Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
								Label	ID	Description/Guidance
	Colour Code Legend					**IMPORTANT:** Only labels and/or IDs will be deprecated, always with replacement version provided. If a term changes in its meaning, a new term will be created.				
	field name in yellow = required									
	field name in purple = recommended									
	field name in white = optional									
Database identifiers		**GENEPIO:0001122**								
Database identifiers	**specimen collector sample ID**	GENEPIO:0001123	The user-defined name for the sample.	Store the collector sample ID. If this number is considered identifiable information, provide an alternative ID. Be sure to store the key that maps between the original and alternative IDs for traceability and follow up if necessary. Every collector sample ID from a single submitter must be unique. It can have any format, but we suggest that you make it concise, unique and consistent within your lab.	ASDFG123			1.0.0	1.0.0	1.0.0
Database identifiers	**specimen collector subsample ID**	GENEPIO:0100752	The user-defined identifier assigned to a portion of the original sample.	Store the ID for the subsample/aliquot.	ASDFG123_12			1.0.0	1.0.0	1.0.0
Database identifiers	**pooled sample ID**	GENEPIO:0100996	The user-defined identifier assigned to a combined (pooled) set of samples.	If the sample being analyzed is the result of pooling individual samples, rename the pooled sample with a new identifier. Store the pooled sample ID.	12345AYZ			1.0.0	1.0.0	1.0.0
Database identifiers	**metagenome-assembled genome (MAG) ID**	GENEPIO:0100753	The user-defined identifier assigned to a genome reconstructed from metagenomic data.	Store the MAG ID.	XYZ1234.1			1.0.0	1.0.0	1.0.0
Database identifiers	**specimen collector project ID**	GENEPIO:0100918	The user-defined project name assigned to a sequencing project.	If the sample was collected or analyzed under the umbrella of a specific project, include the name of that project here.				1.0.0	1.0.0	1.0.0
Database identifiers	**BioProject accession**	GENEPIO:0001136	The INSDC (i.e., ENA, NCBI, or DDBJ) accession number of the BioProject(s) to which the BioSample belongs.	Store the BioProject accession number. BioProjects are an organizing tool that links together raw sequence data, assemblies, and their associated metadata. Each province will be assigned a different bioproject accession number by the National Microbiology Lab. A valid NCBI BioProject accession has prefix PRJN e.g., PRJNA12345, and is created once at the beginning of a new sequencing project.	PRJNA608651			1.0.0	1.0.0	1.0.0
Database identifiers	**BioSample accession**	GENEPIO:0001139	The identifier assigned to a BioSample in INSDC (i.e., ENA, NCBI, or DDBJ) archives.	Store the accession returned from the BioSample submission. NCBI BioSamples will have the prefix SAMN, ENA have the prefix SAMEA, DDBJ have SAMD	SAMN14180202, SAMD00000001, SAMEA00000001			1.0.0	1.0.0	1.0.0
Database identifiers	**GenBank accession (versioned)**	GENEPIO:0100754	The unique identifier assigned to an assembly or consensus sequence in GenBank archives.	Store the versioned GenBank accession assigned to the submitted sequence.	LZ986655.1			1.0.0	1.0.0	1.0.0
Database identifiers	**SRA accession**	GENEPIO:0001142	The Sequence Read Archive (SRA) identifier linking raw read data, methodological metadata and quality control metrics submitted to the INSDC.	Store the accession assigned to the submitted sequence. NCBI-SRA accessions start with SRR.	SRR11177792			1.0.0	1.0.0	1.0.0
Database identifiers	**GISAID accession**	GENEPIO:0001147	The identifier assigned to a sequence in GISAID (the Global Initiative on Sharing All Influenza Data) archives.	Store the accession assigned to the submitted sequence. GISAID accessions start with EPI.	EPI_ISL_402131			1.0.0	1.0.0	1.0.0
Database identifiers	**GISAID virus name**	GENEPIO:0100282	The user-defined GISAID virus name assigned to the sequence.	GISAID virus names should be in the format "hCoV-19/Country/Identifier/year".	hCoV-19/Canada/prov_rona_99/2020			1.0.0	1.0.0	1.0.0
Database identifiers	**ENA accession**	GENEPIO:0100755	The identifier assigned to a sequence in the European Nucleotide Archive (ENA).	Store the accession assigned to the submitted sequence. ENA sequence accessions start with ERR.	ERR123456			1.0.0	1.0.0	1.0.0
Database identifiers	**DRA accession**	GENEPIO:0100757	The identifier assigned to a sequence in DNA Data Bank of Japan (DDBJ) sequence read archives (DRA).	Store the accession assigned to the submitted sequence. DRA accessions start with DRR.	DRR123456			1.0.0	1.0.0	1.0.0
Database identifiers	**GSA accession**	GENEPIO:0100758	The identifier assigned to a sequence in the Genome Sequence Archive (GSA).	Store the accession assigned to the submitted sequence. GSA accessions start with CRR.	CRR123456			1.0.0	1.0.0	1.0.0
Database identifiers	**Enterobase accession**	GENEPIO:0100759	The identifier assigned to a sequence in Enterobase archives.	Store the barcode assigned to the submitted sequence. Enterobase barcodes start with different 3 letter codes depending on the organism.	SAL_AA0019AA_ST			1.0.0	1.0.0	1.0.0
Database identifiers	**sampling site ID**	GENEPIO:0100760	The user-defined identifier assigned to a specific location from which samples are taken.	Store the ID for the site from which a sample was taken. The "site" is user defined (e.g. it may be a building and its environs, a specific entity within an environment). Please use the same site ID for all samples from a given site, regardless of when these samples were taken. Any important changes in site location, should be represented with a new site ID.	Site 12A			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking Label	ID	Description/Guidance
	Colour Code Legend									
Database identifiers	sampling event ID	GENEPIO:0100761	The user-defined identifier assigned to a specific event during which one or more samples are taken, from one or more sites.	Store the ID for the event during which a sample or samples were taken. For example, an event could be one person taking samples from multiple sites, or multiple people taking samples from one site.	Event 120522.1			1.0.0	1.0.0	1.0.0
Sample collection and processing		GENEPIO:0001150								
Sample collection and processing	sample collection data steward name	GENEPIO:0100762	A sample collection data field which describes the name of the individual responsible for the data governance, (meta)data usage and distribution of the sample.	Provide the name of the sample collection data steward.	Joe Bloggs			1.0.0	1.0.0	1.0.0
Sample collection and processing	sample collected by	GENEPIO:0001153	The name of the organization with which the sample collector is affiliated.	The name of the agency should be written out in full, (with minor exceptions) and be consistent across multiple submissions.	Public Health Agency of Canada			1.0.0	1.0.0	1.0.0
Sample collection and processing	sample collector contact email	GENEPIO:0001156	The email address of the contact responsible for follow-up regarding the sample.	The email address can represent a specific individual or lab e.g. johnnyblogs@lab.ca, or RespLab@lab.ca	WaterTester@facility.ca			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc name (country)	GENEPIO:0001181	The country of origin of the sample.	If known, select a value from the pick list.	Canada			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc name (state/province/territory)	GENEPIO:0001185	The state/province/territory of origin of the sample.	Provide the state/province/territory name from the GAZ geography ontology. Search for geography terms here: https://www.ebi.ac.uk/ols/ontologies/gaz	Western Cape			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc name (county/region)	GENEPIO:0100280	The county/region of origin of the sample.	Provide the county/region name from the GAZ geography ontology. Search for geography terms here: https://www.ebi.ac.uk/ols/ontologies/gaz	Derbyshire			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc name (city)	GENEPIO:0001189	The city of origin of the sample.	Provide the city name from the GAZ geography ontology. Search for geography terms here: https://www.ebi.ac.uk/ols/ontologies/gaz	Vancouver			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc name (site)	GENEPIO:0100436	The name of a specific geographical location e.g. Credit River (rather than river).	Provide the name of the specific geographical site using a specific noun (a word that names a certain place, thing).	Credit River			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc latitude	GENEPIO:0100309	The latitude coordinates of the geographical location of sample collection.	Provide latitude coordinates if available. Do not use the centre of the city/region/province/state/country or the location of your agency as a proxy, as this implicates a real location and is misleading. Specify as degrees latitude in format "d[d.dddd] N|S".	38.98 N			1.0.0	1.0.0	1.0.0
