344
MC5328441/

N gene assay target (N1). From <https://pubmed.ncbi.nlm.nih.gov/articles/PMC5328441/>

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://>
† THE INFA1 PRIMER SET IN THE COMPLETE INFA ASSAY. Influenza A 2 gene target. Source: <https://>

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 Testir
gen-qiacyuity-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

bmed.ncbi.nlm.nih.gov/16274752/

bmed.ncbi.nlm.nih.gov/16274752/

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 Respirat
ing of Influenza A, H1pdm09, H3, and H5 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

Respiratory 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_n'

A sampling location other than "wwtp"

vs_sample_matrix

Value Set

raw wastewater

post grit removal

primary sludge

primary effluent

secondary sludge

secondary effluent

septage

holding tank

Description

Wastewater without any form of treatment applied to it

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

Sludge from the primary clarifier

Effluent from the primary clarifier

Sludge from the secondary clarifier

Effluent from the secondary clarifier

Wastewater sampled from within a septic tank

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

vs_sample_typeValue Set

grab

48-hr flow-weighted composite

47-hr flow-weighted composite

46-hr flow-weighted composite

45-hr flow-weighted composite

44-hr flow-weighted composite

43-hr flow-weighted composite

42-hr flow-weighted composite

41-hr flow-weighted composite

40-hr flow-weighted composite

39-hr flow-weighted composite

38-hr flow-weighted composite

37-hr flow-weighted composite

36-hr flow-weighted composite

35-hr flow-weighted composite

34-hr flow-weighted composite

33-hr flow-weighted composite

32-hr flow-weighted composite

31-hr flow-weighted composite

30-hr flow-weighted composite

29-hr flow-weighted composite

28-hr flow-weighted composite

27-hr flow-weighted composite

26-hr flow-weighted composite

25-hr flow-weighted composite

24-hr flow-weighted composite

23-hr flow-weighted composite

22-hr flow-weighted composite

21-hr flow-weighted composite

20-hr flow-weighted composite

19-hr flow-weighted composite

18-hr flow-weighted composite

17-hr flow-weighted composite

16-hr flow-weighted composite

15-hr flow-weighted composite

14-hr flow-weighted composite

13-hr flow-weighted composite

12-hr flow-weighted composite

11-hr flow-weighted composite

10-hr flow-weighted composite

9-hr flow-weighted composite

8-hr flow-weighted composite

7-hr flow-weighted composite
6-hr flow-weighted composite
5-hr flow-weighted composite
4-hr flow-weighted composite
3-hr flow-weighted composite
2-hr flow-weighted composite
1-hr flow-weighted composite
96-hr time-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
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6-hr time-weighted composite
5-hr time-weighted composite
4-hr time-weighted composite
3-hr time-weighted composite
2-hr time-weighted composite
1-hr time-weighted composite
96-hr manual composite
48-hr manual composite
47-hr manual composite
46-hr manual composite
45-hr manual composite
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43-hr manual composite
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8-hr manual composite
7-hr manual composite
6-hr manual composite
5-hr manual composite
4-hr manual composite
3-hr manual composite
2-hr manual composite
1-hr manual composite

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
29-hr passive sample
28-hr passive sample
27-hr passive sample
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25-hr passive sample
24-hr passive sample
23-hr passive sample
22-hr passive sample
21-hr passive sample
20-hr passive sample
19-hr passive sample
18-hr passive sample
17-hr passive sample
16-hr passive sample
15-hr passive sample
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

E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

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E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

E.g., Moore swabs

vs_solids_separation

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

filtration	Filtration to remove solids from a wastewater sample prior to AL
centrifugation	Centrifugation prior to or in the absence of a concentration st AK
gravity settling	Solids separated from liquid by allowing solids to settle by grav\AS
none	
[empty]	

vs_wwtp_jurisdiction

Value Set

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

Description	vs_yn	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	
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Use of semantic versioning began with v2.0.0. A description follows; see <https://semver.org/> for further details. Major changes (indicated by X in version X.Y.Z): not backwards compatible. In the context of NWSS DCIPHER data, this means that the data dictionary will change. Minor changes (indicated by Y in version X.Y.Z): backwards compatible functionality added. In the context of NWSS DCIPHER data, this means that the data dictionary will change. Patches (indicated by Z in version X.Y.Z): backwards compatible bug fixes. In the context of NWSS DCIPHER data, this means that the data dictionary will change.

