Parent Class	Field	Ontology Identifier	Definition	Guidance	Examples	Deprecated Label	Deprecated ID	Version Tracking Label	ID	Description/Guidance
Database Identifiers		**GENEPIO:0001122**								
Database Identifiers	specimen collector sample ID	GENEPIO:0001123	The user-defined name for the sample.	Store the collector sample ID. If this number is considered identifiable information, provide an alternative ID. Be sure to store the key that maps between the original and alternative IDs for traceability and follow up if necessary. Every collector sample ID from a single submitter must be unique. It can have any format, but we suggest that you make it concise, unique and consistent within your lab.	prov_mpox_1234			1.0.0	1.0.0	1.0.0
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			1.0.0	1.0.0	1.0.0
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			1.0.0	1.0.0	1.0.0
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			1.0.0	1.0.0	1.0.0
Database identifiers	INSDC sequence read accession	GENEPIO:0101203	The identifier assigned to a sequence in one of the International Nucleotide Sequence Database Collaboration (INSDC) repositories.	Store the accession assigned to the submitted sequence. European Nucleotide Archive (ENA) sequence accessions start with ERR, NCBI-SRA accessions start with SRR, DNA Data Bank of Japan (DDBJ) accessions start with DRR and Genome Sequence Archive (GSA) accessions start with CRR.	SRR123456, ERR123456, DRR123456, CRR123456			3.0.0	1.0.0	1.0.0
Database identifiers	INSDC assembly accession	GENEPIO:0101204	The versioned identifier assigned to an assembly or consensus sequence in one of the International Nucleotide Sequence Database Collaboration (INSDC) repositories.	Store the versioned accession assigned to the submitted sequence e.g. the GenBank accession version.	LZ986655.1			3.0.0	1.0.0	1.0.0
Database Identifiers	GISAID virus name	GENEPIO:0100282	Identifier of the specific isolate.	Provide the GISAID EpiPox virus name, which should be wri	hMpxV/Canada/UN-NML-12345/2022			1.0.0	1.0.0	1.0.0
Database Identifiers	GISAID accession	GENEPIO:0001147	The GISAID accession number assigned to the sequence.	Store the accession returned from the GISAID submission.	EPI_ISL_436489			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 sample collector should be written out in ful	BC Centre for Disease Control			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.	Sample collection date is critical for surveillance and many types of analyses. Required granularity includes year, month and day. If this date is considered identifiable information, it is acceptable to add "jitter" by adding or subtracting a calendar day (acceptable by GISAID). Alternatively, "received date" may be used as a substitute. 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.	ISO 8601 standard "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 pro	United States of America [GAZ:00002459]			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 where the sample was collected.	Provide the state/province/territory name from the controlled	Saskatchewan			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 coll	Provide latitude coordinates if available. Do not use the cent	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 co	Provide longitude coordinates if available. Do not use the ce	77.11 W			1.0.0	1.0.0	1.0.0
Sample collection and processing	organism	GENEPIO:0001191	Taxonomic name of the organism.	Use "Mpox virus". This value is provided in the template. No	Mpox virus [NCBITaxon:10244]			1.0.0	1.0.0	1.0.0
Sample collection and processing	isolate	GENEPIO:0001644	Identifier of the specific isolate.	This identifier should be an unique, indexed, alpha-numeric	MpxV/human/USA/CA-CDPH-001/2020			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.	As all samples are taken for diagnostic purposes, "Diagnosti	Diagnostic testing [GENEPIO:0100002]			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 public health investigation/surveillance activity/research question. If details are not available, provide a null value.	Symptomology and history suggested Monkeypox diagnosis.			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.	Provide a descriptor if an anatomical material was sampled.	Lesion (Pustule) [NCIT:C78582]			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	Genital area [BTO:0003358]			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,	Provide a descriptor if a body product was sampled. Use the	Pus [UBERON:0000177]			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	Provide a descriptor if an environmental material was sample	Bed linen			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 t	Swab [GENEPIO:0100027]			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 sam	Biopsy [OBI:0002650]			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 s	Critical for interpreting data. Select all the applicable proces	Specimens pooled [OBI:0600016]			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.	5 swabs from different body sites were pooled and further prepared as a single sample during library prep.			1.0.0	1.0.0	1.0.0

Category	Field name	GENEPIO ID	Description	Guidance	Example			v1	v2	v3
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 [GENEPIO:0101018]			3.0.0	3.0.0	3.0.0
