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Submission Portal

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Submission Portal

Submit to the world's largest public repository of biological and scientific information

Type a few words about the sequence data you are submitting and select an option to learn more. You can also browse submission information below.

What do you want to submit?

Enter a few words about your sequence data.

Enter sequence type

Q

Suggest tool

SARS-CoV-2

16S rRNA

genome

ITS

SRA

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Download batch submission template

Note: to update an existing record or recent submission, please email your request.

Short description and brief instructions

+

10 submissions

1 SUBMITTER

2 GENERAL INFO

3 SAMPLE TYPE

4 ATTRIBUTES

5 DESCRIPTION

6 REVIEW & SUBMIT

Submitter

Required fields are marked with \* asterisk

★ First (given) name

Middle name

★ Last (family) name

★ Email (primary)

Email (secondary)

At least one email should be from the organization's domain.

Group for this submission

No group

(affiliation from my personal profile)

4 members

Francisco Gerardo Polotan's shared submissions

★ Submitting organization

Submitting organization URL

★ Department

Research Institute for Tropical Medicine

Molecular Biology Laboratory

Phone

Fax

★ Street

★ City

State/Province

★ Postal code

★ Country

9002 Research Drive

Muntinlupa

NCR

1781

Philippines

Click

EN

Continue

☒

Update my contact information in profile

New

1 SUBMITTER

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General Information

Required fields are marked with \* asterisk

Release date

Note: Release of BioProject or BioSample is also triggered by the release of linked data.

★ When should this submission be released to the public?

☒ Release immediately following processing

☐ Release on specified date or upon publication, whichever is first

★ Specify if you are submitting a single sample or a file containing multiple samples

☒ Batch/Multiple BioSamples

You will be asked to upload a tab-delimited text file that describes each of your samples and their attributes. Submission template files can be downloaded from the Attributes tab or the [templates page](#).

☐ Single BioSample

You will be asked to manually complete a web form to describe one sample and its attributes.

Continue

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Sample Type

Required fields are marked with \* asterisk

★ Select the package that best describes your samples.

All packages

Packages for MAG submitters

Packages for metagenome submitters

(Optional) Filter packages by organism name

Enter the full scientific name of your samples, e.g., Escherichia coli

Reset and show all packages

To filter for relevant BioSample packages, enter the **full scientific name** of the organism of your samples.

If your BioSamples are derived from a species **not represented in NCBI's Taxonomy database**, enter the genus-level name, e.g., *Escherichia*

If your BioSamples are derived from **more than one organism**, enter the common species, genus, or family, e.g., *Enterobacteriaceae*

If your BioSamples are **metagenomic/environmental**, or **metagenome-assembled genomes (MAG)**, select the appropriate tab above

For more information about organism names, see [Organism information](#).

NCBI packages [More...](#)

☒ SARS-CoV-2: clinical or host-associated **Select**

Use for SARS-CoV-2 samples that are relevant to public health. Required attributes include those considered useful for the rapid analysis and trace back of SARS-CoV-2 cases.

☐ SARS-CoV-2: wastewater surveillance

Use for SARS-CoV-2 wastewater surveillance samples that are relevant to public health. Required attributes include those considered useful for the rapid analysis and trace back of SARS-CoV-2 cases.

☐ Pathogen

GSC [MixS](#) packages for genomes, metagenomes, and marker sequences [More...](#)

☐ MIGS Cultured Bacterial/Archaeal

Use for cultured bacterial or archaeal genomic sequences. Organism must have lineage [Bacteria](#) or [Archaea](#).

☐ MIGS Eukaryotic

Use for eukaryotic genomic sequences. Organism must have lineage [Eukaryota](#).

☐ MIGS Viral

Use for virus genomic sequences. Organism must have lineage [Viruses](#).

☐ Metagenome

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Attributes

Required fields are marked with \* asterisk.  
At least one of the fields marked with \*\*, ++ or †† is required.

Package SARS-CoV-2: clinical or host-associated; version 1.0

★ How do you want to provide your BioSample attributes?

☐ Use built-in table editor

☒ Upload a file using Excel or text format (tab-delimited) that includes the attributes for each of your BioSamples

1. Select

★ Attributes file

Choose file

or drag and drop it here

2. Click and Upload

To filter for relevant BioSample packages, enter the **full scientific name** of the organism of your samples.

Template for BioSample package SARS-CoV-2: clinical or host-associated; version 1.0

[Download Excel](#) or [download TSV](#)

For column explanations and examples, please see the [sample attributes page](#).

For more information, please see [creating sample attribute file](#).

Continue

3. Click

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Review & Submit

This BioSample submission will be released **following processing**.

Submitter Information

Submitter

John Doe

john.doe@genomics.org

General Information

Package

SARS-CoV-2: clinical or host-associated; version 1.0

Attribute file

SARS-CoV-2.cl.1.0\_Batch73.xlsx (21.8 KB)

Submit Click

Your submission is not yet complete. Finish your submission to get accession(s) sooner. You may need to upload your data again if your submission remains unfinished.

To proceed, please review your submission, make necessary changes on any tab, then click the 'Submit' button.

Ask for help