Date of change	New file name	Version
20200923	NWSS_DCIPHERForm_DataDictionary_Sent-to-states_9.23.20	0.1.0
20201020	NWSS_DCIPHERForm_DataDictionary_20201020	0.2.0
20201021	NWSS_DCIPHERForm_DataDictionary_20201021	0.3.0
20201103	NWSS_DCIPHERForm_DataDictionary_20201103	0.3.1
20201105	NWSS_DCIPHERForm_DataDictionary_20201104	0.4.0
20201201	NWSS_DCIPHERForm_DataDictionary_20201201	0.5.0
20201204	NWSS_DCIPHERForm_DataDictionary_20201204	1.0.0
20201215	NWSS_DCIPHERForm_DataDictionary_20201215	1.0.1
20201218	NWSS_DCIPHERForm_DataDictionary_20201218	1.0.2
20210111	NWSS_DCIPHERForm_DataDictionary_20210111	1.0.3
20210122	NWSS_DCIPHERForm_DataDictionary_20210122	1.0.4

202101225	NWSS_DCIPHERForm_DataDictionary_20210125	1.0.5
20210127	NWSS_DCIPHERForm_DataDictionary_20210127	1.0.6
202102110	NWSS_DCIPHERForm_DataDictionary_20210210	1.0.7
20210319	NWSS_DCIPHER_Data_Dictionary_v2.0.0_20210323	2.0.0

20210416	NWSS_DCIPHER_Data_Dictionary_v2.0.1_20210416	2.0.1
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20210512	NWSS_DCIPHER_Data_Dictionary_v2.0.2_20210512	2.0.2
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20210621	NWSS_DCIPHER_Data_Dictionary_v2.0.3_20210621	2.0.3
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20210818	NWSS_DCIPHER_Data_Dictionary_v2.1.0_20210818	2.1.0
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20211028	NWSS_DCIPHER_Data_Dictionary_v2.1.1_20211028	2.1.1
20211202	NWSS_DCIPHER_Data_Dictionary_v3.0.0_20211202	3.0.0
20211208	NWSS_DCIPHER_Data_Dictionary_v3.1.0_20211208	3.1.0

20220524	NWSS_DCIPHER_Data_Dictionary_v3.1.1_20220524	3.1.1
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3.1.2

20220906	NWSS Data Dictionary_v3_1_3_20220906	3.1.3
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20221018	NWSS Data Dictionary_v3_1_4_20221018	3.1.4
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20221122	NWSS Data Dictionary_v3_1_5_20221122	3.1.5
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20230322	NWSS Data Dictionary_v4.0.0_20230322	4.0.0
20230606	NWSS Data Dictionary_v5.0.0_2023-06-06	5.0.0
20230710	NWSS Data Dictionary_v5.1.0_2023-07-10	5.1.0
20230905	NWSS Data Dictionary_v5.2.0_2023-09-06	5.2.0
20230926	NWSS Data Dictionary_v5.2.1_2023-09-26	5.2.1
20231109	NWSS Data Dictionary_v5.2.2_2023-11-15	5.2.2
20240628	NWSS Data Dictionary_v5.2.3_2024-06-28	5.2.3
20241007	NWSS Data Dictionary_v5.2.4_2024-10-07	5.2.4
20241122	NWSS Data Dictionary_v5.2.5_2024-11-22	5.2.5
20241220	NWSS Data Dictionary_v5.2.6_2024-12-20	5.2.6

20250128	NWSS Data Dictionary_v5.3.0_2025-01-28	5.3.0
20250312	NWSS Data Dictionary_v5.4.0_2025-03-12	5.4.0
20250317	NWSS Data Dictionary_v5.4.1_2025-03-17	5.4.1
20250409	NWSS Data Dictionary_v5.5.0_2025-04-09	5.5.0
20250529	NWSS Data Dictionary_v6.0.0_2025-05-29	6.0.0
20250812	NWSS Data Dictionary_v6.1.0_2025-08-12	6.1.0

