Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
	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.
Database Identifiers		GENEPIO:0001122					
Database Identifiers	**specimen collector sample ID**	GENEPIO:0001123	The user-defined name for the sample.	Every 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, and as informative as possible.	prov_rona_99		
Database Identifiers	**third party lab service provider name**	GENEPIO:0001202	The name of the third party company or laboratory that provided services.	Provide the full, unabbreviated name of the company or laboratory.	Switch Health		
Database Identifiers	**third party lab sample ID**	GENEPIO:0001149	The identifier assigned to a sample by a third party service provider.	Store the sample identifier supplied by the third party services provider.	SHK123456		
Database Identifiers	**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		
Database Identifiers	**Related specimen primary ID**	GENEPIO:0001128	The primary ID of a related specimen previously submitted to the repository.	Store the primary ID of the related specimen previously submitted to the National Microbiology Laboratory so that the samples can be linked and tracked through the system.	SR20-12345		
Database Identifiers	**IRIDA sample name**	GENEPIO:0001131	The identifier assigned to a sequenced isolate in IRIDA.	Store the IRIDA sample name. The IRIDA sample name will be created by the individual entering data into the IRIDA platform. IRIDA samples may be linked to metadata and sequence data, or just metadata alone. It is recommended that the IRIDA sample name be the same as, or contain, the specimen collector sample ID for better traceability. It is also recommended that the IRIDA sample name mirror the GISAID accession. IRIDA sample names cannot contain slashes. Slashes should be replaced by underscores. See IRIDA documentation for more information regarding special characters (https://irida.corefacility.ca/documentation/user/user/samples/#adding-a-new-sample).	prov_rona_99		
Database Identifiers	**umbrella bioproject accession**	GENEPIO:0001133	The INSDC umbrella accession number of the BioProject to which the BioSample belongs.	Required if submission is linked to an umbrella BioProject. An umbrella BioProject links together related BioProjects. A valid BioProject umbrella accession has prefix PRJN, PRJE or PRJD. Your laboratory can have one or many BioProjects.	PRJNA623807		
Database Identifiers	**bioproject accession**	GENEPIO:0001136	The INSDC accession number of the BioProject(s) to which the BioSample belongs.	Required if submission is linked to a BioProject. BioProjects are an organizing tool that links together raw sequence data, assemblies, and their associated metadata. A valid BioProject accession has prefix PRJN, PRJE or PRJD, e.g., PRJNA12345 and is created once at the beginning of a new sequencing project. Your laboratory can have one or many BioProjects.	PRJNA12345		
Database Identifiers	**biosample accession**	GENEPIO:0001139	The identifier assigned to a BioSample in INSDC archives.	Store the accession returned from the BioSample submission. NCBI BioSamples will have the prefix SAMN, while ENA BioSamples will have the prefix SAMEA.	SAMN14180202		
Database Identifiers	**SRA accession**	GENEPIO:0001142	The Sequence Read Archive (SRA), European Nucleotide Archive (ENA) or DDBJ Sequence Read Archive (DRA) identifier linking raw read data, methodological metadata and quality control metrics submitted to the INSDC.	Store the accession assigned to the submitted "run". NCBI-SRA accessions start with SRR, EBI-ENA runs start with ERR and DRA accessions start with DRR.	SRR11177792		
Database Identifiers	**GenBank accession**	GENEPIO:0001145	The GenBank/ENA/DDBJ identifier assigned to the sequence in the INSDC archives.	Store the accession returned from a GenBank/ENA/DDBJ submission (viral genome assembly).	MN908947.3		
Database Identifiers	**GISAID accession**	GENEPIO:0001147	The GISAID accession number assigned to the sequence.	Store the accession returned from the GISAID submission.	EPI_ISL_123456		
Sample collection and processing		GENEPIO:0001268					
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		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
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 laboratory.	johnnyblogs@lab.ca		
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, State/Province/Region, Country, Postal Code/Zip Code	655 Lab St, Vancouver, British Columbia, V5N 2A2, Canada		
Sample collection and processing	sequence submitted by	GENEPIO:0001159	The name of the agency that generated the sequence.	The name of the agency should be written out in full, (with minor exceptions) and be consistent across multiple submissions.	Centers for Disease Control and Prevention		
Sample collection and processing	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		
Sample collection and processing	sequence submitter contact address	GENEPIO:0001167	The mailing address of the agency submitting the sequence.	The mailing address should be in the format: Street number and name, City, State/Province/Region, Country, Postal Code/Zip Code	123 Sunnybrooke St, Toronto, Ontario, M4P 1L6, Canada		