Sample collection and processing	experimental control details	GENEPIO:0100922	The details regarding the experimental control contained in the sam	Provide details regarding the nature of the reference strain u	Human coronavirus 229E (HCoV-229E) spiked in sample as process control			3.0.0	3.0.0	3.0.0
Host Information		**GENEPIO:0001268**						**1.0.0**	**1.0.0**	**1.0.0**
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. Both can be provided, if known. Use terms from the pick lists in the template. Common name e.g. human.	Human			1.0.0	1.0.0	1.0.0
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. Both can be provided, if known. Use terms from the pick lists in the template. Scientific name e.g. Homo sapiens, If the sample was environmental, put "not applicable	Homo sapiens [NCBITaxon:9606]			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 descriptor from the pick list provided in the template.	Hospitalized [NCIT:C25179]			1.0.0	1.0.0	1.0.0
Host Information	host health outcome	GENEPIO:0001389	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 disease	GENEPIO:0001391	The name of the disease experienced by the host.	Select "Mpox" from the pick list provided in the template. Not	Mpox [MONDO:0002594]			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.	This identifier can be used to link samples from the same individual. Caution: consult the data steward before sharing as this value may be considered identifiable information.	12345B-222			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	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]			1.0.0	1.0.0	1.0.0
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]			1.0.0	1.0.0	1.0.0
Host Information	host residence geo_loc name (country)	GENEPIO:0001396	The country of residence of the host.	Select the country name from pick list provided in the template.	Canada [GAZ:00002560]			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".	2022-05-25			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.	Lesion (Pustule) [NCIT:C78582], Swollen Lymph Nodes [HP:0002716], Myalgia (muscle pain) [HP:0003326]			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.				1.0.0	1.0.0	1.0.0
Host Information	complications	GENEPIO:0001402	Patient medical complications that are believed to have occurred as a result of host disease.	Select all of the complications experienced by the host from the pick list. If the desired term is missing, contact the curation team.	Delayed wound healing (lesion healing) [MP:0002908]			1.0.0	1.0.0	1.0.0
Host Information	antiviral therapy	GENEPIO:0100580	Treatment of viral infections with agents that prevent viral replicatio	Provide details of all current antiviral treatment during the cu	Tecovirimat used to treat current Monkeypox infection; AZT administered for concurrent HIV infe	1.0.0		1.0.0	1.0.0	
Host vaccination information		**GENEPIO:0001403**						**1.0.0**	**1.0.0**	**1.0.0**
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.	Not Vaccinated [GENEPIO:0100102]			1.0.0	1.0.0	1.0.0
Host vaccination information	number of vaccine doses received	GENEPIO:0001406	The number of doses of the vaccine recived by the host.	Record how many doses of the vaccine the host has received.	1			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 1 vaccine name	GENEPIO:0100313	The name of the vaccine administered as the first dose of a vaccine regimen.	Provide the name and the corresponding manufacturer of the Smallpox vaccine administered as the first dose.	IMVAMUNE (Bavarian Nordic)			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination dose 1 vaccination date	GENEPIO:0100314	The date the first dose of a vaccine was administered.	Provide the date the first dose of Smallpox vaccine was administered. The date should be provided in ISO 8601 standard format "YYYY-MM-DD".	2022-06-01			1.0.0	1.0.0	1.0.0
Host vaccination information	vaccination history	GENEPIO:0100321	A description of the vaccines received and the administration dates of a series of vaccinations against a specific disease or a set of diseases.	Free text description of the dates and vaccines administered against a particular disease/set of diseases. It is also acceptable to concatenate the individual dose information (vaccine name, vaccination date) separated by semicolons.	IMVAMUNE (Bavarian Nordic); 2022-06-01			1.0.0	1.0.0	1.0.0
								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	location of exposure geo_loc name (country)	GENEPIO:0001410	The country where the host was likely exposed to the causative agent of the illness.	Select the country name from the pick list provided in the template.	Canada			1.0.0	1.0.0	1.0.0
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.	Select the country name from the pick list provided in the template.	Canada [GAZ:00002560]			1.0.0	1.0.0	1.0.0
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			1.0.0	1.0.0	1.0.0
Host exposure information	destination of most recent travel (state/province/territory)	GENEPIO:0001412	The name of the state/province/territory that was the destination of most recent travel.	Select the province name from the pick list provided in the template.				1.0.0	1.0.0	1.0.0
Host exposure information	destination of most recent travel (state/province/territory)	GENEPIO:0001412	The name of the state/province/territory 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			1.0.0	1.0.0	1.0.0