20250918	NWSS Data Dictionary_v6.2.0_2025-09-18	6.2.0
20250929	NWSS Data Dictionary_v6.2.1_2025-09-29	6.2.1
20260130	NWSS Data Dictionary_v6.2.2_2026_01_30	6.2.2
20260204	NWSS Data Dictionary_v6.2.3_2026_02_04	6.2.3
20260309	NWSS Data Dictionary_v6.2.4_2026_03_09	6.2.4
20260427	NWSS Data Dictionary_v6.2.5_2026_04_27	6.2.5
20260519	NWSS Data Dictionary_v6.3.0_2026_05_19	6.3.0

5.

ata submission, these are changes that would cause submission (see note on Submission Requirements) of a data f
WSS DCIPHER data submission, these may be additions of non-required fields, name changes to non-required field
a submission, these may be clarifications of field descriptions, additions to value sets, or reorganization of the met:

Major changes

NA

None

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

None

None

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

None

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

None

None

None

None

None

None

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';

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

None

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

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'

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

none

none

none

none

none

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

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 not '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', and 'nucleomag (ref. 744220.4) using kingfisher automated instrument'; 'pcr_target' now allows 'RSV'; 'pcr_gene_target' now allows 'InfA1 and InfA2 combined' and 'RSV-A and RSV-B combined'.

1. Add new required field: 'site_id'

1. Changes to value sets: 'extraction_method' now allows 'sciencell viral rna isolation kit', 'thermo magmax viral/pathogen nucleic acid isolation kit', and 'nucleomag (ref. 744220.4) using kingfisher automated instrument'

1. Add new field: 'validated_methods'

1. Changes to value sets: 'extraction_method' now allows 'dneasy powersoil pro kit'.

1. Changes to value sets: 'extraction_method' now allows 'BOMB.bio protocol'; 'pcr_gene_target' description for 'n' that provides a source for gene target. 2. Removing [empty] as an allowed value for 'major_lab_method' and 'major_lab_method_desc'

1. Changes to value sets: pcr_target now allows 'FLUAV pdm H1', 'FLUAV A H5a', 'FLUAV A H5b', 'FLUAV A H5', 'FLUAV A H1', 'FLUAV A H3', 'FLUAV A H7', 'DENV-pan', 'DENV-1', 'DENV-2', 'DENV-3' and 'DENV-4'. 2. Changes to value sets: pcr_gene_target now allows 'INFA_H5 (Verily)', 'INFA_H5b (CDC)', 'FLUAV A H1_Cv1', '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)', and 'INFA_clade 2.3.4.4x (WHO)'. 3. Changes to value sets: reporting_jurisdiction now allows 'TMBCI'

1. Changes to value set: pcr_target now allows 'ev-d68' and 'OROV'. 2. Changes to value set: pcr_gene_target now allows 'vp1', 'OROV_S', 'OROV_Cv1', and 'OROV_Cv2'.

1. Changes to value set: pcr_gene_target now allows 'E3L 393' and '

1. Changes to description for pcr_gene_target value sets: descriptio

1. Changes to the value set: pcr_gene_target now allows INFA_H1pdm09 (CDC), and INFA_H3 (CDC).

1. Changes to the value set: pcr_gene_target now allows hMPXV_Clade_I OPG210 (GT-Digital), MeV_WT (GT-Digital), MeV_M_Gene_WT, and MeV_M_Gene_VA.