Sample collection and processing	sample collection date	GENEPIO:0001174	The date on which the sample was collected.	Record the collection date accurately in the template. Required granularity includes year, month and day. Before sharing this data, ensure this date is not considered identifiable information. If this date is considered identifiable, it is acceptable to add "jitter" to the collection date by adding or subtracting calendar days. Do not change the collection date in your original records. Alternatively, "received date" may be used as a substitute in the data you share. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2020-03-19		
Sample collection and processing	sample collection date precision	GENEPIO:0001177	The precision to which the "sample collection date" was provided.	Provide the precision of granularity to the "day", "month", or "year" for the date provided in the "sample collection date" field. The "sample collection date" will be truncated to the precision specified upon export; "day" for "YYYY-MM-DD", "month" for "YYYY-MM", or "year" for "YYYY".	year		
Sample collection and processing	sample received date	GENEPIO:0001179	The date on which the sample was received.	The date the sample was received by a lab that was not the point of collection. ISO 8601 standard "YYYY-MM-DD".	2020-03-20		
Sample collection and processing	geo_loc name (country)	GENEPIO:0001181	The country of origin of the sample.	Provide the country name from the pick list in the template	South Africa [GAZ:00001094] [1]		
Sample collection and processing	geo_loc name (state/province/territory)	GENEPIO:0001185	The state/province/territory of origin of the sample.	Provide the state/province/territory name from the GAZ geography ontology. Search for geography terms here: https://www.ebi.ac.uk/ols/ontologies/gaz	Western Cape		
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		
Sample collection and processing	organism	GENEPIO:0001191	Taxonomic name of the organism.	Select "Severe acute respiratory syndrome coronavirus 2" if sequencing SARS-CoV-2. If another Coronaviridae is being sequenced, provide the taxonomic name from NCBITaxon. Search for taxonomy terms at https://www.ebi.ac.uk/ols/ontologies/ncbitaxon.	Severe acute respiratory syndrome coronavirus 2 [NCBITaxon:2697049] [2]		
Sample collection and processing	isolate	GENEPIO:0001644	Identifier of the specific isolate.	This identifier should be an unique, indexed, alpha-numeric ID within your laboratory. If submitted to the INSDC, the "isolate" name is propagated throughtout different databases. As such, structure the "isolate" name to be ICTV/INSDC compliant in the following format: "SARS-CoV-2/host/country/sampleID/date".	SARS-CoV-2/human/USA/CA-CDPH-001/2020		
Sample collection and processing	purpose of sampling	GENEPIO:0001198	The reason that the sample was collected.	Select a value from the pick list in the template.	Diagnostic testing [GENEPIO:0100002] [3]		
Sample collection and processing	purpose of sampling details	GENEPIO:0001200	Further details pertaining to the reason the sample was collected.	Provide a free text description of the sampling strategy or samples collected.	Screening of bat specimens in museum collections.		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
Sample collection and processing	NML submitted specimen type	GENEPIO:0001204	The type of specimen submitted to the National Microbiology Laboratory (NML) for testing.	This information is required for upload through the CNPHI LaSER system. Select the specimen type from the pick list provided. If sequence data is being submitted rather than a specimen for testing, select "Not Applicable".	swab		
Sample collection and processing	Related specimen relationship type	GENEPIO:0001209	The relationship of the current specimen to the specimen/sample previously submitted to the repository.	Provide the tag that describes how the previous sample is related to the current sample being submitted from the pick list provided, so that the samples can be linked and tracked in the system.	Specimen sampling methods testing [4]		
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 pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/uberon. If not applicable, leave blank.	Blood [UBERON:0000178] [5]		
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 pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/uberon. If not applicable, leave blank.	Nasopharynx (NP) [UBERON:0001728] [6]		
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 pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/uberon. If not applicable, leave blank.	Feces [UBERON:0001988] [7]		
Sample collection and processing	environmental material	GENEPIO:0001223	A substance obtained from the natural or man-made environment e.g. soil, water, sewage, door handle, bed handrail, face mask.	Provide a descriptor if an environmental material was sampled. Use the pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/envo. If not applicable, leave blank.	Face mask [OBI:0002787] [8]		
