

This is a submission template for batch deposit of 'SARS-CoV-2: wastewater surveillance; version		
GREEN fields are mandatory for NCBI. Your submission will fail if any mandatory fields are not co		
YELLOW fields are optional. Leave optional fields empty (or delete them) if no information is avai		
Purple fields are highly recommended for US submitters		
Hover over field name to view definition, or see https://www.ncbi.nlm.nih.gov/biosample/docs/att		
CAUTION: Be aware that Excel may automatically apply formatting to your data. In particular, tak		
TO MAKE A SUBMISSION:		
1. Complete this template table.		
2. Upload the file on the 'Attributes' tab of the BioSample Submission Portal at https://submit.ncbi		
If you have any questions, please contact us at biosamplehelp@ncbi.nlm.nih.gov .		
*sample_name	sample_title	bioproject_accession
6493.P		PRJNA839090
4119.D		PRJNA839090
3990.C		PRJNA839090

1.0' samples to the NCBI BioSample database (https://www.ncbi.nlm.nih.gov/biosample/).			
Completed. If information is unavailable for any mandatory field, please enter 'not collected', 'not available'.			
tributes/ .			
Please take care with dates, incrementing autofills and special characters like / or -. Doublecheck that you			
.nlm.nih.gov/subs/biosample/ .			
*organism	*collection_date	collection_time	*geo_loc_name
wastewater metagenome	9/21/2022		USA: New Jersey
wastewater metagenome	9/20/2022		USA: Vermont
wastewater metagenome	9/21/2022		USA: Arkansas

applicable' or 'missing' as appropriate.		
r text file is accurate before uploading to BioSample.		
*isolation_source	collection_site_id	project_name
Wastewater	8675	GenomeTrakr
Wastewater	30	GenomeTrakr
Wastewater	9	GenomeTrakr; LFFM ww project

Field Name

sample_name
sample_title
isolation_source
collection_date
collection_time
geo_loc_name
organism

specimen_processing
specimen_processing_id
specimen_processing_details
ww_surv_target_1
ww_surv_target_1_known_prese
ww_sample_matrix
ww_sample_duration
ww_sample_type
ww_population
collection_site_id
project_name
bioproject_accession
collected_by
description
sequenced_by
ww_sample_site
ww_surv_jurisdiction
ww_surv_system_sample_id
ww_population_source
purpose_of_ww_sampling
purpose_of_ww_sequencing
ww_processing_protocol
collection_volume
concentration_method
extraction_method
extraction_control
ww_surv_target_1_conc
ww_surv_target_1_conc_unit
ww_surv_target_1_gene
ww_surv_target_1_protocol
ww_surv_target_2
ww_surv_target_2_conc
ww_surv_target_2_conc_unit
ww_surv_target_2_gene
ww_surv_target_2_known_prese
ww_endog_control_1

ww_endog_control_1_conc
ww_endog_control_1_protocol
ww_endog_control_1_units
ww_endog_control_2
ww_endog_control_2_conc
ww_endog_control_2_protocol
ww_endog_control_2_units
ww_flow
instantaneous_flow
ww_temperature
ww_total_suspended_solids
ww_industrial_effluent_percent
ww_ph
ww_sample_salinity
ww_pre_treatment
ww_primary_sludge_retention_ti

Definition

Sample Name is a name that you choose for the sample. It can have any format, but we suggest that you make it concise, unique, and descriptive.

Title of the sample. If no value is specified, this will be imputed as "SARS-CoV-2: wastewater surveillance sample from Wastewater Surveillance System (WWS) Sample ID: [Sample ID]".

Describes the physical, environmental and/or local geographical source of the biological sample from which the sample was derived.

The date on which the sample was collected; date/time ranges are supported by providing two dates from among the supported date formats.

For grab samples: the time of day the sample was collected in your timezone. 1-12 AM - 1-12 PM.

