Parent Class	Field Colour Code Legend field name in yellow = required field name in purple = recommended field name in white = optional	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label **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.	Deprecated ID	Version Tracking Label	ID	Description/Guidance
	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	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
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
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			1.0.0	1.0.0	1.0.0
Database identifiers	GenBank_accession_(versioned)	GENEPIO:0100754	The versioned 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	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.	Store the accession assigned to the submitted sequence. DRA accessions start with DRR.	DRR123456			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	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_collection_data_steward_contact_email	GENEPIO:0101107	The email address of the individual responsible for the data governance, (meta)data usage and distribution of the sample.	Provide the email address of the sample collection data steward. This may or may not be the same individual/organization that collected the sample. If the contact is the same, provide the same address as the "sample collector contact email".	bloggsj@aglab.ca			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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/ga	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	organism	GENEPIO:0001191	Taxonomic name of the organism.	Provide the official nomenclature for the organism(s) present in the sample. Multiple organisms can be entered, separated by semicolons. Avoid abbreviations. Search for taxonomic names here: ncbi.nlm.nih.gov/taxonomy.	Vibrio cholerae			1.0.0	1.0.0	1.0.0
Sample collection and processing	influenza_subtype	GENEPIO:0101108						1.0.0	1.0.0	1.0.0
Sample collection and processing	influenza_subtyping_scheme_name	GENEPIO:0101109						1.0.0	1.0.0	1.0.0
Sample collection and processing	taxonomic_identification_process	GENEPIO:0100583						1.0.0	1.0.0	1.0.0
Sample collection and processing	virus_identifier	GENEPIO:0101110						1.0.0	1.0.0	1.0.0
Sample collection and processing	WHO/OIE/FAO_H5_clade	GENEPIO:0101111						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. 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 for a continuous sample.	Provide the date that sample collection ended in ISO 8601 format i.e. YYYY-MM-DD	2020-03-18			1.0.0	1.0.0	1.0.0
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

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
Sample collection and processing	sample_collection_time_of_day	GENEPIO:0100765	The descriptive time of day during which the sample was collected.	If known, select a value from the pick list. 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	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 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
Sample collection and processing	host_origin_geo_loc_name (country)	GENEPIO:0100438	The country of origin of the host.	If a sample is from a human or animal host that originated from outside of Canada, provide the the name of the country where the host originated 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.	South Africa [GAZ:00001094]			1.0.0	1.0.0	1.0.0
Sample collection and processing	food_product_origin_geo_loc_name (country)	GENEPIO:0100437	The country of origin of a food product.	If a food product was sampled and the food product was manufactured outside of Canada, provide the name of the country where the food product originated 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.	United States of America [GAZ:00002459]			1.0.0	1.0.0	1.0.0
Sample collection and processing	food_product	GENEPIO:0100444	A material consumed and digested for nutritional value or enjoyment.	This field includes animal feed. If applicable, select the standardized term and ontology ID for the anatomical material from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Feather meal [FOODON:00003927]; Bone meal [ENVO:02000054]; Chicken breast [FOODON:00002703]			1.0.0	1.0.0	1.0.0
Sample collection and processing	food_product_properties	GENEPIO:0100445	Any characteristic of the food product pertaining to its state, processing, a label claim, or implications for consumers.	Provide any characteristics of the food product including whether it has been cooked, processed, preserved, any known information about its state (e.g. raw, ready-to-eat), any known information about its containment (e.g. canned), and any information about a label claim (e.g. organic, fat-free).	Food (chopped) [FOODON:00002777]; Ready-to-eat (RTE) [FOODON:03316636]			1.0.0	1.0.0	1.0.0
Sample collection and processing	food_packaging	GENEPIO:0100447	The type of packaging used to contain a food product.	If known, provide information regarding how the food product was packaged.	Plastic tray or pan [FOODON:03490126]			1.0.0	1.0.0	1.0.0