Sample collection and processing	environmental site	GENEPIO:0001232	An environmental location may describe a site in the natural or built environment e.g. hospital, wet market, bat cave.	Provide a descriptor if an environmental site was sampled. Use the pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/envo. If not applicable, leave blank.	Hospital [ENVO:00002173] [9]		
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 collection device was used for sampling. Use the pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/obi. If not applicable, leave blank.	Swab [GENEPIO:0100027] [10]		
Sample collection and processing	collection method	GENEPIO:0001241	The process used to collect the sample e.g. phlebotomy, necropsy.	Provide a descriptor if a collection method was used for sampling. Use the pick list provided in the template. If a desired term is missing from the pick list, use this look-up service to identify a standardized term: https://www.ebi.ac.uk/ols/ontologies/obi. If not applicable, leave blank.	Bronchoalveolar lavage (BAL) [GENEPIO:0100032] [11]		
Sample collection and processing	collection protocol	GENEPIO:0001243	The name and version of a particular protocol used for sampling.	Provide the name and version of the protocol used to collect the samples.	SC2SamplingProtocol 1.2		
Sample collection and processing	specimen processing	GENEPIO:0001253	Any processing applied to the sample during or after receiving the sample.	Critical for interpreting data. Select all the applicable processes from the pick list. If virus was passaged, include information in "lab host", "passage number", and "passage method" fields. If none of the processes in the pick list apply, put "not applicable".	Virus passage [GENEPIO:0100039] [12]		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
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.	25 swabs were pooled and further prepared as a single sample during library prep.		
Sample collection and processing	**lab host**	GENEPIO:0001255	Name and description of the laboratory host used to propagate the source organism or material from which the sample was obtained.	Type of cell line used for propagation. Select a value form the pick list. If not passaged, put "not applicable".	Vero E6 cell line [BTO:0004755] [13]		
Sample collection and processing	**passage number**	GENEPIO:0001261	Number of passages.	Provide number of known passages. If not passaged, put "not applicable"	3		
Sample collection and processing	**passage method**	GENEPIO:0001264	Description of how organism was passaged.	Free text. Provide a short description. If not passaged, put "not applicable".	AVL buffer+30%EtOH lysate received from Respiratory Lab. P3 passage in Vero-1 via bioreactor large-scale batch passage. P3 batch derived from the SP-2/reference lab strain.		
Sample collection and processing	**biomaterial extracted**	GENEPIO:0001266	The biomaterial extracted from samples for the purpose of sequencing.	Provide the biomaterial extracted from the pick list in the template.	RNA (Total) [OBI:0000895] [14]		
Host information		GENEPIO:0001268					
Host information	**host (common name)**	GENEPIO:0001386	The commonly used name of the host.	Common name or scientific name are required if there was a host. Common name examples e.g. human, bat. Select a value from the pick list. If the sample was environmental, put "not applicable".	Human [NCBITaxon:9606] [15]		
Host information	**host (scientific name)**	GENEPIO:0001387	The taxonomic, or scientific name of the host.	Common name or scientific name are required if there was a host. Scientific name examples e.g. Homo sapiens. Select a value from the pick list. If the sample was environmental, put "not applicable".	Homo sapiens [NCBITaxon:9606] [16]		
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] [17]		
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] [18]		
Host information	**host health outcome**	GENEPIO:0001390	Disease outcome in the host.	If known, select a value from the pick list.	Recovered [NCIT:C49498] [19]		
Host information	**host disease**	GENEPIO:0001391	The name of the disease experienced by the host.	This field is only required if there was a host. If the host was a human select COVID-19 from the pick list. If the host was asymptomatic, this can be recorded under "host health state details". "COVID-19" should still be provided if patient is asymptomatic. If the host is not human, and the disease state is not known or the host appears healthy, put "not applicable".	COVID-19 [MONDO:0100096] [20]		
Host information	**host age**	GENEPIO:0001392	Age of host at the time of sampling.	If known, provide age. Age-binning is also acceptable.	79		
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] [21]		
Host information	**host age bin**	GENEPIO:0001394	The age category of the host at the time of sampling.	Age bins in 10 year intervals have been provided. If a host's age cannot be specified due to provacy concerns, an age bin can be used as an alternative.	50 - 59 [GENEPIO:0100054] [22]		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
Host information	host gender	GENEPIO:0001395	The gender of the host at the time of sample collection.	If known, select a value from the pick list.	Male [NCIT:C46109] [23]		