Sample collection and processing	geo loc longitude	GENEPIO:0100310	The longitude coordinates of the geographical location of sample collection.	Provide longitude coordinates if available. Do not use the centre of the city/region/province/state/country or the location of your agency as a proxy, as this implicates a real location and is misleading. Specify as degrees longitude in format "d[dd.dddd] W|E".	77.11 W			1.0.0	1.0.0	1.0.0
Sample collection and processing	watershed shapefile availability	GENEPIO:0100919	The availability status of a shapefile descriping the catchment contributing to a watershed.	Select a value from the picklist to describe whether or not a watershed shapefile would be available upon request.	watershed shapefile available			1.0.0	1.0.0	1.0.0
Sample collection and processing	watershed shapefile filename	GENEPIO:0100920	The name of the watershed shapefile.	Provide the shapefile filename corresponding to the watershed from which the sample was taken. If there are multiple files associated with the watershed, provide all names separated by commas.	siteAD17.shp, siteAD17.kml			1.0.0	1.0.0	1.0.0
Sample collection and processing	organism	GENEPIO:0001191	Taxonomic name of the organism.	Provide the official nomenclature for the organism present in the sample. Search for taxonomic names here: ncbi.nlm.nih.gov/taxonomy.	Severe acute respiratory syndrome coronavirus 2			1.0.0	1.0.0	1.0.0
Sample collection and processing	purpose of sampling	GENEPIO:0001198	The reason that the sample was collected.	The reason a sample was collected may provide information about potential biases in sampling strategy. Provide the purpose of sampling from the picklist in the template. Most likely, the sample was collected for public health surveillance. The reason why a sample was originally collected may differ from the reason why it was selected for sequencing, which should be indicated in the "purpose of sequencing" field.	Public health surveillance			1.0.0	1.0.0	1.0.0
Sample collection and processing	scale of sampling	GENEPIO:0100877	The range of locations or entities sampled expressed in general terms.	Provide the scale of wastewater sampling by selecting a value from the picklist.	Community-level surveillance			1.0.0	1.0.0	1.0.0
Sample collection and processing	sample received date	GENEPIO:0001179	The date on which the sample was received.	Provide the sample received date in ISO 8601 format, i.e. "YYYY-MM-DD".	2020-03-28			1.0.0	1.0.0	1.0.0
Sample collection and processing	sample collection date	GENEPIO:0001174	The date on which the sample was collected, or sampling began for a continuous sample.	If your sample is a continuous sample please use this field to capture your start date. Sample collection date is critical for surveillance and many types of analyses. Required granularity includes year, month and day. If this date is considered identifiable information, it is acceptable to add "jitter" by adding or subtracting a calendar day (acceptable by GISAID). Alternatively, "received date" may be used as a substitute. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2020-03-16			1.0.0	1.0.0	1.0.0
Sample collection and processing	sample collection end date	GENEPIO:0101071	The date on which sample collection ended fo	Provide the date that sample collection ended in ISO 8601 fo	2020-03-18			1.0.0	1.0.0	1.0.0
Sample collection and processing	sample processing date	GENEPIO:0100763	The date on which the sample was processed.	Provide the sample processed date in ISO 8601 format, i.e. "YYYY-MM-DD". The sample may be collected and processed (e.g. filtered, extraction) on the same day, or on different dates.	2020-03-16			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking Label	ID	Description/Guidance
	Colour Code Legend									
Sample collection and processing	**sample collection start time**	GENEPIO:0101072	The time at which sample collection began.	Provide this time in ISO 8601 24hr format, in your local time.	17:15 PST			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample collection end time**	GENEPIO:0101073	The time at which sample collection ended.	Provide this time in ISO 8601 24hr format, in your local time.	19:15 PST			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample collection time of day**	GENEPIO:0100765	The descriptive time of day during which the sample was collected.	If known, fill in sample collection time. Otherwise, select a value from the pick list for sample collection time of day to approximate the timing. The time of sample processing matters especially for grab samples, as fecal concentration in wastewater fluctuates over the course of the day.	Morning			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample collection time duration value**	GENEPIO:0100766	The amount of time over which the sample was collected.	Provide the numerical value of time.	4			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample collection time duration unit**	GENEPIO:0100767	The units of the time duration measurement of sample collection.	Provide the units from the pick list.	Hour			1.0.0	1.0.0	1.0.0
Sample collection and processing	**presampling activity**	GENEPIO:0100433	The activities or variables upstream of sample collection that may affect the sample.	If there was an activity that would affect the sample prior to collection (this is different than sample processing), provide the activities by selecting one or more values from the template pick list. If the information is unknown or cannot be provided, leave blank or provide a null value.	Agricultural activity			1.0.0	1.0.0	1.0.0
Sample collection and processing	**presampling activity details**	GENEPIO:0100434	The details of the activities or variables that affected the sample collected.	Briefly describe the presampling activities using free text.	Agricultural waste from large farm contributes waste to the site sampled.			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample volume measurement value**	GENEPIO:0100768	The numerical value of the volume measurement of the sample collected.	Provide the numerical value of volume.	5			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample volume measurement unit**	GENEPIO:0100769	The units of the volume measurement of the sample collected.	Provide the units from the pick list.	mL			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample storage method**	GENEPIO:0100448	The process used to store the sample.	Provide details of how the sample was stored from time of collection until time of processing. If there were issues with the cold chain storage, note those here.	The sample was placed in a tube in a cooler bag during transportation (~3 hours) to the lab site. At this point the sample was placed in storage medium and put in a -10C freezer until it was processed and extracted 5 days later.			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample storage medium**	GENEPIO:0100449	The medium in which a sample is stored.	Provide the name of the transport medium or storage medium used for this sample. If none was used, leave blank or write "None".	Cary-Blair transport medium			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample storage duration value**	GENEPIO:0101014	The numerical value of the time measurement during which a sample is in storage.	Provide the numerical value of time.	5			1.0.0	1.0.0	1.0.0
Sample collection and processing	**sample storage duration unit**	GENEPIO:0101015	The units of a measured sample storage duration.	Provide the units from the pick list.	Day			1.0.0	1.0.0	1.0.0
Sample collection and processing	**specimen processing**	GENEPIO:0001253	Any processing applied to the sample during or after receiving the sample.	Select processes from the picklist that were applied to this sample.	Centrifugation			1.0.0	1.0.0	1.0.0
Sample collection and processing	**specimen processing details**	GENEPIO:0100311	The details of the processing applied to the sample during or after receiving the sample.	Briefly describe the processes applied to the sample.	25 samples were pooled and further prepared as a single sample during library prep.			1.0.0	1.0.0	1.0.0
Sample collection and processing	**experimental protocol field**	GENEPIO:0101029	The name of the overarching experimental methodology that was used to process the	Provide the name of the methodology used in your study. If available, provide a link to the protocol.						
