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	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

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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_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 received date	GENEPIO:0001179	The date on which the sample was received.	Provide the sample received date in ISO 8601 for	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

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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:0000109 4]			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:000 0479]; Blood [UBERON:000 0178]			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:000 1988]; Urine [UBERON:000 1088]			1.0.0	1.0.0	1.0.0
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:000 6333]			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

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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 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

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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 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]			1.0.0	1.0.0	1.0.0
Host exposure information		GENEPIO:0001409								
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			1.0.0	1.0.0	1.0.0
Host vaccination information		GENEPIO:0001403								

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Host vaccination information	host vaccination status	GENEPIO:0001404	The vaccination status of the host (fully vaccinated, partially vaccinated, or not vaccinated).	Select the vaccination status of the host from the pick list.	Fully Vaccinated [GENEPIO:0100100]			1.0.0	1.0.0	1.0.0
Host vaccination information	number of vaccine doses received	GENEPIO:0001406	The number of doses of the vaccine received by the host.	Record how many doses of the vaccine the host has received.	2			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 1 vaccine name	GENEPIO:0100313	The name of the vaccine administered as the first dose of a vaccine regimen.	Provide the name and the corresponding manufacturer of the COVID-19 vaccine administered as the first dose by selecting a value from the pick list	Pfizer-BioNTech (Comirnaty)			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 1 vaccination date	GENEPIO:0100314	The date the first dose of a vaccine was administered.	Provide the date the first dose of COVID-19 vaccine was administered. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2021-03-01			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 2 vaccine name	GENEPIO:0100315	The name of the vaccine administered as the second dose of a vaccine regimen.	Provide the name and the corresponding manufacturer of the COVID-19 vaccine administered as the second dose by selecting a value from the pick list	Pfizer-BioNTech (Comirnaty)			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 2 vaccination date	GENEPIO:0100316	The date the second dose of a vaccine was administered.	Provide the date the second dose of COVID-19 vaccine was administered. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2021-09-01			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 3 vaccine name	GENEPIO:0100317	The name of the vaccine administered as the third dose of a vaccine regimen.	Provide the name and the corresponding manufacturer of the COVID-19 vaccine administered as the third dose by selecting a value from the pick list	Pfizer-BioNTech (Comirnaty)			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 3 vaccination date	GENEPIO:0100318	The date the third dose of a vaccine was administered.	Provide the date the third dose of COVID-19 vaccine was administered. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2021-12-30			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 4 vaccine name	GENEPIO:0100319	The name of the vaccine administered as the fourth dose of a vaccine regimen.	Provide the name and the corresponding manufacturer of the COVID-19 vaccine administered as the fourth dose by selecting a value from the pick list	Pfizer-BioNTech (Comirnaty)			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 4 vaccination date	GENEPIO:0100320	The date the fourth dose of a vaccine was administered.	Provide the date the fourth dose of COVID-19 vaccine was administered. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2022-01-15			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination history	GENEPIO:0100321	A description of the vaccines received and the administration dates of a series of vaccinations against a specific disease or a set of diseases.	Free text description of the dates and vaccines administered against a particular disease/set of diseases. It is also acceptable to concatenate the individual dose information (vaccine name, vaccination date) separated by semicolons.	Pfizer-BioNTech (Comirnaty); 2021-03-01; Pfizer-BioNTech (Comirnaty); 2022-01-15			1.0.0	1.0.0	1.0.0
Host treatment information										
Host treatment information	prior influenza antiviral agent administration	GENEPIO:0101113						1.0.0	1.0.0	1.0.0
Host treatment information	prior 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	prior influenza antiviral treatment date	GENEPIO:0101115						1.0.0	1.0.0	1.0.0
Sequence information		GENEPIO:0001441								
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			1.0.0	1.0.0	1.0.0
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		
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/univers ities			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:010 0551]			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.c a			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.pro tocols.io/view/v -4-direct-waste water-rna-captu re-and-purificati on-36wgq581y gk5/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	consensus_sequence_filename	GENEPIO:0101119						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								

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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.	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

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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								
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 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

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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								
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/2Sq1LbI	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						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.	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								
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:010009 25]			1.0.0	1.0.0	1.0.0
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

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking		
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