Sample collection and processing	food_quality_date	GENEPIO:0100615	A date recommended for the use of a product while at peak quality, this date is not a reflection of safety unless used on infant formula.	This date is typically labeled on a food product as "best if used by", best by", "use by", or "freeze by" e.g. 5/24/2020. If the date is known, leave blank or provide a null value.	2020-05-25			1.0.0	1.0.0	1.0.0
Sample collection and processing	food_packaging_date	GENEPIO:0100616	A food product's packaging date as marked by a food manufacturer or retailer.	The packaging date should not be confused with, nor replaced by a Best Before date or other food quality date. If the date is known, leave blank or provide a null value.	2020-05-25			1.0.0	1.0.0	1.0.0
Sample collection and processing	environmental_site	GENEPIO:0001232	An environmental location may describe a site in the natural or built environment e.g. hospital, wet market, bat cave.	If applicable, select the standardized term and ontology ID for the environmental site from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Poultry hatchery [ENVO:01001874]			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, door handle, bed handrail, face mask.	If applicable, select the standardized term and ontology ID for the environmental material from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Soil [ENVO:00001998]; Water [CHEBI:15377]; Wastewater [ENVO:00002001]; Broom [ENVO:03501377]			1.0.0	1.0.0	1.0.0
Sample collection and processing	anatomical_material	GENEPIO:0001211	A substance obtained from an anatomical part of an organism e.g. tissue, blood.	An anatomical material is a substance taken from the body. If applicable, select the standardized term and ontology ID for the anatomical material from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Tissue [UBERON:0000479]; Blood [UBERON:0000178]			1.0.0	1.0.0	1.0.0
Sample collection and processing	body_product	GENEPIO:0001216	A substance excreted/secreted from an organism e.g. feces, urine, sweat.	A body product is a substance produced by the body but meant to be excreted/secreted (i.e. not part of the body). If applicable, select the standardized term and ontology ID for the body product from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Feces [UBERON:0001988]; Urine [UBERON:0001088]			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
Sample collection and processing	anatomical_part	GENEPIO:0001214	An anatomical part of an organism e.g. oropharynx.	An anatomical part is a structure or location in the body. If applicable, select the standardized term and ontology ID for the anatomical material from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Snout [UBERON:0006333]			1.0.0	1.0.0	1.0.0
Sample collection and processing	collection_device	GENEPIO:0001234	The instrument or container used to collect the sample e.g. swab.	This field includes animal feed. If applicable, select the standardized term and ontology ID for the anatomical material from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Drag swab [OBI:0002822]			1.0.0	1.0.0	1.0.0
Sample collection and processing	collection_method	GENEPIO:0001241	The process used to collect the sample e.g. phlebotomy, necropsy.	If applicable, provide the standardized term and ontology ID for the anatomical material from the picklist provided. Multiple values can be provided, separated by a semi-colon.	Rinsing for specimen collection [GENEPIO_00 02116]			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.	milliliter (mL) [UO:0000098]			1.0.0	1.0.0	1.0.0
Sample collection and processing	residual_sample_status	GENEPIO:0101090	The status of the residual sample (whether any sample remains after its original use).	Residual samples are samples that remain after the sample material was used for its original purpose. Select a residual sample status from the picklist. If sample still exists, select "Residual sample remaining (some sample left)".	No residual sample (sample all used) [GENEPIO:010 1088]			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	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_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

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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	GENEPIO:0101029	The name of the overarching experimental methodology that was used to process the biomaterial.	Provide the name of the methodology used in your study. If available, provide a link to the protocol.				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_specimen_details	GENEPIO:0101112						1.0.0	1.0.0	1.0.0
Sample collection and processing	available_data_types	GENEPIO:0100690	The type of data that is available, that may or may not require permission to access.	This field provides information about additional data types that are available that may provide context for interpretation of the sequence data. Provide a term from the picklist for additional data types that are available. Additional data types may require special permission to access. Contact the data provider for more information.	Total coliform count [GENEPIO:0100729]			1.0.0	1.0.0	1.0.0
Sample collection and processing	available_data_type_details	GENEPIO:0101023	Detailed information regarding other available data types.	Use this field to provide free text details describing other available data types that may provide context for interpreting genomic sequence data.	Pooled metagenomes containing extended spectrum beta-lactamase (ESBL) bacteria			1.0.0	1.0.0	1.0.0