Host exposure information	destination of most recent travel (country)	GENEPIO:0001413	The name of the country that was the destination of most recent travel.	Select the country name from the pick list provided in the template.	Canada			1.0.0	1.0.0	1.0.0
Host exposure information	destination of most recent travel (country)	GENEPIO:0001413	The name of the country that was the destination of most recent travel.	Select the country name from the pick list provided in the template.	United Kingdom [GAZ:00002637]			1.0.0	1.0.0	1.0.0

Category	Field	ID	Description	Guidance	Example		v1	v2	v3
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.	2020-03-16		1.0.0	1.0.0	1.0.0
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.	2020-04-26		1.0.0	1.0.0	1.0.0
Host exposure information	travel history	GENEPIO:0001416	Travel history in last six months.	Specify the countries (and more granular locations if known, separated by a comma) travelled in the last six months; can include multiple travels. Separate multiple travel events with a semi-colon. List most recent travel first.	Canada, Vancouver; USA, Seattle; Italy, Milan		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 DataHarmonizer curation team.	Party		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 DataHarmonizer curation team.	Party [PCO:0000035]		1.0.0	1.0.0	1.0.0
Host exposure information	exposure contact level	GENEPIO:0001418	The exposure transmission contact type.	Select exposure contact level from the pick-list.	Contact with infected individual		1.0.0	1.0.0	1.0.0
Host exposure information	exposure contact level	GENEPIO:0001418	The exposure transmission contact type.	Select exposure contact level from the pick-list.	Contact with infected individual [GENEPIO:0100357]		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 DataHarmonizer curation team.	Acquaintance of case		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 DataHarmonizer curation team.	Acquaintance of case [GENEPIO:0100266]		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 DataHarmonizer curation team.	Healthcare Setting		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 DataHarmonizer curation team.	Healthcare Setting [GENEPIO:0100201]		1.0.0	1.0.0	1.0.0
Host exposure information	exposure details	GENEPIO:0001431	Additional host exposure information.	Free text description of the exposure.	Large party, many contacts		1.0.0	1.0.0	1.0.0
Host reinfection information		**GENEPIO:0001434**					**1.0.0**	**1.0.0**	**1.0.0**
Host reinfection information	prior Mpox infection	GENEPIO:0100532	The absence or presence of a prior Mpox infection.	If known, provide information about whether the individual had a previous Mpox infection. Select a value from the pick list.	Prior infection		1.0.0	1.0.0	1.0.0
Host reinfection information	prior Mpox infection	GENEPIO:0100532	The absence or presence of a prior Mpox infection.	If known, provide information about whether the individual had a previous Mpox infection. Select a value from the pick list.	Prior infection [GENEPIO:0100037]		1.0.0	1.0.0	1.0.0
Host reinfection information	prior Mpox infection date	GENEPIO:0100533	The date of diagnosis of the prior Mpox infection.	Provide the date that the most recent prior infection was diagnosed. Provide the prior Mpox infection date in ISO 8601 standard format "YYYY-MM-DD".	2022-06-20		1.0.0	1.0.0	1.0.0
Host reinfection information	prior Mpox antiviral treatment	GENEPIO:0100534	The absence or presence of antiviral treatment for a prior Mpox infection.	If known, provide information about whether the individual had a previous Mpox antiviral treatment. Select a value from the pick list.	Prior antiviral treatment		1.0.0	1.0.0	1.0.0
Host reinfection information	prior Mpox antiviral treatment	GENEPIO:0100534	The absence or presence of antiviral treatment for a prior Mpox infection.	If known, provide information about whether the individual had a previous Mpox antiviral treatment. Select a value from the pick list.	Prior antiviral treatment [GENEPIO:0100037]		1.0.0	1.0.0	1.0.0
Host reinfection information	prior antiviral treatment during prior Mpox infection	GENEPIO:0100535	Antiviral treatment for any infection during the prior Mpox infection period.	Provide a description of any antiviral treatment administered for viral infections (not including Mpox treatment) during the prior Mpox infection period. This field is meant to capture concurrent treatment information.	AZT was administered for HIV infection during the prior Mpox infection.		1.0.0	1.0.0	1.0.0
							1.0.0	1.0.0	1.0.0
							1.0.0	1.0.0	1.0.0
Sequencing		**GENEPIO:0001441**					**1.0.0**	**1.0.0**	**1.0.0**
Sequence information	sequencing project name	GENEPIO:0100472	The name of the project/initiative/program for which sequencing was performed.	Provide the name of the project and/or the project ID here. If the information is unknown or cannot be provided, leave blank or provide a null value.	MPOX-1356		1.0.0	1.0.0	1.0.0
Sequencing	==sequenced by==	GENEPIO:0100416	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. If 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
Sequencing	==sequenced by==	GENEPIO:0100416	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.	Public Health Ontario (PHO)		1.0.0	1.0.0	1.0.0