Host information	host residence geo_loc name (country)	GENEPIO:0001396	The country where the host resides.	If known, select a value from the pick list.	South Africa [GAZ:0000109 4] [24]		
Host information	host residence geo_loc name (state/province/territory)	GENEPIO:0001397	The state/province/territory of residence of the host.	Select the province/territory name from pick list provided in the template.	Quebec		
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		
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		
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]		
Host information	pre-existing conditions and risk factors	GENEPIO:0001401	Patient pre-existing conditions and risk factors.	Select all of the pre-existing conditions and risk factors experienced by the host from the pick list.	Asthma		
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:0001 208] [26]		
Host vaccination information		GENEPIO:0001403					
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:010 0100] [27]		
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		
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-BioNTec h (Comirnaty)		
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		
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-BioNTec h (Comirnaty)		
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		
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-BioNTec h (Comirnaty)		
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		
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-BioNTec h (Comirnaty)		
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		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
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		
Host exposure information		GENEPIO:0001409					
Host exposure information	**location of exposure geo_loc name (country)**	GENEPIO:0001410	The country where the host was likely exposed to the causative agent of the illness.	This location pertains to the country the host was believed to be exposed, and may not be the same as the host's country of residence. If known, provide the country name from the pick list.	South Africa [GAZ:0000109 4] [28]		
Host exposure information	**destination of most recent travel (city)**	GENEPIO:0001411	The name of the city that was the destination of most recent travel.	Provide the name of the city that the host travelled to. Use this look-up service to identify the standardized term: https://www.ebi.ac.uk/ols/ontologies/gaz	New York City		
Host exposure information	**destination of most recent travel (state/province/territory)**	GENEPIO:0001412	The name of the province that was the destination of most recent travel.	Provide the name of the state/province/territory that the host travelled to. Use this look-up service to identify the standardized term: https://www.ebi.ac.uk/ols/ontologies/gaz	California		
Host exposure information	**destination of most recent travel (country)**	GENEPIO:0001413	The name of the country that was the destination of most recent travel.	Provide the name of the country that the host travelled to. Use this look-up service to identify the standardized term: https://www.ebi.ac.uk/ols/ontologies/gaz	United Kingdom [GAZ:0000263 7] [29]		
Host exposure information	**most recent travel departure date**	GENEPIO:0001414	The date of a person's most recent departure from their primary residence (at that time) on a journey to one or more other locations.	Provide the travel departure date in ISO 8601 standard format "YYYY-MM-DD".	2020-03-16		
Host exposure information	**most recent travel return date**	GENEPIO:0001415	The date of a person's most recent return to some residence from a journey originating at that residence.	Provide the travel return date in ISO 8601 standard format "YYYY-MM-DD".	2020-04-26		
Host exposure information	**travel point of entry type**	GENEPIO:0100413	The type of entry point a traveler arrives through.	Select the point of entry type.	Air		
Host exposure information	**border testing test day type**	GENEPIO:0100414	The day a traveller was tested on or after arrival at their point of entry.	Select the test day.	day 1		
Host exposure information	**travel history**	GENEPIO:0001416	Travel history in last six months.	Specify the countries (and more granular locations if known) travelled in the last six months; can include multiple travels. Separate multiple travel events with a semicolon. Provide as free text.	Canada, Vancouver; USA, Seattle; Italy, Milan		
Host exposure information	**exposure event**	GENEPIO:0001417	Event leading to exposure.	If known, select the exposure event from the pick list.	Mass Gathering [GENEPIO:010 0237] [30]		
Host exposure information	**exposure contact level**	GENEPIO:0001418	The exposure transmission contact type.	Select direct or indirect exposure from the pick list.	Direct (human-to-hum an contact) [TRANS:00000 01] [31]		
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.	Patient [OMRSE:00000 030] [32]		
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 [GENEPIO:010 0201] [33]		
Host exposure information	**exposure details**	GENEPIO:0001431	Additional host exposure information.	Free text description of the exposure.	Host role - Other: Bus Driver		
Host reinfection information		GENEPIO:0001434					