2. Changes to the value set: reporting_jurisdiction now allows AZMC.

3. Changes to the value set pcr_target now allows MeV.

1. Replacing all mentions of "DCIPHER" with "1CDP"

2. Changes to the value set pcr_gene_target now allows "MeV2_N_Gene"

3. Changes to the value set institution_type now allows for "airport"

1. Amendment to pcr_gene_target: change INFA_H5b (CDC) to INFA_H5 (CDC).

2. Remove value sets: pcr_target no longer allows FLUAV pdm H1, FLUAV A H5a, nor FLUAV A H5b.

3. Remove value set: pcr_gene_target no longer allows MeV2_N_Gene.

1. Inclusion of "PCR Target to Gene Target Assoc" sheet to highlight pcr_targets and corresponding gene targets.

1. Removed value set: pcr_gene_target no longer allows "E9L-OPX3".

2. Added value sets: pcr_gene_target now allows "hMPXV_Clade_II (GT-Digital)", "RSV (Wadsworth)", "INFA_H1pdm09 (Wadsworth)", "WNV (GT-Digital)", "WNV (Qiagen)", and "WNV_WNENV (CDC)".

3. Added value set: pcr_target now allows "WNV" (West Nile Virus)

1. Added value sets: pcr_target now allows "MeV_WT" and "MeV_VA".

2. Amendment to pcr_target and pcr_gene_target associations.

-The following pcr_gene_targets now correspond to pcr_target "MeV_WT":

"MeV_M_Gene_WT1"
"MeV_M_Gene_WT2"
"MeV_N_Gene_WT (WWScan)"
"MeV_WT (GT-Digital)"
"MeV_M_Gene_WT_Combined"

-The following pcr_gene_target now corresponds to pcr_target "MeV_VA"

"MeV_M_Gene_VA"

1. Addition of soil-transmitted helminths. Pcr_target now allows for: "Name", "Alum", "Aduo", "Ttri", and Sste.

2. Addition of pcr_gene_targets: "Name_ITS-2 (GT-Digital)", "Alum_Sat-DNA (GT-Digital)", "Aduo_ITS-2 (GT-Digital)", "Ttri_ITS-1 (GT-Digital)", "Sste_18S-rRNA (GT-Digital)", "caur_5.8S (GT-Digital)", "InfA_M_Gene (MO)", "InfA_H1_M2_Gene (MO)", "InfA_H3_NP_Gene (MO)", and "InfB_M2_Gene (MO)".

ile, if unaltered, to fail upload. These may include addition of requirements, or changes to value sets, which will not prohibit upload but will be added to the data.

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 "zympo 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 **only** 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'

dD14-16'.

ns changed for InfA1, InfA2, InfA1 and InfA2 combined, and INFA_H.

1. Changes to the value set: pcr_gene_target now allows FLUAV A H

1. Changes to the value set: pcr_gene_target now allows MeV_N_Gene_N3 (CDC), RUBV_gp1_gene, MuV_N_gene_v2 (CDC), MeV_M_Gene_WT1, MeV_M_Gene_WT2, and MeV_N_Gene_WT (WWScan).

2. Changes to the value set: pcr_target now allows RUBV and MuV.

3. Change pcr_gene_target value "MeV_M_Gene_WT" to "MeV_M_Gene_WT_Combined".

4. Amendment to the pcr_gene_target MeV_M_Gene_WT_Combined description.

5. Amendment to pcr_target descriptions for FLUAV A H1 and FLUAV A H5.

1. Amendment to pcr_gene_target descriptions for "n", "RSV-A and RSV-B combined", "InfB", "InfA1 and InfA2 combined", "INFA_H1pdm09 (CDC)", "INFA_H3 (CDC)", and "INFA_H5 (CDC)".

1. Modified the description for pcr_target "MeV".

1. Changes to the value set: pcr_gene_target now allows "FLUAV A H1_Cv3".

1. Add "Applied Biosystems MaxMax Wastewater Ultra Nucleic Acid Isolation Kit" to the list of approved values for extraction_method.

2. Add value sets: pcr_gene_target now allows "MeV_N_Gene_N1 (CDC)".

3. Modify value set: change the description for pcr_gene_target "MeV_N_Gene_N3 (CDC)".

1. Modify extraction_method value: change "Applied Biosystems MaxMax Wastewater Ultra Nucleic Acid Isolation Kit" to "Applied Biosystems MagMax Wastewater Ultra Nucleic Acid Isolation Kit"

1. Add value set: pcr_gene_target now allows "MeV_N_Gene_WT_v2 (WWScan)"

1. Add value set: extraction_method now allows "Zymo Quick-RNA Fecal/Soil Microbe Microprep Kit (Cat R2040)"

2. Add value set: concentration_method now allows "Invitroge Dynabeads Intact Virus Enrichment (Cat 10700D/10701D)"

1. Updated the dependency language for flow_rate.

2. Updated the description of sample_id to now allow for 24 characters.

ed fields or name changes to required fields.
e flagged in on-platform QC checks.