Sequence information	sequenced by laboratory name	GENEPIO:0100470	The specific laboratory affiliation of the responsible for sequencing the isolate's genome.	Provide the name of the specific laboratory that that performed the sequencing in full (avoid abbreviations). If the information is unknown or cannot be provided, leave blank or provide a null value.	Topp Lab		1.0.0	1.0.0	1.0.0
Sequence information	==sequenced by contact name==	GENEPIO:0100471	The name or title of the contact responsible for follow-up regarding the sequence.	Provide the name of an individual or their job title. As personnel turnover may render the contact's name obsolete, it is more prefereable to provide a job title for ensuring accuracy of information and institutional memory. If the information is unknown or cannot be provided, leave blank or provide a null value.	Enterics Lab Manager		1.0.0	1.0.0	1.0.0
Sequencing	sequenced by contact email	GENEPIO:0100422	The email address of the contact responsible for follow-up regarding the sequence.	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
Sequencing	sequenced by contact address	GENEPIO:0100423	The mailing address of the agency submitting the sequence.	The mailing address should be in the format: Street number and name, City, Province/Territory, Postal Code, Country	123 Sunnybrooke St, Toronto, Ontario, M4P 1L6, Canada		1.0.0	1.0.0	1.0.0
Sequencing	==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. If 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

Category	Field name	GENEPIO ID	Description	Guidance	Example	v1	v2	v3
Sequencing	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. If 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
Sequencing	sequence submitter contact email	GENEPIO:0001165	The email address of the agency responsible for submission of the sequence.	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
Sequencing	sequence submitter contact address	GENEPIO:0001167	The mailing address of the agency responsible for submission of the sequence.	The mailing address should be in the format: Street number and name, City, Province/Territory, Postal Code, Country	123 Sunnybrooke St, Toronto, Ontario, M4P 1L6, Canada	1.0.0	1.0.0	1.0.0
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.	Select "Targeted surveillance (non-random sampling)" if the specimen fits any of the following criteria: Specimens attributed to individuals with no known intimate contacts to positive cases;Specimens attributed to youth/minors <18 yrs.;Specimens attributed to vulnerable persons living in transient shelters or congregant settings;Specimens attributed to individuals self-identifying as "female";For specimens with a recent international and/or domestic travel history, please select the most appropriate tag from the following three options: Domestic travel surveillance;International travel surveillance;Travel-associated surveillance;For specimens targeted for sequencing as part of an outbreak investigation, please select: Cluster/Outbreak investigation; In all other cases use: Baseline surveillance (random sampling).	1.0.0	1.0.0	1.0.0
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:0100005]	1.0.0	1.0.0	1.0.0
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 free text. The description may include the importance of the sequences for a particular public health investigation/surveillance activity/research question. Suggested standardized descriotions include: Screened due to travel history, Screened due to close contact with infected individual.	Outbreak in MSM community	1.0.0	1.0.0	1.0.0
Sequencing	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
Sequencing	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
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	1.0.0	1.0.0	1.0.0
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	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	1.0.0	1.0.0	1.0.0
Sequence information	sequencing assay type	GENEPIO:0100997	The overarching sequencing methodology that was used to determine the sequence of a biomaterial.	Example Guidance: Provide the name of the DNA or RNA sequencing technology used in your study. If unsure refer to the protocol documentation, or provide a null value.	whole genome sequencing assay [OBI:0002117]	1.0.0	1.0.0	1.0.0
Sequencing	sequencing instrument	GENEPIO:0001452	The model of the sequencing instrument used.	Select a sequencing instrument from the picklist provided in the template.	Oxford Nanopore MinION	1.0.0	1.0.0	1.0.0
Sequencing	sequencing instrument	GENEPIO:0001452	The model of the sequencing instrument used.	Select a sequencing instrument from the picklist provided in the template.	Oxford Nanopore MinION [GENEPIO:0100142]	1.0.0	1.0.0	1.0.0
Sequence information	sequencing flow cell version	GENEPIO:0101102	The version number of the flow cell used for generating sequence data.	Flow cells can vary in terms of design, chemistry, capacity, etc. The version of the flow cell used to generate sequence data can affect sequence quantity and quality. Record the version of the flow cell used to generate sequence data. Do not include "version" or "v" in the version number.	R.9.4.1	1.0.0	1.0.0	1.0.0
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 metagenomic shotgun sequencing approach. Sequencing was performed using a <fill in> sequencing instrument. Libraries were prepared using <fill in> library kit. "	Viral sequencing was performed following a metagenomic shotgun sequencing approach. Libraries were created using Illumina DNA Prep kits, and sequence data was produced using Miseq Micro v2 (500 cycles) sequencing kits.	1.0.0	1.0.0	1.0.0