Host reinfection information	**prior SARS-CoV-2 infection**	GENEPIO:0001435	Whether there was prior SARS-CoV-2 infection.	If known, provide infromation about whether the individual had a previous SARS-CoV-2 infection. Select a value from the pick list.	Prior infection [GENEPIO:010 0234] [34]		
Host reinfection information	**prior SARS-CoV-2 infection isolate**	GENEPIO:0001436	The identifier of the isolate found in the prior SARS-CoV-2 infection.	Provide the isolate name of the most recent prior infection. Structure the "isolate" name to be ICTV/INSDC compliant in the following format: "SARS-CoV-2/host/country/sampleID/date".	SARS-CoV-2/h uman/USA/CA-CDPH-001/202 0		
Host reinfection information	**prior SARS-CoV-2 infection date**	GENEPIO:0001437	The date of diagnosis of the prior SARS-CoV-2 infection.	Provide the date that the most recent prior infection was diagnosed. Provide the prior SARS-CoV-2 infection date in ISO 8601 standard format "YYYY-MM-DD".	2021-01-23		
Host reinfection information	**prior SARS-CoV-2 antiviral treatment**	GENEPIO:0001438	Whether there was prior SARS-CoV-2 treatment with an antiviral agent.	If known, provide infromation about whether the individual had a previous SARS-CoV-2 antiviral treatment. Select a value from the pick list.	Prior antiviral treatment [GENEPIO:010 0037] [35]		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
Host reinfection information	**prior SARS-CoV-2 antiviral treatment agent**	GENEPIO:0001439	The name of the antiviral treatment agent administered during the prior SARS-CoV-2 infection.	Provide the name of the antiviral treatment agent administered during the most recent prior infection. If no treatment was administered, put "No treatment". If multiple antiviral agents were administered, list them all separated by commas.	Remdesivir		
Host reinfection information	**prior SARS-CoV-2 antiviral treatment date**	GENEPIO:0001440	The date treatment was first administered during the prior SARS-CoV-2 infection.	Provide the date that the antiviral treatment agent was first administered during the most recenrt prior infection. Provide the prior SARS-CoV-2 treatment date in ISO 8601 standard format "YYYY-MM-DD".	2021-01-28		
Sequencing		GENEPIO:0001441					
Sequencing	**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.	Baseline surveillance (random sampling) [GENEPIO:010 0005] [36]		
Sequencing	**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 pick list. The description may include the importance of the sequences for a particular public health investigation/surveillance activity/research question. Suggested standardized descriptions include: Screened for S gene target failure (S dropout), Screened for mink variants, Screened for B.1.1.7 variant, Screened for B.1.135 variant, Screened for P.1 variant, Screened due to travel history, Screened due to close contact with infected individual, Assessing public health control measures, Determining early introductions and spread, Investigating airline-related exposures, Investigating temporary foreign worker, Investigating remote regions, Investigating health care workers, Investigating schools/universities, Investigating reinfection.	Screened for S gene target failure (S dropout)		
Sequencing	**sequencing date**	GENEPIO:0001447	The date the sample was sequenced.	Provide the sequencing date in ISO 8601 standard format "YYYY-MM-DD".	2021-04-26		
Sequencing	**library ID**	GENEPIO:0001448	The user-specified identifier for the library prepared for sequencing.	The library name should be unique, and can be an autogenerated ID from your LIMS, or modification of the isolate ID.	XYZ_123345		
Sequencing	**amplicon size**	GENEPIO:0001449	The length of the amplicon generated by PCR amplification.	Provide the amplicon size, including the units.	300bp		
Sequencing	**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		
Sequencing	**flow cell barcode**	GENEPIO:0001451	The barcode of the flow cell used for sequencing.	Provide the barcode of the flow cell used for sequencing the sample.	FAB06069		
Sequencing	**sequencing instrument**	GENEPIO:0001452	The model of the sequencing instrument used.	Select the sequencing instrument from the pick list.	Oxford Nanopore MinION [GENEPIO:010 0142] [37]		
Sequencing	**sequencing protocol name**	GENEPIO:0001453	The name and version number of the sequencing protocol used.	Provide the name and version of the sequencing protocol.	1D_DNA_MinI ON, ARTIC Network Protocol V3		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
Sequencing	**sequencing protocol**	GENEPIO:0001454	The protocol used to generate the sequence.	Provide a free text description of the methods and materials used to generate the sequence. Suggested text, fill in information where indicated.: "Viral sequencing was performed following a tiling amplicon strategy using the <fill in> primer scheme. Sequencing was performed using a <fill in> sequencing instrument. Libraries were prepared using <fill in> library kit. "	Genomes were generated through amplicon sequencing of 1200 bp amplicons with Freed schema primers. Libraries were created using Illumina DNA Prep kits, and sequence data was produced using Miseq Micro v2 (500 cycles) sequencing kits.		