	Host information	GENEPIO:0001268								
Host information	host_(common_name)	GENEPIO:0001386	The commonly used name of the host.	If the sample is directly from a host, either a common or scientific name must be provided (although both can be included, if known). If known, provide the common name.	Cow [NCBITaxon:9913]; Chicken [NCBITaxon:9913], Human [NCBITaxon:9606]			1.0.0	1.0.0	1.0.0
Host information	host_(scientific_name)	GENEPIO:0001387	The taxonomic, or scientific name of the host.	If the sample is directly from a host, either a common or scientific name must be provided (although both can be included, if known). If known, select the scientific name from the picklist provided.	Bos taurus [NCBITaxon:9913]; Homo sapiens [NCBITaxon:9103]			1.0.0	1.0.0	1.0.0
Host information	host_(ecotype)	GENEPIO:0100450	The biotype resulting from selection in a particular habitat, e.g. the A. thaliana Ecotype Ler.	Provide the name of the ecotype of the host organism.	Sea ecotype			1.0.0	1.0.0	1.0.0
Host information	host_(breed)	GENEPIO:0100451	A breed is a specific group of domestic animals or plants having homogeneous appearance, homogeneous behavior, and other characteristics that distinguish it from other animals or plants of the same species and that were arrived at through selective breeding.	Provide the name of the breed of the host organism.	Holstein			1.0.0	1.0.0	1.0.0
Host information	host_(food production name)	GENEPIO:0100452	The name of the host at a certain stage of food production, which may depend on its age or stage of sexual maturity.	Select the host's food production name from the pick list.	Calf [FOODON:03411349]			1.0.0	1.0.0	1.0.0
Host Information	host_age	GENEPIO:0001392	Age of host at the time of sampling.	If known, provide age. Age-binning is also acceptable.	79			1.0.0	1.0.0	1.0.0
Host Information	host_age_unit	GENEPIO:0001393	The units used to measure the host's age.	If known, provide the age units used to measure the host's age from the pick list.	year [UO:0000036]			1.0.0	1.0.0	1.0.0
Host information	host_age_bin	GENEPIO:0001394	Age of host at the time of sampling, expressed as an age group.	Select the corresponding host age bin from the pick list provided in the template. If not available, provide a null value or leave blank.				1.0.0	1.0.0	1.0.0
	host_gender							1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
Host information	host_disease	GENEPIO:0001391	The name of the disease experienced by the host.	This field is only required if the Pathogen.cl package was selected. If the host was sick, provide the name of the disease.The standardized term can be sourced from this look-up service: https://www.ebi.ac.uk/ols/ontologies/doid If the disease is not known, put "missing".	mastitis, gastroenteritis			1.0.0	1.0.0	1.0.0
Host Information	host_health_state	GENEPIO:0001388	Health status of the host at the time of sample collection.	If known, select a value from the pick list.	Asymptomatic [NCIT:C3833]			1.0.0	1.0.0	1.0.0
Host Information	host_health_status_details	GENEPIO:0001389	Further details pertaining to the health or disease status of the host at time of collection.	If known, select a value from the pick list.	Hospitalized (ICU) [GENEPIO:0100046]			1.0.0	1.0.0	1.0.0
Host Information	host_health_outcome	GENEPIO:0001390	Disease outcome in the host.	If known, select a value from the pick list.	Recovered [NCIT:C49498]			1.0.0	1.0.0	1.0.0
Host Information	host_subject_ID	GENEPIO:0001398	A unique identifier by which each host can be referred to e.g. #131	Should be a unique, user-defined identifier. This ID can help link laboratory data with epidemiological data, however, is likely sensitive information. Consult the data steward.	BCxy123			1.0.0	1.0.0	1.0.0
Host Information	case_ID	GENEPIO:0100281	The identifier used to specify an epidemiologically detected case of disease.	Provide the case identifer. The case ID greatly facilitates linkage between laboratory and epidemiological data. The case ID may be considered identifiable information. Consult the data steward before sharing.	ABCD1234			1.0.0	1.0.0	1.0.0
Host Information	symptom_onset_date	GENEPIO:0001399	The date on which the symptoms began or were first noted.	If known, provide the symptom onset date in ISO 8601 standard format "YYYY-MM-DD".	2020-03-16			1.0.0	1.0.0	1.0.0
Host Information	signs_and_symptoms	GENEPIO:0001400	A perceived change in function or sensation, (loss, disturbance or appearance) indicative of a disease, reported by a patient.	Select all of the symptoms experienced by the host from the pick list.	Cough [HP:0012735], Fever [HP:0001945], Rigors (fever shakes) [HP:0025145]			1.0.0	1.0.0	1.0.0
Host Information	pre-existing_conditions_and_risk_factors	GENEPIO:0001401	Patient pre-existing conditions and risk factors. Pre-existing condition: A medical condition that existed prior to the current infection. Risk Factor: A variable associated with an increased risk of disease or infection.	Select all of the pre-existing conditions and risk factors experienced by the host from the pick list. If the desired term is missing, contact the curation team.	Asthma [HP:0002099]			1.0.0	1.0.0	1.0.0