Sample collection and processing	**environmental site**	GENEPIO:0001232	An environmental location may describe a site in the natural or built environment e.g. contact surface, metal can, hospital, wet market, bat cave.	Provide a descriptor of the environmental site sampled. Use the picklist provided in the template. If not applicable, choose a null value.	Meat processing plant			1.0.0	1.0.0	1.0.0
Sample collection and processing	**environmental material**	GENEPIO:0001223	A substance obtained from the natural or man-made environment e.g. soil, water, sewage.	Provide a descriptor of the environmental material sampled. Use the picklist provided in the template. If not applicable, choose a null value.	Raw wastewater			1.0.0	1.0.0	1.0.0
Sample collection and processing	**environmental material properties**	GENEPIO:0100770	The properties, characteristics and qualities of a substance obtained from an environment.	Provide the environmental material properties by selecting descriptors from the pick list.	Stagnant			1.0.0	1.0.0	1.0.0
Sample collection and processing	**wastewater system type**	GENEPIO:0100771	The type or classification of a wastewater system e.g. sanitary sewer, combined sewer	Provide the classification of the wastewater system by selecting from the provided pick list.	Sanitary sewer			1.0.0	1.0.0	1.0.0
Sample collection and processing	**experimental specimen role type**	GENEPIO:0100921	The type of role that the sample represents in the experiment.	Samples can play different types of roles in experiments. A sample under study in one experiment may act as a control or be a replicate of another sample in another experiment. This field is used to distinguish samples under study from controls, replicates, etc. If the sample acted as an experimental control or a replicate, select a role type from the picklist. If the sample was not a control, leave blank or select "Not Applicable".	Positive experimental control			1.0.0	1.0.0	1.0.0
Sample collection and processing	**experimental control details**	GENEPIO:0100922	The details regarding the type of control that the sample represents in the experiment.	Provide details regarding the nature of the reference strain used as a control, or what is was used to monitor.	Human coronavirus 229E (HCoV-229E) spiked in sample as process control			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	Colour Code Legend							Label	ID	Description/Guidance
Sample collection and processing	collection device	GENEPIO:0001234	The instrument or container used to collect the sample e.g. *grab sampler*.	Provide a descriptor of the device used for sampling. Use the picklist provided in the template. If not applicable, choose a null value.	Automatic flow-proportional sampler			1.0.0	1.0.0	1.0.0
Sample collection and processing	collection method	GENEPIO:0001241	The process used to collect the sample.	Provide a descriptor of the collection method used for sampling. Use the picklist provided in the template. If not applicable, choose a null value.	Automatic composite sampling			1.0.0	1.0.0	1.0.0
Sample collection and processing	nucleic acid extraction method	GENEPIO:0100939	The process used to extract genomic material from a sample.	Briefly describe the extraction method used.	Direct wastewater RNA capture and purification via the "Sewage, Salt, Silica and SARS-CoV-2 (4S)" method v4 found at https://www.protocols.io/view/v-4-direct-wastewater-rna-capture-and-purification-36wgq581ygk5/v4			1.0.0	1.0.0	1.0.0
Sample collection and processing	nucleic acid extraction kit	GENEPIO:0100772	The kit used to extract genomic material from a sample	Provide the name of the genomic extraction kit used.	QIAamp PowerFecal Pro DNA Kit			1.0.0	1.0.0	1.0.0
Sample collection and processing	endogenous control details	GENEPIO:0100923	The description of the endogenous controls included when extracting a sample.	Provide the names of endogenous controls that were used as a reference during extraction. If relevant, include titers of these controls, as well as whether any controls were expected but not identified in the sample.	Pepper mild mottle virus (PMMoV) detected			1.0.0	1.0.0	1.0.0
Sample collection and processing	extraction recovery efficiency measurement value	GENEPIO:0100924	The recovery efficiency of an extraction, calculated as the amount of a synthetic or endogenous compound identified in the sample relative to the amount expected.	Provide value as a percent.	25			1.0.0	1.0.0	1.0.0
Sample collection and processing	extraction recovery efficiency measurement method	GENEPIO:0100925	The method by which recovery efficiency of an extraction was calculated.	Provide a brief description of how extraction recovery efficiency was measured or estimated.	Spiked in synthetic material into wastewater sample and into water control and compared recovery.			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements		**GENEPIO:0100940**								
Environmental conditions and measurements	water catchment area human population measurement value	GENEPIO:0100773	The numerical value of the human population measurement that contributes to the composition of water in a catchment area.	Where known, provide the numerical value of population size, i.e. the number of people.	10,500			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	water catchment area human population bin	GENEPIO:0100774	The human population range of the water catchment that contributes effluent to a wastewater site.	Where catchment population is not well known, provide an estimation of population size by selecting a value from the picklist.	1,000 - 10,000 people			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	water catchment area human population measurement method	GENEPIO:0100775	The method by which a water catchment 's human population size was measured or estimated	Provide a brief description of how catchment population size was measured or estimated.	population of jurisdiction encompassing the wastewater service area			1.0.0	1.0.0	1.0.0
Environmental conditions and	water catchment area human population	GENEPIO:0100776	The numerical value describing the number	Provide the numerical value of the population density in the	4			1.0.0	1.0.0	1.0.0
Environmental conditions and	water catchment area human population	GENEPIO:0100777	The unit describing the number of humans	Provide the unit of the population density in the catchment	persons per Km^2			1.0.0	1.0.0	1.0.0
Environmental conditions and	populated area type	GENEPIO:0100778	A type of area that is populated by humans	Provide the populated area type from the pick list.	Urban area			1.0.0	1.0.0	1.0.0
Environmental conditions and	sampling weather conditions	GENEPIO:0100779	The state of the atmosphere at a place and	Provide the weather conditions at the time of sample	Rain			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	presampling weather conditions	GENEPIO:0100780	Weather conditions prior to collection that may affect the sample.	Provide the weather conditions prior to sample collection.	Drizzle			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	precipitation measurement value	GENEPIO:0100911	The amount of water which has fallen during a precipitation process.	Provide the quantity of precipitation in the area leading up to the time of sample collection.	12			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	precipitation measurement unit	GENEPIO:0100912	The units of measurement for the amount of water which has fallen during a precipitation process.	Provide the units of precipitation by selecting a value from the pick list.	inch			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	precipitation measurement method	GENEPIO:0100913	The process used to measure the amount of water which has fallen during a precipitation process.	Provide the name of the procedure or method used to measure precipitation.	Rain gauge over a 12 hour period prior to sample collection			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	ambient temperature measurement value	GENEPIO:0100935	The numerical value of a measurement of the ambient temperature.	Provide the numerical value of the measured temperature.	