Sequencing	sequencing kit number	GENEPIO:0001455	The manufacturer's kit number.	Alphanumeric value.	AB456XYZ789	1.0.0	1.0.0	1.0.0
Sequencing	DNA fragment length	GENEPIO:0100843	The length of the DNA fragment generated by mechanical shearing or enzymatic digestion for the purposes of library preparation.	Provide the fragment length in base pairs (do not include the units).	400	1.0.0	1.0.0	1.0.0
Sequencing	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	3.0.0	3.0.0	3.0.0
Sequencing	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	3.0.0	3.0.0	3.0.0
Sequencing	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.	enrichment was done using Illumina Target Enrichment methodology with the Illumina DNA Prep with enrichment kit.	3.0.0	3.0.0	3.0.0
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.	MPXV Sunrise 3.1	1.0.0	1.0.0	1.0.0
Sequencing	amplicon size	GENEPIO:0001449	The length of the amplicon generated by PCR amplification.	Provide the amplicon size expressed in base pairs.	300bp	1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics		**GENEPIO:0001457**				**1.0.0**	**1.0.0**	**1.0.0**

Category	Field name	GENEPIO ID	Description	Guidance	Example			v1	v2	v3
Bioinformatics and QC metrics	quality control method name	GENEPIO:0100557	The name of the method used to assess whether a sequence passed a predetermined quality control threshold.	Providing the name of the method used for quality control is very important for interpreting the rest of the QC information. Method names can be provided as the name of a pipeline or a link to a GitHub repository. Multiple methods should be listed and separated by a semi-colon. Do not include QC tags in other fields if no method name is provided.	ncov-tools			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control method version	GENEPIO:0100558	The version number of the method used to assess whether a sequence passed a predetermined quality control threshold.	Methods updates can make big differences to their outputs. Provide the version of the method used for quality control. The version can be expressed using whatever convention the developer implements (e.g. date, semantic versioning). If multiple methods were used, record the version numbers in the same order as the method names. Separate the version numbers using a semi-colon.	1.2.3			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control determination	GENEPIO:0100559	The determination of a quality control assessment.	Select a value from the pick list provided. If a desired value is missing, submit a new term request to the PHA4GE QC Tag GitHub issuetracker using the New Term Request form.	sequence failed quality control			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control determination	GENEPIO:0100559						1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control issues	GENEPIO:0100560	The reason contributing to, or causing, a low quality determination in a quality control assessment.	Select a value from the pick list provided. If a desired value is missing, submit a new term request to the PHA4GE QC Tag GitHub issuetracker using the New Term Request form.	low average genome coverage			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	quality control issues	GENEPIO:0100560						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 names of the software and version number used for raw data processing such as removing barcodes, adapter trimming, filtering etc.	Provide the software name followed by the version e.g. Trimmomatic v. 0.38, Porechop v. 0.2.3	Porechop 0.2.3			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	raw sequence data processing method	GENEPIO:0001458	The names of the software and version number used for raw data processing such as removing barcodes, adapter trimming, filtering etc.	Provide the software name followed by the version e.g. Trimmomatic v. 0.38, Porechop v. 0.2.3	Porechop 0.2.3			1.0.0		
Bioinformatics and QC metrics	==dehosting method==	GENEPIO:0001459	The method used to remove host reads from the pathogen sequence.	Provide the name and version number of the software used to remove host reads.	Nanostripper			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	dehosting method	GENEPIO:0001459	The method used to remove host reads from the pathogen sequence.	Provide the name and version number of the software used to remove host reads.	Nanostripper			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	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	consensus sequence name	GENEPIO:0001460	The name of the consensus sequence.	Provide the name and version number of the consensus sequence.	mpxvassembly3			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	genome sequence file name	GENEPIO:0101715	The name of the consensus 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			3.0.0	3.0.0	3.0.0
Bioinformatics and QC metrics	genome sequence file path	GENEPIO:0101716	The filepath of the consensus sequence file.	Provide the filepath of the genome sequence FASTA file.	/User/Documents/ViralLab/Data/mpxvassembly.fasta			3.0.0	3.0.0	3.0.0