Geographical origin of the sample; use the appropriate name from this list <http://www.insdc.org/documents/country-qualifier-values>.

The most descriptive organism name for this sample (to the species, if possible). It is OK to submit an organism name that is not in the NCBI Taxonomy database.

Any laboratory processing applied to the sample from the point of collection through RNA extraction.

Identifier used to distinguish specimen processing treatments.

Detailed description of the specimen processing steps employed.

Taxonomic name of the surveillance target. For the COVID-19 response, use 'SARS-CoV-2'.

Is genetic material of the surveillance target(s) known to the submitter to be present in this wastewater sample? Presence detected by sequencing.

The wastewater matrix that was sampled.

Duration of composite sample collected, in units of hours, e.g., 24. Specify integer values. If the sample is not a composite sample, specify 0.

Type of wastewater sample collected

Number of persons contributing wastewater to this sample collection site; if unknown, estimate to the nearest order of magnitude.

ID that uniquely identifies the sample collection site among other sample collection sites in this BioProject. It must be unique across all BioProjects.

A concise name that describes the overall project, for example "Analysis of sequences collected from Antarctic soil"

The accession number of the BioProject(s) to which the BioSample belongs. If the BioSample belongs to more than one BioProject, list all accession numbers.

Name of persons or institute who collected the sample

Description of the sample.

The name of the agency that generated the sequence, e.g., Centers for Disease Control and Prevention.

The type of site where the wastewater sample was collected.

A jurisdiction identifier that can be used to support linking the sample to a public health surveillance system, e.g., va.

The sample ID used for submission to a public health surveillance system (e.g., CDC's National Wastewater Surveillance System).

Source of value specified in 'ww_population', e.g., wastewater utility billing records, population of jurisdiction encompassing the collection site.

The reason the sample was collected.

The reason the sample was sequenced, e.g., identification of mutations within a specific region, presence of clinically known mutations.

The protocol used to process the wastewater sample. Processing includes laboratory procedures prior to and including nucleic acid extraction.

The method used to concentrate a target organism, nucleic acid, organelle, etc within a sample.

The protocol used to extract nucleic acids (DNA or RNA) from a sample

Organism (or nucleic acid) used in the extraction protocol to determine successful extraction.

The concentration of the wastewater surveillance target specified in 'ww_surv_target_1' on a per wastewater unit basis, e.g., copies/L wastewater.

The units of the value specified in 'ww_surv_target_1_conc', e.g., copies/L wastewater.

The name of the gene quantified for the the surveillance target specified in 'ww_surv_target_1', e.g., N gene.

The protocol used to quantify 'ww_surv_target_1'. Specify a reference, website, or brief description.

Taxonomic name of the second surveillance target, if any

The concentration of the wastewater surveillance target specified in 'ww_surv_target_2' on a per wastewater unit basis, e.g., copies/L wastewater.

The units of the value specified in 'ww_surv_target_2_conc', e.g., copies/L wastewater.

The name of the gene quantified for the the surveillance target specified in 'ww_surv_target_2', e.g., ORF1-ORF2 junction.

Is genetic material of the surveillance target(s) known to the submitter to be present in this wastewater sample? Presence detected by sequencing.

The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., pepper mild mottle virus.

The concentration of the endogenous control specified in 'ww_endog_control_1' on a per wastewater unit basis, e.g., 700000

The protocol used to quantify 'ww_endog_control_1'. Specify a reference, website, or brief description.

The units of the value specified in 'ww_endog_control_1_conc', e.g., copies/L wastewater.

The name of an organism, gene, or compound used as an endogenous wastewater control, e.g., crassphage.

The concentration of the endogenous control specified in 'ww_endog_control_2' on a per wastewater unit basis, e.g., 140000

The protocol used to quantify 'ww_endog_control_2'. Specify a reference, website, or brief description.

The units of the value specified in 'ww_endog_control_2_conc', e.g., copies/L wastewater.

Daily volumetric flow through collection site, in units of liters per day, e.g., 110000000.