Sequencing	**sequencing kit number**	GENEPIO:0001455	The manufacturer's kit number.	Alphanumeric value.	AB456XYZ789		
Sequencing	**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.	https://github.com/joshquick/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019.tsv		
Bioinformatics and QC metrics		GENEPIO:0001457					
Bioinformatics and QC metrics	**raw sequence data processing method**	GENEPIO:0001458	The method used for raw data processing such as removing barcodes, adapter trimming, filtering etc.	Provide the name and version numbers of the software used to process the raw data.	Porechop 0.2.3		
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 1.2.3		
Bioinformatics and QC metrics	**consensus sequence name**	GENEPIO:0001460	The name of the consensus sequence.	Provide the name and version number of the consensus sequence.	ncov123assembly3		
Bioinformatics and QC metrics	**consensus sequence filename**	GENEPIO:0001461	The name of the consensus sequence file.	Provide the name and version number of the consensus sequence FASTA file.	ncov123assembly.fasta		
Bioinformatics and QC metrics	**consensus sequence filepath**	GENEPIO:0001462	The filepath of the consensus sequence file.	Provide the filepath of the consensus sequence FASTA file.	/User/Documents/RespLab/Data/ncov123assembly.fasta		
Bioinformatics and QC metrics	**consensus sequence software name**	GENEPIO:0001463	The name of software used to generate the consensus sequence.	Provide the name of the software used to generate the consensus sequence.	Ivar		
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		
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%		
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.	400x		
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.	100x		
Bioinformatics and QC metrics	**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		
Bioinformatics and QC metrics	**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		
Bioinformatics and QC metrics	**r1 fastq filepath**	GENEPIO:0001478	The filepath of the r1 FASTQ file.	Provide the filepath of the r1 FASTQ file.	/User/Documents/RespLab/Data/ABC123_S1_L001_R1_001.fastq.gz		
Bioinformatics and QC metrics	**r2 fastq filepath**	GENEPIO:0001479	The filepath of the r2 FASTQ file.	Provide the filepath of the r2 FASTQ file.	/User/Documents/RespLab/Data/ABC123_S1_L001_R2_001.fastq.gz		
Bioinformatics and QC metrics	**fast5 filename**	GENEPIO:0001480	The user-specified filename of the FAST5 file.	Provide the FAST5 filename.	batch1a_sequences.fast5		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
Bioinformatics and QC metrics	**fast5 filepath**	GENEPIO:0001481	The filepath of the FAST5 file.	Provide the filepath of the FAST5 file.	/User/Documents/RespLab/Data/batch1a_sequences.fast5		
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		
Bioinformatics and QC metrics	**consensus genome length**	GENEPIO:0001483	Size of the assembled genome described as the number of base pairs.	Provide a numerical value (no need to include units).	38677		
Bioinformatics and QC metrics	**Ns per 100 kbp**	GENEPIO:0001484	The number of N symbols present in the consensus fasta sequence, per 100kbp of sequence.	Provide a numerical value (no need to include units).	300		
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		
Bioinformatics and QC metrics	**bioinformatics protocol**	GENEPIO:0001489	The name and version number of the bioinformatics protocol used.	Further details regarding the methods used to process raw data, and/or generate assemblies, and/or generate consensus sequences can be provided in an SOP or protocol. Provide the name and version number of the protocol, or a link if deposited in a protocol repository.	https://www.protocols.io/groups/cphln-sarscov2-sequencing-consortium/members		
Lineage and Variant information		GENEPIO:0001498					
Lineage and Variant information	**lineage/clade name**	GENEPIO:0001500	The name of the lineage or clade.	Provide the Pangolin or Nextstrain lineage/clade name.	B.1.1.7		
Lineage and Variant information	**lineage/clade analysis software name**	GENEPIO:0001501	The name of the software used to determine the lineage/clade.	Provide the name of the software used to determine the lineage/clade.	Pangolin		
Lineage and Variant information	**lineage/clade analysis software version**	GENEPIO:0001502	The version of the software used to determine the lineage/clade.	Provide the version of the software used ot determine the lineage/clade.	2.1.10		
Lineage and Variant information	**variant designation**	GENEPIO:0001503	The variant classification of the lineage/clade i.e. variant, variant of concern.	If the lineage/clade is considered a Variant of Concern, select Variant of Concern from the pick list. If the lineage/clade contains mutations of concern (mutations that increase transmission, clincal severity, or other epidemiological fa ctors) but it not a global Variant of Concern, select Variant. If the lineage/clade does not contain mutations of concern, leave blank.	Variant of Concern (VOC) [GENEPIO:0100083] [38]		
Lineage and Variant information	**variant evidence**	GENEPIO:0001504	The evidence used to make the variant determination.	Select whether the sample was screened using RT-qPCR or by sequencing from the pick list.	RT-qPCR		
Lineage and Variant information	**variant evidence details**	GENEPIO:0001505	Details about the evidence used to make the variant determination.	Provide the assay and list the set of lineage-defining mutations used to make the variant determination. If there are mutations of interest/concern observed in addition to lineage-defining mutations, describe those here.	Lineage-defining mutations: ORF1ab (K1655N), Spike (K417N, E484K, N501Y, D614G, A701V), N (T205I), E (P71L).		