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			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	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	r1 fastq filename	GENEPIO:0001476	The user-specified filename of the r1 FASTQ file.	Provide the r1 FASTQ filename. This information aids in data management.	ABC123_S1_L001_R1_001.fastq.gz			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	r2 fastq filename	GENEPIO:0001477	The user-specified filename of the r2 FASTQ file.	Provide the r2 FASTQ filename. This information aids in data management.	ABC123_S1_L001_R2_001.fastq.gz			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	r1 fastq filepath	GENEPIO:0001478	The location of the r1 FASTQ file within a user's file system.	Provide the filepath for the r1 FASTQ file. This information aids in data management.	/User/Documents/ViralLab/Data/ABC123_S1_L001_R1_001.fastq.gz			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	r2 fastq filepath	GENEPIO:0001479	The location of the r2 FASTQ file within a user's file system.	Provide the filepath for the r2 FASTQ file. This information aids in data management.	/User/Documents/ViralLab/Data/ABC123_S1_L001_R2_001.fastq.gz			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	fast5 filename	GENEPIO:0001480	The user-specified filename of the FAST5 file.	Provide the FAST5 filename. This information aids in data management.	mpxv123seq.fast5			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	fast5 filepath	GENEPIO:0001481	The location of the FAST5 file within a user's file system.	Provide the filepath for the FAST5 file. This information aids in data management.	/User/Documents/RespLab/Data/mpxv123seq.fast5			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	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			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.	100x			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).	2639019			1.0.0	1.0.0	1.0.0
Bioinformatics and QC metrics	consensus genome length	GENEPIO:0001483	Size of the reconstructed genome described as the number of base pairs.	Provide a numerical value (no need to include units).	197063			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	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	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	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 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	reference genome accession	GENEPIO:0001485	A persistent, unique identifier of a genome database entry.	Provide the accession number of the reference genome.	NC_063383.1				
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/monkeypox-nf				
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/monkeypox-nf		3.0.0	3.0.0	3.0.0
							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	assay target name	GENEPIO:0101206					1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 1	GENEPIO:0001507	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	MPX (orf B6R)		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 1	GENEPIO:0001507	The name of the gene used in the diagnostic RT-PCR test.	Provide the full name of the gene used in the 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	MPX (orf B6R)		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	diagnostic pcr Ct value 1	GENEPIO:0001509	The Ct value result from a diagnostic SARS-CoV-2 RT-PCR test.	Provide the CT value of the sample from the diagnostic RT-PCR test.	21		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 2	GENEPIO:0001510	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	OVP (orf 17L)		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 2	GENEPIO:0001510	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	OVP (orf 17L)		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	diagnostic pcr Ct value 2	GENEPIO:0001512	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.	36		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 3	GENEPIO:0001513	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	OPHA (orf B2R)		1.0.0	1.0.0	1.0.0
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	OPHA (orf B2R)		1.0.0	1.0.0	1.0.0
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.	19		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 4	GENEPIO:0100576	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	G2R_G (TNFR)		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	diagnostic pcr Ct value 4	GENEPIO:0100577	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.	27		1.0.0	1.0.0	1.0.0
Pathogen diagnostic testing	gene name 5	GENEPIO:0100578	The name of the gene used in the diagnostic RT-PCR test.	Select the name of the gene used for the diagnostic PCR from the standardized pick list.	RNAse P				
Pathogen diagnostic testing	diagnostic pcr Ct value 5	GENEPIO:0100579	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		1.0.0	1.0.0	1.0.0
							1.0.0	1.0.0	1.0.0
	Contributor acknowledgement	GENEPIO:0001516							
Contributor acknowledgement	authors	GENEPIO:0001517	Names of individuals contributing to the processes of sample collec	Include the first and last names of all individuals that should	Tejinder Singh, Fei Hu, Joe Blogs				
Contributor acknowledgement	DataHarmonizer provenance	GENEPIO:0001518	The DataHarmonizer software and template version provenance.	The current software and template version information will be	DataHarmonizer v1.4.3, Mpox v3.3.1				