Host Information	complications	GENEPIO:0001402	Patient medical complications that are believed to have occurred as a result of host disease.	Select all of the complications experienced by the host from the pick list.	Acute respiratory failure [MONDO:0001208]					
	Host exposure information	GENEPIO:0001409						1.0.0	1.0.0	1.0.0
Host exposure information	exposure event	GENEPIO:0001417	Event leading to exposure.	Select an exposure event from the pick list provided in the template. If the desired term is missing, contact the curation team.	Social Gathering			1.0.0	1.0.0	1.0.0
Host exposure information	exposure contact level	GENEPIO:0001418	The exposure transmission contact type.	Select direct or indirect exposure from the pick-list.	Direct			1.0.0	1.0.0	1.0.0
Host exposure information	host role	GENEPIO:0001419	The role of the host in relation to the exposure setting.	Select the host's personal role(s) from the pick list provided in the template. If the desired term is missing, contact the curation team.	Inpatient			1.0.0	1.0.0	1.0.0
Host exposure information	exposure setting	GENEPIO:0001428	The setting leading to exposure.	Select the host exposure setting(s) from the pick list provided in the template. If a desired term is missing, contact the curation team.	Healthcare Setting			1.0.0	1.0.0	1.0.0
Host exposure information	exposure details	GENEPIO:0001431	Additional host exposure information.	Free text description of the exposure.	Case infected family at home					
	Host vaccination information	GENEPIO:0001403						1.0.0	1.0.0	1.0.0
Host vaccination information	host_vaccination_status	GENEPIO:0001404	#REF!					1.0.0	1.0.0	1.0.0
Host vaccination information	number_of_vaccine_doses_received	GENEPIO:0001406						1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination_dose_1_vaccine_name	GENEPIO:0100313						1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination_dose_1_vaccination_date	GENEPIO:0100314						1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination_dose_2_vaccine_name	GENEPIO:0100315						1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination_dose_2_vaccination_date	GENEPIO:0100316						1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination history	GENEPIO:0100321						1.0.0	1.0.0	1.0.0
	Host treatment information							1.0.0	1.0.0	1.0.0
Host treatment information	influenza_antiviral_treatment_administration menu	GENEPIO:0101113						1.0.0	1.0.0	1.0.0
Host treatment information	influenza_antiviral_agent	GENEPIO:0101114	A substance that destroys or inhibits replication of viruses.					1.0.0	1.0.0	1.0.0
Host treatment information	influenza_antiviral_treatment_date	GENEPIO:0101115								
	Environmental conditions and measurements							1.0.0	1.0.0	1.0.0
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_range	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

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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					
Environmental conditions and measurements	water catchment area human population density value	GENEPIO:0100776	The numerical value describing the number of humans per geographical area in a water catchment.	Provide the numerical value of the population density in the catchement area.	4			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	water catchment area human population density unit	GENEPIO:0100777	The unit describing the number of humans per geographical area in a water catchment.	Provide the unit of the population density in the catchement area.	persons per Km^2			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	populated area type	GENEPIO:0100778	A type of area that is populated by humans to different degrees.	Provide the populated area type from the pick list.	Urban area			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sampling weather conditions	GENEPIO:0100779	The state of the atmosphere at a place and time as regards heat, dryness, sunshine, wind, rain, etc.	Provide the weather conditions at the time of sample collection.	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	water_depth	GENEPIO:0100440	The depth of some water.	Provide the numerical depth only of water only (without units).	5			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	water_depth_units	GENEPIO:0101025	The units of measurement for water depth.	Provide the units of measurement for which the depth was recorded.	meter (m) [UO:0000008]			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sediment_depth	GENEPIO:0100697	The depth of some sediment.	Provide the numerical depth only of the sediment (without units).	2			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	sediment_depth_units	GENEPIO:0101026	The units of measurement for sediment depth.	Provide the units of measurement for which the depth was recorded.	meter (m) [UO:0000008]			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	air_temperature	GENEPIO:0100441	The temperature of some air.	Provide the numerical value for the temperature of the air (without units).	25			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	air_temperature_units	GENEPIO:0101027	The units of measurement for air temperature.	Provide the units of measurement for which the temperature was recorded.	degree Celsius (C) [UO:0000027]			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	water_temperature	GENEPIO:0100698	The temperature of some water.	Provide the numerical value for the temperature of the water (without units).	4			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	water_temperature_units	GENEPIO:0101028	The units of measurement for water temperature.	Provide the units of measurement for which the temperature was recorded.	degree Celsius (C) [UO:0000027]			1.0.0	1.0.0	1.0.0