70			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	ambient temperature measurement unit	GENEPIO:0100936	The units of a measurement of the ambient temperature.	Provide the units of the measured temperature.	degree Celsius (C)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	pH measurement value	GENEPIO:0001736	The measured pH value indicating the acidity or basicity(alkalinity) of an aqueous solution.	Provide the numerical value of the measured pH.	7.4			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	pH measurement method	GENEPIO:0100781	The process used to measure pH value.	Provide the name of the procedure or technology used to measure pH.	pH test strip (litmus test)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total daily flow rate measurement value	GENEPIO:0100905	The numerical value of a measured fluid flow rate over the course of a day.	Provide the numerical value of the measured flow rate.	10			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total daily flow rate measurement unit	GENEPIO:0100906	The units of a measured fluid flow rate over the course of a day.	Provide the units of the measured flow rate by selecting a value from the pick list.	million gallons per day (MGD)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total daily flow rate measurement method	GENEPIO:0100907	The process used to measure total daily fluid flow rate.	Provide the name of the procedure or technology used to measure flow rate.	Flow meter			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	instantaneous flow rate measurement value	GENEPIO:0100908	The numerical value of a measured instantaneous fluid flow rate.	Provide the numerical value of the measured flow rate.	25			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	instantaneous flow rate measurement unit	GENEPIO:0100909	The units of a measured instantaneous fluid flow rate.	Provide the units of the measured flow rate by selecting a value from the pick list.	cubic meter per hour (m^3/h)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	instantaneous flow rate measurement method	GENEPIO:0100910	The process used to measure instantaneous fluid flow rate.	Provide the name of the procedure or technology used to measure flow rate.	Flow meter			1.0.0	1.0.0	1.0.0

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	Colour Code Legend									
Environmental conditions and measurements	turbidity measurement value	GENEPIO:0100783	The numerical value of a measurement of turbidity.	Provide the numerical value of the measured turbidity.	0.02			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	turbidity measurement unit	GENEPIO:0100914	The units of a measurement of turbidity.	Provide the units of the measured turbidity by selecting a value from the pick list.	nephelometric turbidity unit (NTU)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	turbidity measurement method	GENEPIO:0101013	The process used to measure turbidity.	Provide the name of the procedure or technology used to measure turbidity.	Nephelometric method			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	dissolved oxygen measurement value	GENEPIO:0100915	The numerical value of a measurement of dissolved oxygen.	Provide the numerical value of the measured dissolved oxygen.	5			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	dissolved oxygen measurement unit	GENEPIO:0100784	The units of a measurement of dissolved oxygen.	Provide the units of the measured dissolved oxygen by selecting a value from the pick list.	part per million (ppm)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	dissolved oxygen measurement method	GENEPIO:0100785	The method used to measure dissolved oxygen.	Provide the name of the procedure or technology used to measure dissolved oxygen.	Dissolved oxygen meter in vertical direction			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	oxygen reduction potential (ORP) measurement value	GENEPIO:0100917	The numerical value of a measurement of oxygen reduction potential (ORP).	Provide the numerical value of the measured oxygen reduction potential.	-50			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	oxygen reduction potential (ORP) measurement unit	GENEPIO:0100786	The units of a measurement of oxygen reduction potential (ORP).	Provide the units of the measured oxygen reduction potential by selecting a value from the pick list.	milliVolt (mV)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	oxygen reduction potential (ORP) measurement method	GENEPIO:0100787	The method used to measure oxygen reduction potential (ORP).	Provide the name of the procedure or technology used to measure oxygen reduction potential.	ORP sensor			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	chemical oxygen demand (COD) measurement value	GENEPIO:0100788	The measured value from a chemical oxygen demand (COD) test.	Provide the numerical value of the COD test result.	26			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	chemical oxygen demand (COD) measurement unit	GENEPIO:0100789	The units associated with a value from a chemical oxygen demand (COD) test.	Provide the units of the COD test result.	milligram per liter (mg/L)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	chemical oxygen demand (COD) measurement method	GENEPIO:0100790	The method used to measure chemical oxygen demand (COD).	Provide the name of the procedure or technology used to measure COD.	Hach LCK test kit			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	carbonaceous biochemical oxygen demand (CBOD) measurement value	GENEPIO:0100791	The numerical value of a measurement of carbonaceous biochemical oxygen demand (CBOD).	Provide the numerical value of the measured CBOD.	20			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	carbonaceous biochemical oxygen demand (CBOD) measurement unit	GENEPIO:0100792	The units of a measurement of carbonaceous biochemical oxygen demand (CBOD).	Provide the units of the measured CBOD by selecting a value from the pick list.	milligram per liter (mg/L)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	carbonaceous biochemical oxygen demand (CBOD) measurement method	GENEPIO:0100793	The method used to measure carbonaceous biochemical oxygen demand (CBOD).	Provide the name of the procedure or technology used to measure CBOD.	CBOD measurement by optical probe			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total suspended solids (TSS) measurement value	GENEPIO:0100794	The mass of suspended particulates, both organic and inorganic in a sample.	Provide the numerical value of the measured TSS.	8			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total suspended solids (TSS) measurement unit	GENEPIO:0100795	The units associated with a value from a total suspended solids (TSS) test.	Provide the units of the measured TSS.	percent (%)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total suspended solids (TSS) measurement method	GENEPIO:0100796	The method used to measure total suspended solids (TSS).	Provide the name of the procedure or technology used to measure TSS.	Vacuum filter through a 2-micron filter, then oven-dried and weighed sample			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total dissolved solids (TDS) measurement value	GENEPIO:0100797	The numerical value from a total dissolved solids (TDS) test.	Provide the numerical value of the measured TDS.	2			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total dissolved solids (TDS) measurement unit	GENEPIO:0100798	The units associated with a value from a total dissolved solids (TDS) test.	Provide the units of the measured TDS.	percent (%)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total dissolved solids (TDS) measurement method	GENEPIO:0100799	The method used to measure total dissolved solids (TDS).	Provide the name of the procedure or technology used to measure TDS.	Subtract calculated TSS from calculated TS			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total solids (TS) measurement value	GENEPIO:0100800	The numerical value from a total solids (TS) test.	Provide the numerical value of the measured TS.	10			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total solids (TS) measurement unit	GENEPIO:0100801	The units associated with a value from a total solids (TS) test.	