Pathogen diagnostic testing		GENEPIO:0001506					
Pathogen diagnostic testing	**gene name 1**	GENEPIO:0001507	The name of the gene used in the diagnostic RT-PCR test.	Select a gene from the pick list. If the gene of interest is not in the list, provide the full name of the gene or the gene symbol (short form of gene name). Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1LbI	E gene (orf4) [GENEPIO:0100151] [39]		
Pathogen diagnostic testing	**diagnostic pcr protocol 1**	GENEPIO:0001508	The name and version number of the protocol used for diagnostic marker amplification.	The name and version number of the protocol used for carrying out a diagnostic PCR test. This information can be compared to sequence data for evaluation of performance and quality control.	PCREGene 2.0		
Pathogen diagnostic testing	**diagnostic pcr Ct value 1**	GENEPIO:0001509	The cycle threshold (Ct) value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the cycle threshold (Ct) value of the sample from the diagnostic RT-PCR test.	21		
Pathogen diagnostic testing	**gene name 2**	GENEPIO:0001510	The name of the gene used in the diagnostic RT-PCR test.	Select a gene from the pick list. If the gene of interest is not in the list, provide the full name of the gene or the gene symbol (short form of gene name). Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1LbI	RdRp gene (nsp12) [GENEPIO:0100168] [40]		
Pathogen diagnostic testing	**diagnostic pcr protocol 2**	GENEPIO:0001511	The name and version number of the protocol used for diagnostic marker amplification.	The name and version number of the protocol used for carrying out a second diagnostic PCR test. This information can be compared to sequence data for evaluation of performance and quality control.	PCRRdRpGene 3.0		

Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID
Pathogen diagnostic testing	**diagnostic pcr Ct value 2**	GENEPIO:0001512	The cycle threshold (Ct) value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the cycle threshold (Ct) value of the sample from the second diagnostic RT-PCR test.	36		
Pathogen diagnostic testing	**gene name 3**	GENEPIO:0001513	The name of the gene used in the diagnostic RT-PCR test.	Provide the full name of another gene used in an RT-PCR test. The gene symbol (short form of gene name) can also be provided. Standardized gene names and symbols can be found in the Gene Ontology using this look-up service: https://bit.ly/2Sq1Lbl	RdRp gene (nsp12)		
Pathogen diagnostic testing	**diagnostic pcr protocol 3**	GENEPIO:0001514	The name and version number of the protocol used for diagnostic marker amplification.	The name and version number of the protocol used for carrying out a second diagnostic PCR test. This information can be compared to sequence data for evaluation of performance and quality control.	RdRpGenePCRTest 3		
Pathogen diagnostic testing	**diagnostic pcr Ct value 3**	GENEPIO:0001515	The Ct value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the CT value of the sample from the second diagnostic RT-PCR test.	30		
Contributor Acknowledgement		GENEPIO:0001516					
Contributor Acknowledgement	**authors**	GENEPIO:0001517	Names of individuals contributing to the processes of sample collection, sequence generation, analysis, and data submission.	Include the first and last names of all individuals that should be attributed, separated by a comma.	Tejinder Singh, Fei Hu, Johnny Blogs		

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