For grab samples: enter the an instantaneous volumetric flow measurement. The time of this measurement should correspond to the time of sampling.

Temperature of the wastewater sample at the time of sampling in Celsius, e.g., 25.

Total concentration of solids in raw wastewater influent sample including a wide variety of material, such as silt, decaying plant matter, etc., e.g., 1000.

Percentage of industrial effluents received by wastewater treatment plant, e.g., 10.

pH measurement of the sample, or liquid portion of sample, or aqueous phase of the fluid, e.g., 7.2.

Salinity is the total concentration of all dissolved salts in a liquid or solid (in the form of an extract obtained by centrifugation) e.g., 1000.

Describe any process of pre-treatment that removes materials that can be easily collected from the raw wastewater, e.g., flow through screens.

The time primary sludge remains in tank in hours, e.g., 4.

NWSS Requirement GenomeTrakr requirement

mandatory	mandatory
optional	optional
mandatory	mandatory
mandatory	mandatory
optional	optional
mandatory	mandatory
mandatory	mandatory
optional	optional
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optional	optional
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US FDA guidance for LFFM-funded laboratories

Biosamples are created at the extraction level (each RNA extraction will get a unique Bi
Enter the following "SARS-CoV-2: wastewater surveillance sample from Wastewater me
Describes the physical, environmental and/or local geographical source of the biological
The date on which the sample was collected; date/time ranges are supported by providin
For grab samples: the time of day the sample was collected in your timezone. 1:00 AM - :
Geographical origin of the sample. Use the appropriate country names from this list <http>
For all wastewater surveillance samples using this attribute package, use "wastewater
Critical for interpreting data. If the sample is a replicate, specify the type of replicate usin
Identifier used to distinguish specimen processing treatments, for example IDs used to inc
Detailed description of the specimen processing steps employed.
If a target for wastewater surveillance activity known, please list all. If looking for e
Select from "yes" or "no" picklist. Presence defined as microbiological evidence of the ta
Select a value from the pick list.
Specify integer values. If the sample is not a composite sample, use 0.
Select a value from the pick list.
Specify a numeric value. If unknown, estimate to the nearest order of magnitude. If no e
ID that uniquely identifies the sample collection site among other sample collection sites
Name of the coordinated sequencing efforts or project within which the sequencing was
Required if submission is linked to a BioProject. BioProjects are an organizing tool that
Name of person, lab, organization, or jurisdiction that led the program or study for whic
Opportunity to add additional free text metadata (was the sample a replicate?)
Name of the laboratory that generated the sequence data
Select a value from the pick list.
A jurisdiction identifier that can be used to support linking the sample to a public health
Not relevant for GenomeTrakr labs, unless a laboratory is also reporting results of this s
Provide a brief description. The purpose of this field is to provide a sense of the accurac
The reason the sample was collected. For GenomeTrakr labs, this is likely "public health
Describe the reason(s) for sequencing the wastewater sample, which will be dependent o
Populate the individual protocol attributes instead of summarizing here.
Enter the volume of the sample collected
The method used to concentrate a target organism, nucleic acid, organelle, etc within a s
The protocol used to extract nucleic acids (DNA or RNA) from a sample
The extraction control used to spike samples prior to processing and used to determine si
Submitters should report Ct values for RT qPCR and concentration values for ddPCR.
Suggested units for liquid wastewater samples are "Ct values", "copies per liter wastewa
For example, "N gene" for quantification of SARS-CoV-2 RNA using the US CDC N1 or N2 a
Specify a reference, website, or brief description.
If a target for wastewater surveillance activity known, please list all. If looking for emergi
For example, SARS-CoV-2 concentrations measured by RT-qPCR would be provided units
Units should be on a per unit of wastewater basis. Suggested units for liquid wastewater
For example, "N gene" for quantification of SARS-CoV-2 RNA using the US CDC N1 or N2 a
Select from "yes" or "no" picklist. Presence defined as microbiological evidence of the ta
Provide the name of the organism, gene, or compound used as an endogenous wastewat

Specify the concentration in units per liter wastewater or gram of sludge; the same units
Specify a reference, website, or brief description.

