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# SARS-CoV-2 EBI submission protocol: ENA, BioSample, and BioProject

Forked from [SARS-CoV-2 NCBI submission protocol: SRA, BioSample, and BioProject](#)

Nabil-Fareed Alikhan<sup>1</sup>, Ruth Timme<sup>2</sup>, Emma Griffiths<sup>3</sup>, Duncan MacCannell<sup>4</sup>

<sup>1</sup>Quadram Institute Bioscience; <sup>2</sup>US Food and Drug Administration; <sup>3</sup>University of British Columbia;

<sup>4</sup>US Center for Disease Control and Prevention

1 Works for me [dx.doi.org/10.17504/protocols.io.bhwdj7a6](https://dx.doi.org/10.17504/protocols.io.bhwdj7a6)

GenomeTrakr

Tech. support email: [genomeTrakr@fda.hhs.gov](mailto:genomeTrakr@fda.hhs.gov)



Nabil-Fareed Alikhan

Quadram Institute Bioscience

## ABSTRACT

**This protocol provides the steps needed to establish a new EBI submission environment for your laboratory, including BioProject(s). Once established, this protocol covers raw read submission to EBI and sample metadata to BioSample.**

For new submitters, there's quite a bit of groundwork that needs to be established before a laboratory can start its first data submission. We recommend that one person in the laboratory take a few days to get everything set up in advance of when you expect to do your first data submission.

Two protocols cover the PHA4GE guidance for SARS-CoV-2 submission to EBI

## Complete in order (1 then 2):

### 1. SARS-CoV-2 EBI submission protocol: ENA, BioSample, and BioProject (included protocol)

- Step-by-step instructions for establishing a new EBI (Webin) submission account and for creating and linking a new BioProject to an existing umbrella effort.
- SARS-CoV-2 raw data submission to ENA (European Nucleotide Archive) and metadata to BioSample.

### 2. SARS-CoV-2 EBI assembly submission protocol

*Required:* established BioProject and BioSamples

- Submit SARS-CoV-2 assemblies to EBI, linking to existing BioProject, BioSamples, and raw data.

## DOI

[dx.doi.org/10.17504/protocols.io.bhwdj7a6](https://dx.doi.org/10.17504/protocols.io.bhwdj7a6)

## PROTOCOL CITATION

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[dx.doi.org/10.17504/protocols.io.bhwdj7a6](https://dx.doi.org/10.17504/protocols.io.bhwdj7a6)

## FORK FROM

Forked from [SARS-CoV-2 NCBI submission protocol: SRA, BioSample, and BioProject](#), Ruth Timme

## KEYWORDS

metadata, INSDC, ERC000033, ENA, EBI, SARS-Cov2, COVID-19

## LICENSE

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Jun 25, 2020

LAST MODIFIED

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PROTOCOL INTEGER ID

38565

## Preamble and other documentation

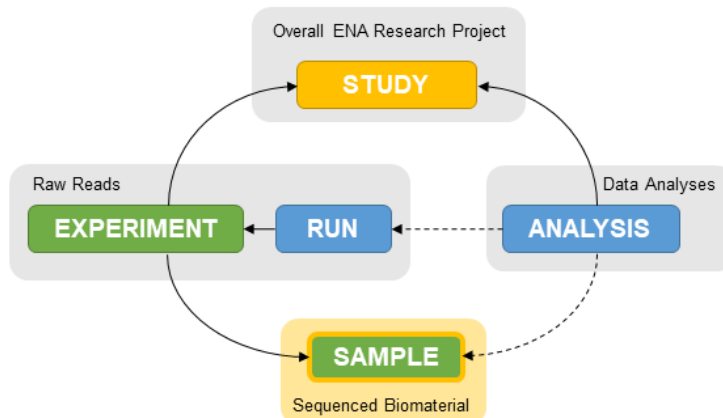
### 1 How data is structured in ENA

Data in ENA are structured in a hierarchy. Data is grouped under a "STUDY," which contains multiple "SAMPLES", which in turn have multiple "RUNS/EXPERIMENTS", and from these are derived "ANALYSES".

- **STUDY:** records overarching information about the organisation, list of authors, and an abstract about the study. This is also referred to as a PROJECT.
- **SAMPLES:** records the contextual information about how the sample was collected. E.g. Host, geographic location, collection dates.
- **EXPERIMENT/RUNS:** records the details about how the sequence was produced, e.g. sequencing platform and library preparation and points to the read data.
- **ANALYSES:** records and data derived from the sequence data, such as *de novo* genome assemblies.