Environmental conditions and measurements	weather_type	GENEPIO:0100442	The state of the atmosphere at a place and time as regards heat, dryness, sunshine, wind, rain, etc.	Provide the weather conditions at the time of sample collection.	Rain [ENVO:01001564]			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
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

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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 numerical value from a total suspended solids (TSS) test.	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			1.0.0	1.0.0	1.0.0
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

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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.	Urobilin Concentration Test			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
	Sequence information	GENEPIO:0001441						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.	Every "library 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, and as informative as possible.	LS_2010_NP_123446			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 [OBI:0002117]			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					
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

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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]			1.0.0	1.0.0	1.0.0
Sequence information	sequenced_by_laboratory_name	GENEPIO:0100470	The specific laboratory affiliation of the responsible for sequencing the isolate's genome.	Provide the name of the specific laboratory that that performed the sequencing in full (avoid abbreviations). If the information is unknown or cannot be provided, leave blank or provide a null value.	Topp Lab			1.0.0	1.0.0	1.0.0
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 prefereable 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			1.0.0	1.0.0	1.0.0
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 prefereable 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			1.0.0	1.0.0	1.0.0
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
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.				1.0.0	1.0.0	1.0.0
Sequence information	sequencing_project_name	GENEPIO:0100472	The name of the project/initiative/program for which sequencing was performed.	Provide the name of the project and/or the project ID here. If the information is unknown or cannot be provided, leave blank or provide a null value.	AMR-GRDI (PA-1356)			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:000 1923]			1.0.0	1.0.0	1.0.0

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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								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	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 (bait-capture) [GENEPIO:0001950]			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. Note: If bait-capture methods were used for enrichment, provide the panel name and version number (or a URL providing that information).	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
Sequence information	**sequencing_flow_cell_version**	GENEPIO:0101102	The version number of the flow cell used for generating sequence data.	Flow cells can vary in terms of design, chemistry, capacity, etc. The version of the flow cell used to generate sequence data can affect sequence quantity and quality. Record the version of the flow cell used to generate sequence data. Do not include "version" or "v" in the version number.	R.9.4.1			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?version_warning=no			1.0.0	1.0.0	1.0.0
Sequence information	**r1_fastq_filename**	GENEPIO:0001476	The user-specified filename of the r1 FASTQ file.	Provide the r1 FASTQ filename.	ABC123_S1_L001_R1_001.fastq.gz			1.0.0	1.0.0	1.0.0
Sequence information	**r2_fastq_filename**	GENEPIO:0001477	The user-specified filename of the r2 FASTQ file.	Provide the r2 FASTQ filename.	ABC123_S1_L001_R2_001.fastq.gz			1.0.0	1.0.0	1.0.0
Sequence information	**fast5_filename**	GENEPIO:0001480	The user-specified filename of the FAST5 file.	Provide the FAST5 filename.	batch1a_sequences.fast5			1.0.0	1.0.0	1.0.0
Sequence information	**genome sequence file name**	GENEPIO:0101715	The name of the sequence file.	Provide the name and version number, with the file extension, of the processed genome sequence file e.g. a consensus sequence FASTA file or a genome assembly file.	mpxvassembly.fasta			1.0.0	1.0.0	1.0.0
Sequence information	**assembly_filename**	GENEPIO:0001461	The user-defined filename of the FASTA file.	Provide the FASTA filename.	pathogenassembly123.fasta			1.0.0	1.0.0	1.0.0
