Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking			Editor Notes
								Label	ID	Description/Guidance	
				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.							
Database Identifiers		GENEPIO:0001122									
Database Identifiers	isolate ID	GENEPIO:0100456	The user-defined identifier for the isolate, as provided by the laboratory that originally isolated the isolate.	Provide the identifier created by the lab for the organism after isolation. This value maps to the "Strain ID#" in the Alberta Microbiota Repository (AMBR) Master file.	SA01			1.0.0	1.0.0	1.0.0	
Database Identifiers	alternative isolate ID	GENEPIO:0100457	An alternative isolate_ID assigned to the isolate by another organization.	Provide the identifier that represents the site code, source and/or patient identifier, media type, strain identifier, colony number, growth condition and dilution factor as a single code. This value corresponds maps to the "Label ID" in the Alberta Microbiota Repository (AMBR) Master file.	3411301			1.0.0	1.0.0	1.0.0	
Database Identifiers	specimen collector sample ID	GENEPIO:0001123	The user-defined name for the sample.	Provide the sample ID provided by the original sample collector. This value is different from the "isolate_ID" as it represents the original material sampled rather than the organism that was isolated from the sampled material. This identifier may or may not be available.	Lake_Louise_Water23			1.0.0	1.0.0	1.0.0	
Sample collection and processing		GENEPIO:0001150									
Sample collection and processing	sample collected by	GENEPIO:0001153	The name of the agency that collected the original sample.	The name of the institution of the original sample collector should be written out in full, (no abbreviations, with minor exceptions) and be consistent across multiple submissions e.g. University of Calgary, Alberta Health Services. The sample collector specified is at the discretion of the data provider (i.e. may be hospital, provincial public health lab, or other).	University of Calgary			1.0.0	1.0.0	1.0.0	
Sample collection and processing	sample_collection_project_name	GENEPIO:0100429	The name of the project/initiative/program for which the sample was collected.	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.	Children's Hospital biofilm study (A3-701-01)			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	RespLab@lab.ca			1.0.0	1.0.0	1.0.0	
Sample collection and processing	sample collector contact address	GENEPIO:0001158	The mailing address of the agency submitting the sample.	The mailing address should be in the format: Street number and name, City, Province/Territory, Postal Code, Country	655 Lab St, Vancouver, British Columbia, V5N 2A2, Canada			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.	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.	The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2020-03-20			1.0.0	1.0.0	1.0.0	
Sample collection and processing	geo_loc_name (country)	GENEPIO:0001181	The country where the sample was collected.	Provide the country name from the controlled vocabulary provided.	Canada			1.0.0	1.0.0	1.0.0	
Sample collection and processing	geo_loc_name (state/province/territory)	GENEPIO:0001185	The province/territory where the sample was collected.	Provide the province/territory name from the controlled vocabulary provided.	Saskatchewan			1.0.0	1.0.0	1.0.0	
Sample collection and processing	geo_loc_name (city)	GENEPIO:0001189	The city where the sample was collected.	Provide the city name. Use this look-up service to identify the standardized term: https://www.ebi.ac.uk/ols/ontologies/gaz	Medicine Hat			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).	Lake Louise			1.0.0	1.0.0	1.0.0	
Sample collection and processing	organism	GENEPIO:0001191	Taxonomic name of the organism.	Provide the confirmed taxonomic name of the species. This value maps to the "Recommended identification" in the Alberta Microbiota Repository (AMBR) Master file.	Staphylococcus aureus			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. 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. Motivation for sampling may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Targeted surveillance			1.0.0	1.0.0	1.0.0	
Sample collection and processing	purpose of sampling details	GENEPIO:0001200	The description of why the sample was collected, providing specific details.	Provide an expanded description of why the sample was collected using free text. The description may include the importance of the sample for a particular investigation/surveillance activity/research question. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	ProvLab/IPC routine monitoring			1.0.0	1.0.0	1.0.0	
Sample collection and processing	original sample description	GENEPIO:0100439	The original sample description provided by the sample collector.	Provide the sample description provided by the original sample collector or the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file. The original description is useful as it may provide further details, or can be used to clarify higher level classifications.	ACH coupons-water study, isolates 2010, 2011 see appendix 3 (Alberta Chil			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.	Provide a descriptor if an anatomical material was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Wound tissue (injury)			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.	Provide a descriptor if an anatomical part was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Nasal cavity			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.	Provide a descriptor if a body product was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Feces			1.0.0	1.0.0	1.0.0	
Sample collection and processing	environmental material	GENEPIO:0001223	A substance obtained from the natural or man-made environment e.g. soil, water, sewage.	Provide a descriptor if an environmental material was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Bandage			1.0.0	1.0.0	1.0.0	
Sample collection and processing	environmental site	GENEPIO:0001232	An environmental location may describe a site in the natural or built environment e.g. contact surface, metal can, hospital, wet market, bat cave.	Provide a descriptor if an environmental site was sampled. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Hospital			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.	Provide a descriptor if a device was used for sampling. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Swab			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. phlebotamy, necropsy.	Provide a descriptor if a collection method was used for sampling. Use the picklist provided in the template. If a desired term is missing from the picklist, contact emma_griffiths@sfu.ca. If not applicable, do not leave blank. Choose a null value. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Biopsy			1.0.0	1.0.0	1.0.0	
Sample collection and processing	collection protocol	GENEPIO:0001243	The name and version of a particular protocol used for sampling.	Free text. Information for populating this field may be available in the "Source of Isolation" field in the Alberta Microbiota Repository (AMBR) Master file.	Collection_protocol_Children's Hospital biofilm study (A3-701-01)			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.	If multiple PCR products were generated from the isolate using different primer sets, indicate that the sequence records represents the same isolate by selecting "Biological replicate" in the "specimen processing" field. Every different sequence experiment should have its own record (i.e. if different amplicons have the same sequence but were generated using different primer sets, these should be stored as separate entries/lines in the spreadsheet). Information about replicates may be available in the "Top-hit taxon (taxa)" or "Trimmed Ribosomal Sequence" fields if there are multiple values for the same "Strain ID#" in the Alberta Microbiota Repository (AMBR) Master file.	Biological replicate			1.0.0	1.0.0	1.0.0	
Sample collection and processing	specimen processing details	GENEPIO:0100311	Detailed information regarding the processing applied to a sample during or after receiving the sample.	Provide a free text description of any processing details applied to a sample. Information about replicates may be available in the "Top-hit taxon (taxa)" or "Trimmed Ribosomal Sequence" fields if there are multiple values for the same "Strain ID#" in the Alberta Microbiota Repository (AMBR) Master file.	Multiple amplicons generated for isolate SA32 using different primer sets			1.0.0	1.0.0	1.0.0	