Units should be on a per unit of wastewater basis. Suggested units for liquid wastewater

Provide the name of the organism, gene, or compound used as an endogenous wastewat

Specify the concentration in units per liter wastewater or gram of sludge and specify the

Specify a reference, website, or brief description.

Units should be on a per unit of wastewater basis. Suggested units for liquid wastewater

Daily volumetric flow through collection site, in units of liters per day, e.g., 110000000.

For grab samples: enter the an instantaneous volumetric flow measurement. The time of

Temperature of the wastewater sample at the time of sampling in Celsius, e.g., 25.

[none]

[none]

[none]

[none]

Processes within the sewer distribution system or wastewater treatment plant that remo

[none]

US CDC guidance for ELC-funded laboratories	Example Data
wwtp12_raw_20210609	[none]
SARS-CoV-2: wastewater surveillance sample from Wastewater meta	[none]
Wastewater	[none]
12:00 PM	5/1/2021 sample_collect_date
USA:Virginia	8:00 AM
wastewater metagenome	[none]
g the options in the dropdown.	[none]
Identify replicates.	technical replicate, biological replicate_1, rep_1
SARS-CoV-2	Grabbed sample was separate
yes	[none]
	[none]
	raw wastewater
	24
	composite
	93000 population_served
Use an anonymized ID that does not identify the wastewater utility un	C.C. Williams Wastewater Trea
GenomeTrakr; LFFM ww project	
PRJNA99999	[none]
virginia department of health	[none]
	[Any useful descriptive metad:
	virginia division of consolidate
	wastewater treatment plant
	reporting_jurisdiction
va	sample_id
s123456	[none]
census block approximation of service area polygon	[none]
public health surveillance community-level	[none]
detection of target organism by RT PCR or ddPCR	[none]
	1L
peg precipitation + ultracentrifugation	[none]
	qiagen rneasy kit
murine norovirus	[none]
	200000 sars_cov2_avg_conc
copies/L wastewater	sars_cov2_units
issay.	N gene
	author et al, title, journal, year
ng pathogens, use "unknown". If no target specified, put "NA". For	[none]
For example, SARS-CoV-2 concentrations measured by RT-qPCR would	24000
Units should be on a per unit of wastewater basis. Suggested units for	copies/L wastewater
For example, "N gene" for quantification of SARS-CoV-2 RNA using the	ORF1-ORF2 junction
Select from "yes" or "no" picklist. Presence defined as microbiological	yes
pepper mild mottle virus	hum_frac_target_mic, hum_f

copies/L wastewater crassphage	700000000 hum_frac_mic_conc, hum_fra author et al, title, journal, year hum_frac_mic_unit, hum_frac hum_frac_target_mic, hum_f
copies/L wastewater Numeric value in units of liters per day. If only an instantaneous flow r this measurement should correspond to when the grab sample was taken, and should be reported in	140000000 hum_frac_mic_conc, hum_fra author et al, title, journal, year hum_frac_mic_unit, hum_frac
flow equilibration basin promotes settling of some solids	[none]
	110000000 25 500 10 7.2 100 4

