

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 <a href="https://www.ncbi.nlm.nih.gov/biosample/docs/att">https://www.ncbi.nlm.nih.gov/biosample/docs/att</a>		
CAUTION: Be aware that Excel may automatically apply formatting to your data. In particular, tak		
<b>TO MAKE A SUBMISSION:</b>		
1. Complete this template table.		
2. Upload the file on the 'Attributes' tab of the BioSample Submission Portal at <a href="https://submit.ncbi">https://submit.ncbi</a>		
If you have any questions, please contact us at <a href="mailto:biosamplehelp@ncbi.nlm.nih.gov">biosamplehelp@ncbi.nlm.nih.gov</a> .		
<b>*sample_name</b>	<b>sample_title</b>	<b>bioproject_accession</b>
6493.P		PRJNA839090
4119.D		PRJNA839090
3990.C		PRJNA839090

1.0' samples to the NCBI BioSample database ( <a href="https://www.ncbi.nlm.nih.gov/biosample/">https://www.ncbi.nlm.nih.gov/biosample/</a> ).			
Completed. If information is unavailable for any mandatory field, please enter 'not collected', 'not available'.			
<a href="#">tributes/</a> .			
Please take care with dates, incrementing autofills and special characters like / or -. Doublecheck that you			
<a href="https://www.ncbi.nlm.nih.gov/subs/biosample/">.nlm.nih.gov/subs/biosample/</a> .			
<b>*organism</b>	<b>*collection_date</b>	<b>collection_time</b>	<b>*geo_loc_name</b>
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.		
<b>*isolation_source</b>	<b>collection_site_id</b>	<b>project_name</b>
Wastewater	8675	GenomeTrakr
Wastewater	30	GenomeTrakr
Wastewater	9	GenomeTrakr; LFFM ww project





<b>ww_surv_jurisdiction</b>	<b>ww_population_source</b>	<b>ww_sample_matrix</b>	<b>ww_sample_type</b>
nj		post grit removal	composite
vt		raw wastewater	grab
ar		raw wastewater	composite

<b>collection_volume</b>	<b>ww_sample_duration</b>	<b>ww_temperature</b>	<b>ww_ph</b>
	24		
	0		
	24		

<b>ww_industrial_effluent_percent</b>	<b>ww_sample_salinity</b>	<b>ww_total_suspended_solids</b>



<b>ww_surv_system_sample_id</b>	<b>ww_pre_treatment</b>	<b>ww_primary_sludge_retention_time</b>
6493.P		
4119.D		
3990.C		



<b>specimen_processing_details</b>

<b>ww_processing_protocol</b>	<b>concentration_method</b>
Pasteurized; virus captured w	ceres nanotrap
Pasteurized; virus captured w	ceres nanotrap
Pasteurized; virus captured w	ceres nanotrap

<b>extraction_method</b>
thermo magmax microbiome ultra nucleic acid isolation kit
thermo magmax microbiome ultra nucleic acid isolation kit
thermo magmax microbiome ultra nucleic acid isolation kit





ww_endog_control_2_con	ww_endog_control_2_protoco	ww_endog_control_2_units





<b>ww_surv_target_1_protocol</b>
RT-qPCR Detection of SARS-CoV-2 from Wastewater Using the AB 7500 (protocols.io)
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





<b>w_surv_target_2_conc_ur</b>	<b>ww_surv_target_2_gene</b>	<b>ww_surv_target_2_known_present</b>

<b>purpose_of_ww_sequencing</b>	<b>sequenced_by</b>
	Ginkgo Bioworks clinical laboratory
	Ginkgo Bioworks clinical laboratory
	Ginkgo Bioworks clinical laboratory

<b>description</b>

## 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) site".

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-qualified>.

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 determined 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 determined 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

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

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)

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

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

**NWSS Requirement GenomeTrakr requirement**

mandatory	mandatory
optional	optional
mandatory	mandatory
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optional	mandatory



## 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]
	5/1/2021 sample_collect_date
12:00 PM	8:00 AM
USA:Virginia	[none]
wastewater metagenome	[none]
g the options in the dropdown.	technical replicate, biological
Identify replicates.	replicate_1, rep_1
	Grabbed sample was separate
SARS-CoV-2	[none]
yes	[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	
PRJNA999999	[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
	110000000 25 500 10 7.2 100
flow equilibration basin promotes settling of some solids	[none]
	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

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protocols have occurred on the same  
grab or composite sample

specimen processing

speciman processing details

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environmental site

pecific

pecific

<b>organism</b>	<b>geo_loc_name</b>	<b>isolation_source</b>
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

<b>ww_surv_target_1</b>	<b>ww_surv_target_1_known_present</b>	<b>ww_surv_target_1_gene</b>
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