Note that at each level, there can be multiple records pointing to the parent e.g. multiple sequence runs pointing to a single sample, or multiple genome assemblies pointing to a set of sequence data.



Relationship of the different data records in ENA



As data depends on another data records, you will need to submit them in a particular order. i.e. STUDY > SAMPLE > EXP/RUN > ANALYSIS.

There are many ways to submit data to ENA:

- **INTERACTIVE WEB (This protocol)**

This is done through a web browser. This is the easiest method to get started, but will become tedious with large submission (> 50 records).

#### ■ WEBIN CLI CLIENT

This is a Java program you can download that will accept prepared plain text files (MANIFESTS). These manifests specify the same information you would enter in the interactive web client, but it is easier to generate programatically. The program also submits data (reads, assemblies) for you. This is also the ONLY way to submit assembled sequences. For any sequencing centre producing data *en masse*, this would be the best option. See <https://ena-docs.readthedocs.io/en/latest/submit/general-guide/webin-cli.html> for more information.

#### ■ MANUAL XML SUBMISSION

This requires creating XML documents with the same information you would submit via the interactive web option. These files can then be submitted through <https://www.ebi.ac.uk/ena/submit/webin/>. If you generate these XML files you can test them out here: <https://wwwdev.ebi.ac.uk/ena/submit/webin/>

#### ■ PROGRAMATIC XML SUBMISSION

This requires the XML files again but the files can be submitted through an API.

In this protocol, we will use the INTERACTIVE WEB submission system, which is through a web browser. This should be the the easiest way to get started. As you get used to the system, you can try the more advanced methods for bulk submissions.

There is a detailed protocol for filling out the submission contextual data (metadata) here. <https://www.protocols.io/private/AC87DEE56E44C12B5F731895CC821F65>

The protocol will take you through how to create a submission account, and how to set up Projects, Samples and Runs. There is a separate protocol dealing with assemblies/consensus sequences.

## 2 Test your submission first!

We highly recommend doing a run through of your submission through the TEST service first.

There are two interactive Webin submission services. One for test submissions and another for production submissions:

- Test service URL: <https://wwwdev.ebi.ac.uk/ena/submit/sra>
- Production service URL: <https://www.ebi.ac.uk/ena/submit/sra>

## 3 Important resources

- ENA Documentation: [https://ena-browser-docs.readthedocs.io/en/latest/help\\_and\\_guides/sars-cov-2-submissions.html](https://ena-browser-docs.readthedocs.io/en/latest/help_and_guides/sars-cov-2-submissions.html)
- ENA Submission site: <https://www.ebi.ac.uk/ena/submit/sra/#studies>
- COVID-19 data portal <https://www.covid19dataportal.org/>



If you have any queries or require assistance with your SARS-CoV2 submission please contact: [virus-dataflow@ebi.ac.uk](mailto:virus-dataflow@ebi.ac.uk).

Creating a submission account

5m

## 4 Create an Webin user account at ENA

5m

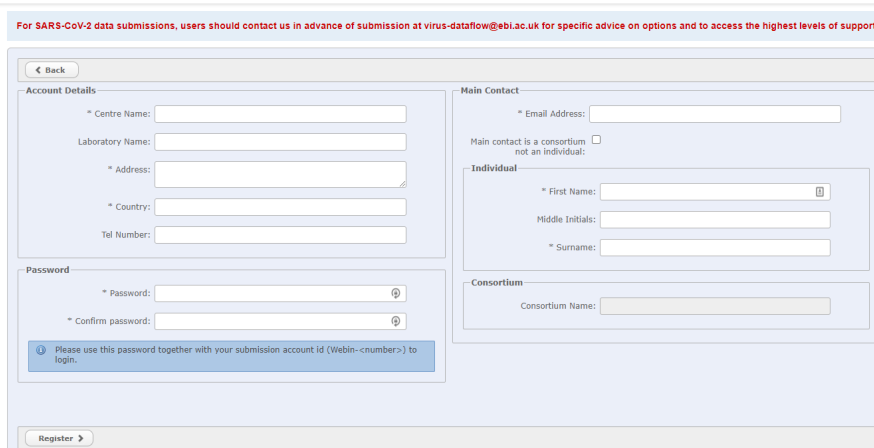
There is a form to fill in at <https://wwwdev.ebi.ac.uk/ena/submit/sra/#registration>



This account should be shared with all members of your submission team. This does mean sharing the

username and password.