Provide the units of the measured TS.	percent (%)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total solids (TS) measurement method	GENEPIO:0100802	The method used to measure total solids (TS).	Provide the name of the procedure or technology used to measure TS.	Gravimetric method by oven drying, then weighing			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	alkalinity measurement value	GENEPIO:0100878	The numerical value of a measurement of alkalinity.	Provide the numerical value of the measured alkalinity.	3			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	alkalinity measurement unit	GENEPIO:0100879	The units of a measurement of alkalinity.	Provide the units of the measured alkalinity.	milligram per liter of calcium carbonate (mg/L CaCO3)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	alkalinity measurement method	GENEPIO:0100880	The process used to measure alkalinity.	Provide the name of the procedure or technology used to measure alkalinity.	Titration method			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	conductivity measurement value	GENEPIO:0100916	The numerical value of a measurement of conductivity.	Provide the numerical value of the measured conductivity.	1412			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	conductivity measurement unit	GENEPIO:0100803	The units of a measurement of conductivity.	Provide the units of the measured conductivity.	microSiemen per centimeter (µS/cm)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	conductivity measurement method	GENEPIO:0100804	The method used to measure conductivity.	Provide the name of the procedure or technology used to measure conductivity.	Conductivity electrode and meter			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	salinity measurement value	GENEPIO:0100805	The numerical value of a measurement of salinity.	Provide the numerical value of the measured salinity.	35			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	salinity measurement unit	GENEPIO:0100806	The units of a measurement of salinity.	Provide the units of the measured salinity.	practical salinity unit (PSU)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	salinity measurement method	GENEPIO:0100807	The method used to measure salinity.	Provide the name of the procedure or technology used to measure salinity.	conductivity meter			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total nitrogen (TN) measurement value	GENEPIO:0100808	The numerical value of a measurement of total nitrogen (TN).	Provide the numerical value of the measured TN.	120					

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking Label	ID	Description/Guidance
	Colour Code Legend									
Environmental conditions and measurements	total nitrogen (TN) measurement unit	GENEPIO:0100809	The units of a measurement of total nitrogen (TN).	Provide the units of the measured TN.	milligram per liter (mg/L)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total nitrogen (TN) measurement method	GENEPIO:0100810	The method used to measure total nitrogen (TN).	Provide the name of the procedure or technology used to measure TN.	Hach total nitrogen spectrophotometric test			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total phosphorus (TP) measurement value	GENEPIO:0100811	The numerical value of a measurement of total phosphorus (TP).	Provide the numerical value of the measured TP.	2			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total phosphorus (TP) measurement unit	GENEPIO:0100812	The units of a measurement of total phosphorus (TP).	Provide the units of the measured TP.	milligrams orthophosphate as phosphorus per liter (mg PO4-P/L)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	total phosphorus (TP) measurement method	GENEPIO:0100813	The method used to measure total phosphorus (TP).	Provide the name of the procedure or technology used to measure TP.	Merck phosphate spectrophotometric test kit			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal contamination indicator	GENEPIO:0100814	A gene, virus, bacteria, or substance used to measure the sanitary quality of water in regards to fecal contamination.	If a fecal contamination indicator was measured, select it from the picklist.	crAssphage			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal contamination value	GENEPIO:0100815	The numerical value of a measurement of fecal contamination.	Provide the numerical value of the measured fecal contamination.	10			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal contamination unit	GENEPIO:0100816	The units of a measurement of fecal contamination.	Provide the units of the measured fecal contamination.	cycle threshold (Ct) / quantification cycle (Cq)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal contamination method	GENEPIO:0100817	The method used to measure fecal contamination.	Provide the name of the procedure or technology used to measure fecal contamination.	quantitative PCR assay			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal coliform count value	GENEPIO:0100818	The numerical value of a measurement of fecal coliforms within a sample.	Provide the numerical value of the measured fecal coliforms.	3			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal coliform count unit	GENEPIO:0100819	The units of a measurement of fecal coliforms.	Provide the units of the measured fecal coliforms.	most probable number per milliliter (MPN/mL)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	fecal coliform count method	GENEPIO:0100820	The method used to measure fecal coliforms.	Provide the name of the procedure or technology used to measure fecal coliforms.	MPN method via serial dilutions until lack of growth			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	urinary contamination indicator	GENEPIO:0100837	A gene, virus, bacteria, or substance used to measure the sanitary quality of water in regards to urinary contamination.	If a urinary contamination indicator was measured, select it from the picklist.	urobilin			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	urinary contamination value	GENEPIO:0100838	The numerical value of a measurement of urinary contamination.	Provide the numerical value of the measured urinary contamination.	3			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	urinary contamination unit	GENEPIO:0100839	The units of a measurement of urinary contamination.	Provide the units of the measured urinary contamination.	nanograms per liter			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	urinary contamination method	GENEPIO:0100840	The method used to measure urinary contamination.	Provide the name of the procedure or technology used to measure urinary contamination.				1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sample temperature value (at collection)	GENEPIO:0100821	The numerical value of a measurement of temperature of a sample at collection.	Provide the numerical value of the measured temperature.	20			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sample temperature unit (at collection)	GENEPIO:0100822	The units of a measurement of temperature of a sample at the time of collection.	Provide the units of the measured temperature.	degree Celsius (C)			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sample temperature value (when received)	GENEPIO:0100823	The numerical value of a measurement of temperature of a sample upon receipt.	Provide the numerical value of the measured temperature.	22			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sample temperature unit (when received)	GENEPIO:0100824	The units of a measurement of temperature of a sample at the time upon receipt.	Provide the units of the measured temperature.	degree Celsius (C)			1.0.0	1.0.0	1.0.0
Strain and isolation information		GENEPIO:0100453								
Strain and isolation information	microbiological method	GENEPIO:0100454	The laboratory method used to grow, prepare,	Provide the name and version number of the microbiological	MFHPB-30			1.0.0	1.0.0	1.0.0