	Bioinformatics and QC metrics	GENEPIO:0001457						1.0.0	1.0.0	1.0.0

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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					
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.	Raw data processing can have a significant impact on data quality and how it can be used. Provide the names and version numbers of software used for trimming adaptors, quality filtering, etc (e.g. Trimmomatic v. 0.38, Porechop v. 0.2.3), or a link to a GitHub protocol.	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	**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	**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	**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

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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**	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	**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	**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
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-artic-nf			1.0.0	1.0.0	1.0.0
	Taxonomic identification information	GENEPIO:0101082						1.0.0	1.0.0	1.0.0
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					
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 results of a taxonomic analysis.	Provide the filename of the report containing the results of the taxonomic analysis.	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 provide context for tool and reference database versions. Provide the date that the taxonomic analysis was performed in ISO 8601 format, i.e. "YYYY-MM-DD".	2024-02-01			1.0.0	1.0.0	1.0.0

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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
	Pathogen diagnostic testing	GENEPIO:0001506						1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**genetic target name**	GENEPIO:0101116	The name of the genetic marker used for testing.	Provide the full name of the gene used in the test. Standardized gene names can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1Lbl	gyrase A			1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**genetic target region**	GENEPIO:0101117						1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	genetic target region reference genome	GENEPIO:0101118								
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.	diagnostic target 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 (no need to include units).	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.	cycle threshold (Ct)			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 determined.	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
Pathogen diagnostic testing	**diagnostic testing threshold value**	GENEPIO:0101104						1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**diagnostic testing threshold units**	GENEPIO:0101105						1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	**diagnostic testing details**	GENEPIO:0101106						1.0.0	1.0.0	1.0.0
	Risk assessment information	GENEPIO:0100478						1.0.0	1.0.0	1.0.0
Risk assessment information	**prevalence_metrics**	GENEPIO:0100480	Metrics regarding the prevalence of the pathogen of interest obtained from a surveillance project.	Risk assessment requires detailed information regarding the quantities of a pathogen in a specified location, commodity, or environment. As such, it is useful for risk assessors to know what types of information are available through documented methods and results. Provide the metric types that are available in the surveillance project sample plan by selecting them from the pick list. The metrics of interest are " Number of total samples collected", "Number of positive samples", "Average count of hazard organism", "Average count of indicator organism". You do not need to provide the actual values, just indicate that the information is available.	Number of total samples collected, Number of positive samples			1.0.0	1.0.0	1.0.0
Risk assessment information	**prevalence_metrics_details**	GENEPIO:0100481	The details pertaining to the prevalence metrics from a surveillance project.	If there are details pertaining to samples or organism counts in the sample plan that might be informative, provide details using free text.	Hazard organism counts (i.e. Salmonella) do not distinguish between serovars.			1.0.0	1.0.0	1.0.0
Risk assessment information	stage_of_production	GENEPIO:0100482	The stage of food production.	Provide the stage of food production as free text.	Abattoir [ENVO:01000925]					
Risk assessment information	**experimental_intervention**	GENEPIO:0100483	The category of the experimental intervention applied in the food production system.	In some surveys, a particular intervention in the food supply chain in studied. If there was an intervention specified in the sample plan, select the intervention category from the pick list provided.	Vaccination [NCIT:C15346]			1.0.0	1.0.0	1.0.0
Risk assessment information	**experiment_intervention_details**	GENEPIO:0100484	The details of the experimental intervention applied in the food production system.	If an experimental intervention was applied in the survey, provide details in this field as free text.	2% cranberry solution mixed in feed			1.0.0	1.0.0	1.0.0