US NWSS Data Dictionary	NCBI validation (value format)	Field Source
NA		SARS-CoV-2: clinical or host-associ
NA		SARS-CoV-2: clinical or host-associ
NA	{text}	PHA4GE
sample_collect_date	{timestamp}	SARS-CoV-2: clinical or host-associ
sample_collect_time	custom attribute	
wwtp_jurisdiction	{term};{term};{text}	SARS-CoV-2: clinical or host-associ
Enter the following "SARS-CoV-2: wastewater surv		SARS-CoV-2: clinical or host-associ
NA	custom attribute	
NA	custom attribute	
NA	custom attribute	
pcr_target	{text}	Wastewater surveillance-specific
NA	no yes	Wastewater surveillance-specific
sample_matrix	raw wastewater sewer pi	Wastewater surveillance-specific
composite_freq	{integer}{text}	Wastewater surveillance-specific
sample_type	grab composite swab-gr	Wastewater surveillance-specific
population_served	{integer}	Wastewater surveillance-specific
NA	custom attribute	Wastewater surveillance-specific
NA	custom attribute	
NWSS Umbrella linked local BioProject		SARS-CoV-2: clinical or host-associ
NA	{text}	SARS-CoV-2: clinical or host-associ
NA	{text}	SARS-CoV-2: clinical or host-associ
NA	{text}	SARS-CoV-2: clinical or host-associ
institution_type	correctional facility lon	Wastewater surveillance-specific
reporting_jurisdiction	{text}	Wastewater surveillance-specific
sample_id	{text}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
NA	public health surveillance c	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
pretreatment_specify	{text}	Wastewater surveillance-specific
NA	custom attribute	
concentration_method	custom attribute	Wastewater surveillance-sp
extraction_method	custom attribute	Wastewater surveillance-sp
NA (e.g. murine norovirucustom attribute		
pcr_target_avg_conc	{integer}	Wastewater surveillance-specific
pcr_target_units	{text}	Wastewater surveillance-specific
pcr_gene_target	{text}	Wastewater surveillance-specific
pcr_target_ref	{text}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
NA	{integer}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
NA	no yes	Wastewater surveillance-specific
hum_frac_target_mic	{text}	Wastewater surveillance-specific

hum_frac_mic_conc	{integer}	Wastewater surveillance-specific
hum_frac_target_mic_re	{text}	Wastewater surveillance-specific
hum_frac_mic_unit	{text}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
NA	{integer}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
NA	{text}	Wastewater surveillance-specific
flow_rate	{integer}	Wastewater surveillance-specific
NA	custom attribute	
collection_water_temp	{integer}	Wastewater surveillance-specific
tss	{integer}	Wastewater surveillance-specific
industrial_input	{integer}	Wastewater surveillance-specific
ph	{integer}	Wastewater surveillance-specific
conductivity	{integer}	Wastewater surveillance-specific
pretreatment	{text}	Wastewater surveillance-specific
NA	{integer}	Wastewater surveillance-specific

Notes/Questions

PHA4GE synonym

lated

lated

lated

lated

lated

protocols have occurred on the same grab or composite sample

specimen processing

speciman processing details

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lated

environmental site

pecific

pecific

organism	geo_loc_name	isolation_source
wastewater metagenome	USA: Alabama	Wastewater
	USA: Alaska	Clinical
	USA: Arizona	Animal
	USA: Arkansas	Missing
	USA: California	Restricted Access
	USA: Canal Zone	
	USA: Colorado	
	USA: Connecticut	
	USA: Delaware	
	USA: District of Columbia	
	USA: Florida	
	USA: Georgia	
	USA: Guam	
	USA: Hawaii	
	USA: Idaho	
	USA: Illinois	
	USA: Indiana	
	USA: Iowa	
	USA: Kansas	
	USA: Kentucky	
	USA: Louisiana	
	USA: Maine	
	USA: Maryland	
	USA: Massachusetts	
	USA: Michigan	
	USA: Minnesota	
	USA: Mississippi	
	USA: Missouri	
	USA: Montana	
	USA: Nebraska	
	USA: Nevada	
	USA: New Hampshire	
	USA: New Jersey	
	USA: New Mexico	
	USA: New York	
	USA: North Carolina	
	USA: North Dakota	
	USA: Ohio	
	USA: Oklahoma	
	USA: Oregon	
	USA: Pennsylvania	
	USA: Puerto Rico	
	USA: Rhode Island	
	USA: South Carolina	