Strain and isolation information	strain	GENEPIO:0100455	The strain identifier.	If the isolate represents or is derived from, a lab reference st	K12			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolate ID	GENEPIO:0100456	The user-defined identifier for the isolate, as p	Provide the isolate_ID created by the lab that first isolated th	SA20131043			1.0.0	1.0.0	1.0.0
Strain and isolation information	alternative isolate ID	GENEPIO:0100457	An alternative isolate_ID assigned to the isola	Alternative isolate IDs should be provided in the in a prescrib	GHIF3456[PHAC]; QWICK222[CFIA]			1.0.0	1.0.0	1.0.0
Strain and isolation information	progeny isolate ID	GENEPIO:0100458	The identifier assigned to a progenitor isolate	If your sequence data pertains to progeny of an original isola	SUB_ON_1526			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolated by	GENEPIO:0100461	The name of the agency, organization or instit	Provide the name of the agency, organization or institution th	Public Health Agency of Canada (PHAC) [GENEPIO:0100551]			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolated by laboratory name	GENEPIO:0100462	The specific laboratory affiliation of the individ	Provide the name of the specific laboratory that that isolated	Topp Lab			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolated by contact name	GENEPIO:0100463	The name or title of the contact responsible fo	Provide the name of an individual or their job title. As person	Enterics Lab Manager			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolated by contact email	GENEPIO:0100464	The email address of the contact responsible	Provide the email associated with the listed contact. As pers	enterics@lab.ca			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolation date	GENEPIO:0100465	The date on which the isolate was isolated fro	Provide the date according to the ISO 8601 standard "YYYY-	2020-10-30			1.0.0	1.0.0	1.0.0
Strain and isolation information	isolate received date	GENEPIO:0100466	The date on which the isolate was received by	Provide the date according to the ISO 8601 standard "YYYY-	2020-11-15			1.0.0	1.0.0	1.0.0
Strain and isolation information	serovar	GENEPIO:0100467	The serovar of the organism.	Only include this information if it has been determined by tra	Heidelberg			1.0.0	1.0.0	1.0.0
Strain and isolation information	serotyping method	GENEPIO:0100468	The method used to determine the serovar.	If the serovar was determined via traditional serotyping meth	SISTR 1.0.1			1.0.0	1.0.0	1.0.0
Strain and isolation information	phagetype	GENEPIO:0100469	The phagetype of the organism.	Provide if known. If unknown, put "missing".	47			1.0.0	1.0.0	1.0.0
Sequence information		GENEPIO:0001441								
Sequence information	purpose of sequencing	GENEPIO:0001445	The reason that the sample was sequenced.	The reason why a sample was originally collected may differ from the reason why it was selected for sequencing. The reason a sample was sequenced may provide information about potential biases in sequencing strategy. Provide the purpose of sequencing from the picklist in the template. The reason for sample collection should be indicated in the "purpose of sampling" field.	Travel-associated surveillance			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	Colour Code Legend							Label	ID	Description/Guidance
Sequence information	**purpose of sequencing details**	GENEPIO:0001446	The description of why the sample was sequenced providing specific details.	Provide an expanded description of why the sample was sequenced using free text. The description may include the importance of the sequences for a particular public health investigation/surveillance activity/research question. Suggested standardized descriptions include: Assessing public health control measures, Determining early introductions and spread, Investigating airline-related exposures, Investigating remote regions, Investigating health care workers, Investigating schools/universities.	Investigating schools/universities			1.0.0	1.0.0	1.0.0
Sequence information	**sequenced by**	GENEPIO:0100416	The name of the agency, organization or institution responsible for sequencing the isolate's genome.	Provide the name of the agency, organization or institution that performed the sequencing in full (avoid abbreviations). If the information is unknown or cannot be provided, leave blank or provide a null value.	Public Health Agency of Canada (PHAC) [GENEPIO:0100551]			3.0.0	3.0.0	3.0.0
Sequence information	**sequenced by contact name**	GENEPIO:0100471	The name or title of the contact responsible for follow-up regarding the sequence.	Provide the name of an individual or their job title. As personnel turnover may render the contact's name obsolete, it is more preferable to provide a job title for ensuring accuracy of information and institutional memory. If the information is unknown or cannot be provided, leave blank or provide a null value.	Enterics Lab Manager			3.0.0	3.0.0	3.0.0
Sequence information	**sequenced by contact email**	GENEPIO:0100422	The email address of the contact responsible for follow-up regarding the sequence.	Provide the email associated with the listed contact. As personnel turnover may render an individual's email obsolete, it is more preferable to provide an address for a position or lab, to ensure accuracy of information and institutional memory. If the information is unknown or cannot be provided, leave blank or provide a null value.	enterics@lab.ca			3.0.0	3.0.0	3.0.0
Sequence information	**sequence submitted by**	GENEPIO:0001159	The name of the agency that submitted the sequence to a database.	The name of the agency should be written out in full, (with minor exceptions) and be consistent across multiple submissions. For Canadian institutions submitting specimens rather than sequencing data, please put the "National Microbiology Laboratory (NML)".	Public Health Ontario (PHO)			1.0.0	1.0.0	1.0.0
Sequence information	**sequence submitter contact email**	GENEPIO:0001165	The email address of the contact responsible for follow-up regarding the sequence.	The email address can represent a specific individual or laboratory.	RespLab@lab.ca			1.0.0	1.0.0	1.0.0
Sequence information	**sequencing date**	GENEPIO:0001447	The date the sample was sequenced.	ISO 8601 standard "YYYY-MM-DD".	2020-06-22			1.0.0	1.0.0	1.0.0
Sequence information	**library ID**	GENEPIO:0001448	The user-specified identifier for the library prepared for sequencing.	The library name should be unique, and can be an autogenerated ID from your LIMS, or modification of the isolate ID.	XYZ_123345			1.0.0	1.0.0	1.0.0
Sequence information	**sequencing platform**	GENEPIO:0100473	The platform technology used to perform the sequencing.	Provide the name of the company that created the sequencing instrument by selecting a value from the template pick list. If the information is unknown or cannot be provided, leave blank or provide a null value.	Illumina [GENEPIO:0001923]			1.0.0	1.0.0	1.0.0
Sequence information	**sequencing instrument**	GENEPIO:0001452	The model of the sequencing instrument used.	Provide the model sequencing instrument by selecting a value from the template pick list. If the information is unknown or cannot be provided, leave blank or provide a null value.	Illumina HiSeq 2500 [GENEPIO:0100117]			1.0.0	1.0.0	1.0.0
Sequence information	**sequencing assay type**	GENEPIO:0100997	The overarching sequencing methodology that was used to determine the sequence of a biomaterial.	Example Guidance: Provide the name of the DNA or RNA sequencing technology used in your study. If unsure refer to the protocol documentation, or provide a null value.	whole genome sequencing assay			1.0.0	1.0.0	1.0.0
Sequence information	**library preparation kit**	GENEPIO:0001450	The name of the DNA library preparation kit used to generate the library being sequenced.	Provide the name of the library preparation kit used.	Nextera XT			1.0.0	1.0.0	1.0.0
Sequence information	**sequencing protocol**	GENEPIO:0001454	The protocol or method used for sequencing.	Provide the name and version of the procedure or protocol used for sequencing. You can also provide a link to a protocol online.	https://www.protocols.io/view/ncov-2019-sequencing-protocol-bbmuik6w?versionwarning=no			1.0.0	1.0.0	1.0.0
