

| Parent Class | Field | Ontology Identifier | Definition | Guidance | Examples | Deprecated Label | Deprecated ID | Version Tracking | ID | Description/Guidance |
|----------------------------------|---|---------------------|---|---|-----------------------------------|---|---------------|------------------|-------|----------------------|
| | Colour Code Legend field name in yellow = required field name in purple = recommended field name in white = optional | | | | | 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. | | 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 | SAMN1418020 2. 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@facity.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[dd.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_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 |

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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 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 | 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 |
| 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_0002116] | | | 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:0101088] | | | 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. | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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. | | | 1.0.01.0.01.0.0 |
| 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. | | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| Sample collection and processing | experimental_specimen_details | GENEPIO:0101112 | | | | | | 1.0.01.0.01.0.0 |
| 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] | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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] | | | 1.0.01.0.01.0.0 |

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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 [NCBI:Taxon:9913]; Homo sapiens [NCBI:Taxon: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 identifier. 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] | | | | | |
| 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 | | | | | | 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 | | | | | |
| 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 | | | | | | 1.0.0 | 1.0.0 | 1.0.0 |

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| 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 | A substance that destroys or inhibits replication of viruses. | | | | | 1.0.0 | 1.0.0 | 1.0.0 |
| Host treatment information | influenza_antiviral_agent | GENEPIO:0101114 | | | | | | | | |
| Host treatment information | influenza_antiviral_treatment_date | GENEPIO:0101115 | | | | | | 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] | | | | | |
| 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 |
| 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 preferable to provide a job title for ensuring accuracy of information and institutional memory. If the information is unknown or cannot be provided, leave blank or provide a null value. | Enterics Lab Manager | | | 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 preferable to provide an address for a position or lab, to ensure accuracy of information and institutional memory. If the information is unknown or cannot be provided, leave blank or provide a null value. | enterics@lab.ca | | | 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 |

| Parent Class | Field | Ontology Identifier | Definition | Guidance | Examples | Deprecated Label | Deprecated ID | Version Tracking |
|----------------------------------|--|---------------------|--|--|--|------------------|---------------|------------------|
| 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 | | | 1.0.01.0.01.0.0 |
| 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/v4-direct-waste-water-rna-capture-and-purification-36wgq581y-gk5/v4 | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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. | | | | 1.0.01.0.01.0.0 |
| 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) | | | 1.0.01.0.01.0.0 |
| Sequence information | sequencing_platform | GENEPIO:0100473 | The platform technology used to perform the sequencing. | Provide the name of the company that created the sequencing instrument by selecting a value from the template pick list. If the information is unknown or cannot be provided, leave blank or provide a null value. | Illumina [GENEPIO:0001923] | | | 1.0.01.0.01.0.0 |
| Sequence information | sequencing_instrument | GENEPIO:0001452 | The model of the sequencing instrument used. | Provide the model sequencing instrument by selecting a value from the template pick list. If the information is unknown or cannot be provided, leave blank or provide a null value. | Illumina HiSeq 2500 [GENEPIO:0100117] | | | 1.0.01.0.01.0.0 |
| Sequence information | | | | | | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| 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] | | | 1.0.01.0.01.0.0 |
| 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/fixd-panels/respiratory-virus-research-panel | | | 1.0.01.0.01.0.0 |
| 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 | | | 1.0.01.0.01.0.0 |
| Sequence information | amplicon_size | GENEPIO:0001449 | The length of the amplicon generated by PCR amplification. | Provide the amplicon size expressed in base pairs. | 300 | | | 1.0.01.0.01.0.0 |

| Parent Class | Field | Ontology Identifier | Definition | Guidance | Examples | Deprecated Label | Deprecated ID | Version Tracking | | |
|-------------------------------|-------------------------------------|---------------------|--|--|---|------------------|---------------|------------------|-------|-------|
| 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=n | | | 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 |
| 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 | | | | | |
| 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 issue tracker 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 issue tracker 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. | Nanostrripper | | | 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 | 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 |
| 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 |

| Parent Class | Field | Ontology Identifier | Definition | Guidance | Examples | Deprecated Label | Deprecated ID | Version Tracking | | |
|---|---|---------------------|---|--|---|------------------|---------------|------------------|-------|-------|
| 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-article-f | | | 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 | | | | | |
| 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 analysis 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 |
| 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/2Sq1LbI | gyrase A | | | 1.0.0 | 1.0.0 | 1.0.0 |
| Pathogen diagnostic testing | genetic target region | GENEPIO:0101117 | | | | | | | | |
| 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 |

| Parent Class | Field | Ontology Identifier | Definition | Guidance | Examples | Deprecated Label | Deprecated ID | Version Tracking | | |
|-----------------------------|---------------------------------|---------------------|--|---|---|------------------|---------------|------------------|-------|-------|
| 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 quantiles 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. | | | | | |
| 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] | | | 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 is 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 | 2% cranberry solution mixed in feed | | | | | | |