USA: South Dakota
USA: Tennessee
USA: Texas
USA: Utah
USA: Vermont
USA: Virgin Islands
USA: Virginia
USA: Washington
USA: West Virginia
USA: Wisconsin
USA: Wyoming
Afghanistan
Albania
Algeria
American Samoa
Andorra
Angola
Anguilla
Antarctica
Antigua and Barbuda
Argentina
Armenia
Aruba
Ashmore and Cartier Islands
Australia
Austria
Azerbaijan
Bahamas
Bahrain
Baker Island
Bangladesh
Barbados
Bassas da India
Belarus
Belgium
Belize
Benin
Bermuda
Bhutan
Bolivia
Borneo
Bosnia and Herzegovina
Botswana
Bouvet Island
Brazil

British Virgin Islands
Brunei
Bulgaria
Burkina Faso
Burundi
Cambodia
Cameroon
Canada
Cape Verde
Cayman Islands
Central African Republic
Chad
Chile
China
Christmas Island
Clipperton Island
Cocos Islands
Colombia
Comoros
Cook Islands
Coral Sea Islands
Costa Rica
Cote d'Ivoire
Croatia
Cuba
Curacao
Cyprus
Czech Republic
Democratic Republic of the Congo
Denmark
Djibouti
Dominica
Dominican Republic
Ecuador
Egypt
El Salvador
Equatorial Guinea
Eritrea
Estonia
Eswatini
Ethiopia
Europa Island
Falkland Islands (Islas Malvinas)
Faroe Islands
Fiji

Finland
France
French Guiana
French Polynesia
French Southern and Antarctic Lands
Gabon
Gambia
Gaza Strip
Georgia
Germany
Ghana
Gibraltar
Glorioso Islands
Greece
Greenland
Grenada
Guadeloupe
Guam
Guatemala
Guernsey
Guinea
Guinea-Bissau
Guyana
Haiti
Heard Island and McDonald Islands
Honduras
Hong Kong
Howland Island
Hungary
Iceland
India
Indonesia
Iran
Iraq
Ireland
Isle of Man
Israel
Italy
Jamaica
Jan Mayen
Japan
Jarvis Island
Jersey
Johnston Atoll
Jordan

Juan de Nova Island
Kazakhstan
Kenya
Kerguelen Archipelago
Kingman Reef
Kiribati
Kosovo
Kuwait
Kyrgyzstan
Laos
Latvia
Lebanon
Lesotho
Liberia
Libya
Liechtenstein
Line Islands
Lithuania
Luxembourg
Macau
Madagascar
Malawi
Malaysia
Maldives
Mali
Malta
Marshall Islands
Martinique
Mauritania
Mauritius
Mayotte
Mexico
Micronesia
Midway Islands
Moldova
Monaco
Mongolia
Montenegro
Montserrat
Morocco
Mozambique
Myanmar
Namibia
Nauru
Navassa Island

Nepal
Netherlands
New Caledonia
New Zealand
Nicaragua
Niger
Nigeria
Niue
Norfolk Island
North Korea
North Macedonia
North Sea
Northern Mariana Islands
Norway
Oman
Pakistan
Palau
Panama
Papua New Guinea
Paracel Islands
Paraguay
Peru
Philippines
Pitcairn Islands
Poland
Portugal
Puerto Rico
Qatar
Republic of the Congo
Reunion
Romania
Ross Sea
Russia
Rwanda
Saint Helena
Saint Kitts and Nevis
Saint Lucia
Saint Pierre and Miquelon
Saint Vincent and the Grenadines
Samoa
San Marino
Sao Tome and Principe
Saudi Arabia
Senegal
Serbia