Sequence information	**DNA fragment length**	GENEPIO:0100843	The length of the DNA fragment generated by mechanical shearing or enzymatic digestion for the purposes of library preparation.	Provide the fragment length in base pairs (do not include the units).	400			1.0.0	1.0.0	1.0.0
Sequence information	**genomic target enrichment method**	GENEPIO:0100966	The molecular technique used to selectively capture and amplify specific regions of interest from a genome.	Provide the name of the enrichment method	hybrid selection method			1.0.0	1.0.0	1.0.0
Sequence information	**genomic target enrichment method details**	GENEPIO:0100967	Details that provide additional context to the molecular technique used to selectively capture and amplify specific regions of interest from a genome.	Provide details that are applicable to the method you used.	enrichment was done using Twist's respiratory virus research panel: https://www.twistbioscience.com/products/ngs/fixed-panels/respiratory-virus-research-panel			1.0.0	1.0.0	1.0.0
Sequence information	**amplicon pcr primer scheme**	GENEPIO:0001456	The specifications of the primers (primer sequences, binding positions, fragment size generated etc) used to generate the amplicons to be sequenced.	Provide the name and version of the primer scheme used to generate the amplicons for sequencing.	artic v3			1.0.0	1.0.0	1.0.0
Sequence information	**amplicon size**	GENEPIO:0001449	The length of the amplicon generated by PCR amplification.	Provide the amplicon size expressed in base pairs.	300			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics		GENEPIO:0001457								

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	Colour Code Legend									
Bioinformatics and QC metrics	quality control method name	GENEPIO:0100557	The name of the method used to assess whether a sequence passed a predetermined quality control threshold.	Providing the name of the method used for quality control is very important for interpreting the rest of the QC information. Method names can be provided as the name of a pipeline or a link to a GitHub repository. Multiple methods should be listed and separated by a semi-colon. Do not include QC tags in other fields if no method name is provided.	ncov-tools			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control method version	GENEPIO:0100558	The version number of the method used to assess whether a sequence passed a predetermined quality control threshold.	Methods updates can make big differences to their outputs. Provide the version of the method used for quality control. The version can be expressed using whatever convention the developer implements (e.g. date, semantic versioning). If multiple methods were used, record the version numbers in the same order as the method names. Separate the version numbers using a semi-colon.	1.2.3			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control determination	GENEPIO:0100559	The determination of a quality control assessment.	Select a value from the pick list provided. If a desired value is missing, submit a new term request to the PHA4GE QC Tag GitHub issuetracker using the New Term Request form.	sequence failed quality control			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control issues	GENEPIO:0100560	The reason contributing to, or causing, a low quality determination in a quality control assessment.	Select a value from the pick list provided. If a desired value is missing, submit a new term request to the PHA4GE QC Tag GitHub issuetracker using the New Term Request form.	low average genome coverage			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control details	GENEPIO:0100561	The details surrounding a low quality determination in a quality control assessment.	Provide notes or details regarding QC results using free text.	CT value of 39. Low viral load. Low DNA concentration after amplification.			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	raw sequence data processing method	GENEPIO:0001458	The method used for raw data processing such as removing barcodes, adapter trimming, filtering etc.	Provide the software name followed by the version or a link to the github protocol e.g. Trimmomatic v. 0.38, Porechop v. 0.2.3	Porechop 0.2.3			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	dehosting method	GENEPIO:0001459	The method used to remove host reads from the pathogen sequence.	Provide the name and version number of the software used to remove host reads.	Nanostripper			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	consensus sequence software name	GENEPIO:0001463	The name of the software used to generate the consensus sequence.	Provide the name of the software used to generate the consensus sequence.	iVar			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	consensus sequence software version	GENEPIO:0001469	The version of the software used to generate the consensus sequence.	Provide the version of the software used to generate the consensus sequence.	1.3			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	sequence assembly software name	GENEPIO:0100825	The name of the software used to assemble a sequence.	Provide the name of the software used to assemble the sequence.	SPAdes Genome Assembler, Canu, wtdbg2, velvet			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	sequence assembly software version	GENEPIO:0100826	The version of the software used to assemble a sequence.	Provide the version of the software used to assemble the sequence.	3.15.5			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	breadth of coverage value	GENEPIO:0001472	The percentage of the reference genome covered by the sequenced data, to a prescribed depth.	Provide value as a percent.	95			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	depth of coverage value	GENEPIO:0001474	The average number of reads representing a given nucleotide in the reconstructed sequence.	Provide value as a fold of coverage.	400			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	depth of coverage threshold	GENEPIO:0001475	The threshold used as a cut-off for the depth of coverage.	Provide the threshold fold coverage.	100			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	genome completeness	GENEPIO:0100844	The percentage of expected genes identified in the genome being sequenced. Missing genes indicate missing genomic regions (incompleteness) in the data.	Provide the genome completeness as a percent (no need to include units).	85			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	number of base pairs sequenced	GENEPIO:0001482	The number of total base pairs generated by the sequencing process.	Provide a numerical value (no need to include units).	387566			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	number of total reads	GENEPIO:0100827	The total number of non-unique reads generated by the sequencing process.	Provide a numerical value (no need to include units).	423867			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	number of unique reads	GENEPIO:0100828	The number of unique reads generated by the sequencing process.	Provide a numerical value (no need to include units).	248236			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	minimum post-trimming read length	GENEPIO:0100829	The threshold used as a cut-off for the minimum length of a read after trimming.	Provide a numerical value (no need to include units).	150			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	number of contigs	GENEPIO:0100937	The number of contigs (contiguous sequences) in a sequence assembly.	Provide a numerical value.	10			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	percent Ns across total genome length	GENEPIO:0100830	The percentage of the assembly that consists of ambiguous bases (Ns).	Provide a numerical value (no need to include units).	2			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	Ns per 100 kbp	GENEPIO:0001484	The number of ambiguous bases (Ns) normalized per 100 kilobasepairs (kbp).	Provide a numerical value (no need to include units).	342			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	N50 value	GENEPIO:0100938	The length of the shortest read that, together with other reads, represents at least 50% of the nucleotides in a set of sequences.	Provide the N50 value in Mb.	150			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	percent read contamination	GENEPIO:0100845	The percent of the total number of reads identified as contamination (not belonging to the target organism) in a sequence dataset.	Provide the percent contamination value (no need to include units).	2			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	consensus genome length	GENEPIO:0001483	The length of the genome defined by the most common nucleotides at each position.	Provide a numerical value (no need to include units).	38677			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