5b(CDC). 2. Change to value set: pcr_gene_target now allows INFA_H5 (GT-Digital) and FLUAV A H1_Cv2

I3_Cv2

[illegible]

omicron		
NVO	Non-Variolla Orthopoxvirus. Source: CDC https://www.cdc.gov/mmwr/volumes/71/wr/mm7128e1.htm	
hMPXV		
hMPXV Clade I	https://www.cdc.gov/mpox/outbreaks/2023/index.html	

hMPXV Clade II		
caur	Candida auris. Source: KEGG	
NoV GI	Norovirus GI. Source: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3446575/ https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3446575/	
NoV GII	Norovirus GII. Source: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3446575/	
FLUAV	Influenza A. Source: Bacterial and Viral Bioinformatics Resource Center (BV-BRC)	
FLUBV	Influenza B. Source: Bacterial and Viral Bioinformatics Resource Center (BV-BRC)	
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	
FLUAV A H5	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	
FLUAV A H1	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	

FLUAV A H3	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	
FLUAV A H7	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	
DENV-pan	Dengue viruses https://www.cdc.gov/dengue/index.html	
DENV-1	dengue serotype 1 https://www.cdc.gov/dengue/index.html	
DENV-2	dengue serotype 2 https://www.cdc.gov/dengue/index.html	
DENV-3	dengue serotype 3 https://www.cdc.gov/dengue/index.html	
DENV-4	dengue serotype 4 https://www.cdc.gov/dengue/index.html	
OROV	Oropouche virus: https://www.cdc.gov/oropouche/about/index.html	
MeV_WT	Wildtype Measles Virus	
MeV_VA	Vaccine-associated Measles Virus	
MeV	Pan-Measles, that does not distinguish vaccine-associated and wild-type measles virus	
RUBV	Rubella Virus	
MuV	Mumps Virus	
WNV	West Nile Virus	
EV-D68	Enterovirus D68 target	
Name	Necator americanus	
Alum	Ascaris lumbricoide	
Aduo	Ancylostoma duodenale	
Ttri	Trichuris trichiura	
Sste	Strongyloides stercoralis	

vs_pcr_gene_target
Value Set
n
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
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
B6R
gtmol_hMPXV
C3L
hMPXV_Clade_I OPG210 (GT-Digital)

E3L 393
dD14-16
G2R_WA
hMPXV_Clade_II (GT-Digital)
caur
caur_5.8S (GT-Digital)
NoV GI
NoV GII
InfA1
InfA2
InfA_M_Gene (MO)
InfA1 and InfA2 combined
InfB
InfB_M2_Gene (MO)
Cjejuni
HAdV-F
MCR-1.1
VanA-A
blaNDM
blaKPC
blaOXA-48
blaVIM
blaCTX-M-1
blaCMY
blaTEM
blaSHV
blaIMP
Class I Integrase
TetW
RSV-A and RSV-B combined
RSV (Wadsworth)
INFA_H5 (Verily)
INFA_H5 (CDC)
INFA_H5 (GT-Digital)
INFA_H5Nx (WHO)
INFA_clade 2.3.4.4x (WHO)
FLUAV A H1_Cv1
FLUAV A H1_Cv2
FLUAV A H1_Cv3
INFA_H1pdm09 (CDC)
INFA_H1pdm09 (Wadsworth)
InfA_H1_M2_Gene (MO)