Seychelles
Sierra Leone
Singapore
Sint Maarten
Slovakia
Slovenia
Solomon Islands
Somalia
South Africa
South Georgia and the South Sandwich Islands
South Korea
South Sudan
Spain
Spratly Islands
Sri Lanka
State of Palestine
Sudan
Suriname
Svalbard
Swaziland
Sweden
Switzerland
Syria
Taiwan
Tajikistan
Tanzania
Thailand
Timor-Leste
Togo
Tokelau
Tonga
Trinidad and Tobago
Tromelin Island
Tunisia
Turkey
Turkmenistan
Turks and Caicos Islands
Tuvalu
USA
Uganda
Ukraine
United Arab Emirates
United Kingdom
Uruguay
Uzbekistan

Vanuatu
Venezuela
Viet Nam
Virgin Islands
Wake Island
Wallis and Futuna
West Bank
Western Sahara
Yemen
Zambia
Zimbabwe
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

purpose_of_ww_sampling

public health surveillance community-level
public health surveillance institution-level
public health surveillance building-level
research
other: define
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

project_name

GenomeTrakr
GenomeTrakr; LFFM ww project
CDC NWSS

ww_sample_type

grab
composite
swab - grab
swab - composite
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

ww_sample_site

correctional facility
long-term care facility
hospital
child day care
school
college or university
social services shelter
other residential building
ship
airplane
airport
septic tank
other holding tank
wastewater treatment plant
wastewater lagoon
sewer pipeline
food or meat processing plant
other: define
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

ww_sample_matrix

raw wastewater
sewer pipeline sediments
post grit removal
primary sludge
primary effluent
secondary sludge
secondary effluent
other: define
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

ww_surv_target_1	ww_surv_target_1_known_present	ww_surv_target_1_gene
SARS-CoV-2	Yes	E gene (orf4)
Not Applicable	No	M gene (orf5)
Not Collected		N gene (orf9)
Not Provided		N gene (N1)
Missing		N gene (N2)
Restricted Access		Spike gene (orf2)
		S gene
		orf1ab (rep)
		orf1a (pp1a)
		nsp11
		nsp1
		nsp2
		nsp3
		Nsp4
		nsp5
		nsp6
		nsp7
		nsp8
		nsp9
		nsp10
		RdRp gene (nsp12)
		hel gene (nsp13)
		exoN gene (nsp14)
		nsp15
		nsp16
		orf3a
		orf3b
		orf6 (ns6)
		orf7a
		orf7b (ns7b)
		orf8 (ns8)
		orf9b
		orf9c
		orf10
		orf14
		SARS-COV-2 5' UTR
		Not Applicable
		Not Collected
		Not Provided
		Missing
		Restricted Access

ww_surv_target_1_protocol

RT-qPCR Detection of SARS-CoV-2 from Wastewater Using the AB 7500 (protocols.io)

RT-qPCR Detection of SARS-CoV-2 using Luna Probe One-Step RT-qPCR 4X Mix with UDG kit

RTqPCR of SARS-CoV-2 N1 Target on ABI 7500 Fast Using Promega GoTaq Enviro Wastewater

ddPCR detection of SARS-CoV-2 using the BioRad PREvalence Kit on the BioRad QXOne

GT-Digital SARS-CoV-2 Wastewater Surveillance Assay For QIAcuity dPCR

Not Applicable

Not Collected

Not Provided

Missing

Restricted Access

ww_surv_target_1_conc_unit

cycles (Ct value)

copies/L

copies/uL

specimen_processing

technical replicate

biological replicate

specimens pooled

Not Applicable

Not Collected

Not Provided

Missing

Restricted Access

concentration_method

membrane filtration with addition of mgcl2

amicon ultrafiltration

beef extract flocculation

centricon ultrafiltration

ceres nanotrap

hollow fiber dead end ultrafiltration

innovaprep ultrafiltration

membrane filtration with acidification and mgcl2

membrane filtration with acidification and mgcl2, membrane recombined with separated solids

membrane filtration with addition of mgcl2, membrane recombined with separated solids

membrane filtration with no amendment

membrane filtration with no amendment, membrane recombined with separated solids

membrane filtration with sample acidification

membrane filtration with sample acidification, membrane recombined with separated solids