	Colour Code Legend							Label	ID	Description/Gui dance
Bioinformatics and QC metrics	**sequence assembly length**	GENEPIO:0100846	The length of the genome generated by assembling reads using a scaffold or by reference-based mapping.	Provide a numerical value (no need to include units).	34272			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	**reference genome accession**	GENEPIO:0001485	A persistent, unique identifier of a genome database entry.	Provide the accession number of the reference genome.	NC_045512.2			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	**deduplication method**	GENEPIO:0100831	The method used to remove duplicated reads in a sequence read dataset.	Provide the deduplication software name followed by the version, or a link to a tool or method.	DeDup 0.12.8			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	**bioinformatics protocol**	GENEPIO:0001489	A description of the overall bioinformatics strategy used.	Further details regarding the methods used to process raw data, and/or generate assemblies, and/or generate consensus sequences can. This information can be provided in an SOP or protocol or pipeline/workflow. Provide the name and version number of the protocol, or a GitHub link to a pipeline or workflow.	https://github.com/phac-nml/ncov2019-arti c-nf			1.0.0	1.0.0	1.0.0
Taxonomic identification information		**GENEPIO:0101082**								
Taxonomic identification information	**read mapping software name**	GENEPIO:0100832	The name of the software used to map sequence reads to a reference genome or set of reference genes.	Provide the name of the read mapping software.	Bowtie2, BWA-MEM, TopHat			1.0.0	1.0.0	1.0.0
Taxonomic identification information	**read mapping software version**	GENEPIO:0100833	The version of the software used to map sequence reads to a reference genome or set of reference genes.	Provide the version number of the read mapping software.	2.5.1			1.0.0	1.0.0	1.0.0
Taxonomic identification information	**taxonomic reference database name**	GENEPIO:0100834	The name of the taxonomic reference database used to identify the organism.	Provide the name of the taxonomic reference database.	NCBITaxon			1.0.0	1.0.0	1.0.0
Taxonomic identification information	**taxonomic reference database version**	GENEPIO:0100835	The version of the taxonomic reference database used to identify the organism.	Provide the version number of the taxonomic reference database.	1.3			1.0.0	1.0.0	1.0.0
Taxonomic identification information	**taxonomic analysis report filename**	GENEPIO:0101074	The filename of the report containing the resul	Provide the filename of the report containing the results of th	WWtax_report_Feb1_2024.doc			1.0.0	1.0.0	1.0.0
Taxonomic identification information	**taxonomic analysis date**	GENEPIO:0101075	The date a taxonomic analysis was performed	Providing the date that an analyis was performed can help pr	2024-02-01			1.0.0	1.0.0	1.0.0
Taxonomic identification information	**read mapping criteria**	GENEPIO:0100836	A description of the criteria used to map reads to a reference sequence.	Provide a description of the read mapping criteria.	Phred score >20			1.0.0	1.0.0	1.0.0
AMR detection information		**GENEPIO:0100479**								
AMR detection information	**AMR analysis software name**	GENEPIO:0101076	The name of the software used to perform an	Provide the name of the software used for AMR analysis.	Resistance Gene Identifier			1.0.0	1.0.0	1.0.0
AMR detection information	**AMR analysis software version**	GENEPIO:0101077	The version number of the software used to p	Provide the version number of the software used for AMR an	6.0.3			1.0.0	1.0.0	1.0.0
AMR detection information	**AMR reference database name**	GENEPIO:0101078	Thr name of the reference database used to p	Provide the name of the reference database used for AMR a	Comprehensive Antibiotic Resistance Database (CARD)			1.0.0	1.0.0	1.0.0
AMR detection information	**AMR reference database version**	GENEPIO:0101079	The version number of the reference database	Provide the version number of the reference database used f	3.2.9			1.0.0	1.0.0	1.0.0
AMR detection information	**AMR analysis report filename**	GENEPIO:0101080	The filename of the report containing the resul	Provide the filename of the report containing the results of th	WWAMR_report_Feb1_2024.doc			1.0.0	1.0.0	1.0.0
Lineage/clade information		**GENEPIO:0001498**								
Lineage/clade information	**lineage/clade name**	GENEPIO:0001500	The name of the lineage or clade.	Provide the Pangolin or Nextstrain lineage/clade name. Multi	B.1.1.7			1.0.0	1.0.0	1.0.0
Lineage/clade information	**lineage/clade analysis software name**	GENEPIO:0001501	The name of the software used to determine tl	Provide the name of the software used to determine the linea	Freyja			1.0.0	1.0.0	1.0.0
Lineage/clade information	**lineage/clade analysis software version**	GENEPIO:0001502	The version of the software used to determine	Provide the version of the software used ot determine the lin	1.5.0			1.0.0	1.0.0	1.0.0
Lineage/clade information	**lineage/clade analysis report filename**	GENEPIO:0101081	The filename of the report containing the resul	Provide the filename of the report containing the results of th	aggregated-WWSC2-ABC-b_1234.tsv			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing		**GENEPIO:0001506**								
Pathogen diagnostic testing	**organism**	GENEPIO:0001191	The taxonomic name of the organism.	Put the genus and species (and subspecies if applicable) if known.The standardized term can be sourced from this look-up service: https://www.ebi.ac.uk/ols4/ontologies/ncbitaxon	Severe acute respiratory syndrome coronavirus 2			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**gene name**	GENEPIO:0100655	The name of the gene used in the diagnostic RT-PCR test.	Provide the full name of the gene used in the test. The gene symbol (short form of gene name) can also be provided. Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1LbI	E gene (orf4)			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**diagnostic target presence**	GENEPIO:0100962	The binary value of the result from a diagnostic test.	Select a value from the pick list provided, to describe whether a target was determined to be present or absent within a sample.	present			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**diagnostic measurement value**	GENEPIO:0100963	The value of the result from a diagnostic test.	Provide the numerical result of a diagnostic test.	1000			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**diagnostic measurement unit**	GENEPIO:0100964	The unit of the result from a diagnostic test.	Select a value from the pick list provided, to describe the units of the given diagnostic test.	CFU/mL			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**diagnostic measurement method**	GENEPIO:0100965	The method by which a diagnostic result was received.	Select a value from the pick list provided to describe the method used for a given diagnostic test.	qPCR			1.0.0	1.0.0	1.0.0
Contributor acknowledgement		**GENEPIO:0001516**								
Contributor acknowledgement	**authors**	GENEPIO:0001517	Names of individuals contributing to the processes of sample collection, sequence generation, analysis, and data submission.	Include the first and last names of all individuals that should be attributed, separated by a comma.	Tejinder Singh, Fei Hu, Joe Blogs			1.0.0	1.0.0	1.0.0