FLUAV A H3_Cv1
INFA_H3 (CDC)
FLUAV A H3_Cv2
InfA_H3_NP_Gene (MO)
FLUAV A H7_Cv1
DENV-pan1
DENV-1-NS5
vp1
DENV-2-E gene
DENV-3-prM
DENV-4-prM
OROV_S
OROV_Cv1
OROV_Cv2
MeV_M_Gene_WT1
MeV_M_Gene_WT2
MeV_N_Gene_WT (WWScan)
MeV_WT (GT-Digital)
MeV_M_Gene_WT_Combined
MeV_N_Gene_WT_v2 (WWScan)
MeV_M_Gene_VA
MeV_N_Gene_N3 (CDC)
MeV_N_Gene_N1 (CDC)
RUBV_gp1_gene
MuV_N_gene_v2 (CDC)
WNV (GT-Digital)
WNV (Qiagen)
WNV_WNENV (CDC)
vp1
Name_ITS-2 (GT-Digital)
Alum_Sat-DNA (GT-Digital)
Aduo_ITS-2 (GT-Digital)
Ttri_ITS-1 (GT-Digital)
Sste_18S-rRNA (GT-Digital)

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[illegible]

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THIS ENTRY SHOULD ONLY BE CHOSEN AFTER CONSULTATION WITH THE NWSS PROGRAM. THIS PRIMER SET IS INTENDED
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Influenza A M gene target developed by Univerisity of Missouri
Influenza A gene target; Detection of InfA1 and InfA2 targets is performed in a single fluoescence channel, such that distir
Transcription PCR for Influenza A Virus, Influenza B Virus, and Severe Acute Respiratory Syndrome Coronavirus 2, https://v
A, H1pdm09, H3, and H5 from Wastewater IFU for wastewater testing; Also includes commercial kits that use the CDC infA
Multiplex Assay Kit for the QIAcuity™ Digital PCR System.
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Colistin AMR gene target. Source: ARG-ANNOT
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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
Beta-Lactamase AMR gene target. Source: ARG-ANNOT
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Protocol 2: Real-time RT-PCR for Influenza A(H5) HA gene https://cdn.who.int/media/docs/default-source/influenza/mole
Protocol 2: Real-time RT-PCR for Influenza A(H5) HA gene https://cdn.who.int/media/docs/default-source/influenza/mole
Verily NWSS commercial contract
Verily NWSS commercial contract
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Singleplex Digital PCR Testing of Influenza A, H1pdm09, H3, and H5 from Wastewater IFU for wastewater testing.
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Singleplex Digital PCR Testing of Influenza A, H1pdm09, H3, and H5 from Wastewater IFU for wastewater testing.
Verily NWSS commercial contract H3 v2
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Verily NWSS commercial contract
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GT-Molecular Digital Necator
americanus (NecA) ITS-2 Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: https://www.gtmolecular.com/product/gt-digital-necator-americanus-its-2-gene
GT-Molecular Digital Ascaris lumbricoides (AscL) Satellite DNA Gene from Soil-Transmitted Helminths Wastewater Surveillance Panel v1.0, for example: https://www.gtmolecular.com/product/gt-digital-ascaris-lumbricoides-satellite-dna-gene
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ga*MTI4MjM1MDg0My4xNzQ1NDI4MTE5*_ga_N4HPZP2900*czE3NTI0OTg2MjkkbzE4JGcxJHQxNzUyNDk4N

gene target. Source: <https://www.cdc.gov/flu/php/laboratories/influenza-sars-cov-2-multiplex-assay.html>

gene target. Source: <https://www.cdc.gov/flu/php/laboratories/influenza-sars-cov-2-multiplex-assay.html>

). CDC IFU Source: Qiagen QIAcuity® Digital PCR (dPCR) Duplex Assay for Detection and Quantification of SAR

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

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2JGoxMyRsMCRoMA..; <https://www.gtmolecular.com/product/gt-digital-nvompox-assay-kit-for-the-qiacl>

S-CoV-2 and Respiratory Syncytial Virus (RSV) in Wastewater (Version 2).

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[illegible]

⌂NzQ1NDI4MTE5*_ga_N4HPZP2900*czE3NTI0OTg2MjkkbzE4JGcxJHQxNzUyNDk4OTIyJGozMyRsMCRoMA..

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