no liquid concentration, liquid recombined with separated solids

peg precipitation

peg precipitation + ultracentrifugation

promega wastewater large volume tna capture kit

skimmed milk flocculation

ultracentrifugation

zymo environ water rna kit

zymo water concentration buffer

Not Applicable

Not Collected

Not Provided

Missing

Restricted Access

extraction_method

qiagen allprep powerviral dna/rna kit
4s method (<https://www.protocols.io/view/v-4-direct-wastewater-r>)
ceres magnetic beads
chemagic viral dna/rna 300 kit
macherey-nagel nucleomag dna/rna water kit
neb monarch total rna miniprep kit
neb monarch total rna miniprep kit + zymo onestep pcr inhibitor rer
nuclisens automated magnetic bead extraction kit
nuclisens manual magnetic bead extraction kit
omega-biotek on the hamilton robot
phenol chloroform
promega automated tna kit
promega ht tna kit
promega manual tna kit
promega wastewater large volume tna capture kit
qiagen allprep dna/rna kit
qiagen allprep powerfecal dna/rna kit
qiagen powerwater kit
qiagen qiaamp buffers with epoch columns
qiagen qiaamp viral rna mini kit
qiagen rneasy kit
qiagen rneasy powermicrobiome kit
thermofisher magmax microbiome ultra nucleic acid isolation kit
thermofisher magmax viral/pathogen nucleic acid isolation kit
trizol, zymo mag beads w/ zymo clean and concentrator
zymo quick-rna fungal/bacterial miniprep #r2014
zymo quick-rna viral kit
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

collected_by

Arizona State Department of Health Services
California Department of Public Health
Indiana State Department of Health
Kentucky State Cabinet for Health and Family Services
Massachusetts State Department of Public Health
New Jersey State Department of Agriculture
New Jersey State Department of Health and Senior Services
New Mexico State University - Las Cruces
North Carolina State University - Raleigh
Ohio State Department of Agriculture
Pennsylvania State University - University Park
Rhode Island Department of Health
South Carolina Department of Health and Environmental Control
South Dakota State University
Texas Department of State Health Services
Nevada State Public Health Laboratory
Virginia Division of Consolidated Laboratory Services
Washington State Department of Agriculture
Washington State Department of Health
West Virginia Department of Agriculture
FDA Center for Food Safety and Applied Nutrition
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

sequenced_by

Arizona State Department of Health Services
California Department of Public Health
Indiana State Department of Health
Kentucky State Cabinet for Health and Family Services
Massachusetts State Department of Public Health
New Jersey State Department of Agriculture
New Jersey State Department of Health and Senior Services
New Mexico State University - Las Cruces
North Carolina State University - Raleigh
Ohio State Department of Agriculture
Pennsylvania State University - University Park
Rhode Island Department of Health
South Carolina Department of Health and Environmental Control
South Dakota State University
Texas Department of State Health Services
Nevada State Public Health Laboratory
Virginia Division of Consolidated Laboratory Services
Washington State Department of Agriculture
Washington State Department of Health
West Virginia Department of Agriculture
FDA Center for Food Safety and Applied Nutrition
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

purpose_of_sequencing

detection of target by RT PCR or ddPCR

reporting_jurisdiction

- AL
- AK
- AS
- AZ
- AR
- CA
- CI
- CO
- MP
- CT
- DE
- DC
- FM
- FL
- GA
- GU
- HI
- HO
- ID
- IL
- IN
- IA
- KS
- KY
- LC
- LA
- ME
- MD
- MA
- MI
- MN
- MS
- MO
- MT
- NE
- NV
- NH
- NJ
- NM
- NY
- NZ
- NC
- ND
- OH

OK
OR
PA
PH
PR
MH
PW
RI
SC
SD
TN
TX
VI
UT
VT
VA
WA
WV
WI
WY
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access