For SARS-CoV-2 data submissions, users should contact us in advance of submission at [virus-dataflow@ebi.ac.uk](mailto:virus-dataflow@ebi.ac.uk) for specific advice on options and to access the highest levels of support.



Registration form for a new submission (Webin) account.

You can now log in into the submission service .

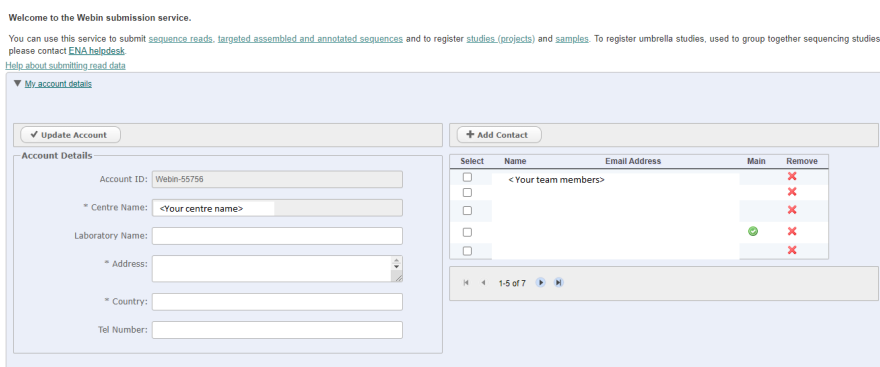
## 5 Add additional contacts for your lab.

5m

Under *Home > My account details* you can add extra contacts for data submissions. These contacts will be notified if there are any major changes to data submissions and they will be listed as contacts on public data.

Welcome to the Webin submission service.

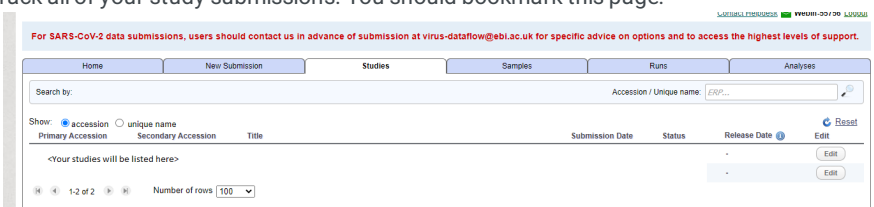
You can use this service to submit [sequence reads](#), [targeted assembled and annotated sequences](#) and to register [studies \(projects\)](#) and [samples](#). To register umbrella studies, used to group together sequencing studies, please contact [ENA helpdesk](#).  
[Help about submitting read data](#)



Form to update details about your organisation

## 6 Bookmark "Studies" at ENA: <https://www.ebi.ac.uk/ena/submit/sra/#studies>. This is the page where you view and track all of your study submissions. You should bookmark this page.

1m




Studies page at ENA is a good place to start your submissions.

## 7 Starting a new submission

You can start a new submission under "New Submission". From here you can do multiple different types of submissions. Remember that there is a particular order for data submissions i.e. STUDY > SAMPLE > EXP/RUN > ANALYSIS. So we will start with "Register STUDY"

Webin - New submission page

 If you get stuck at any stage there is a "Restart Submission" link at the bottom

Creating a new project

1w

## 8 Identify or establish new BioProjects (Umbrella and/or Data BioProjects)

1w

**Umbrella projects/studies.** If you are already part of a surveillance network, (e.g. SPHERES, COG-UK, CanCOGeN, etc) you should link your study to one of their established umbrella projects. For reference, here are some of the umbrella projects established for SARS-CoV-2 surveillance:

SPHERES (US): PRJNA615625  
CanCOGeN (Canada), PRJNA623807

You will need to talk to your consortium about having your new study linked with their umbrella project.

**Data BioProjects.** Does your consortium have an established data BioProject for this effort? You should ask them to act as a broker and submit the data on your behalf.

### Countries with single data projects (not exhaustive):

COG-UK (United Kingdom): PRJEB37886  
Turkey: PRJNA636004  
Switzerland: PRJEB38472  
South Africa: PRJNA624358

Once you have confirmed that there are no existing projects that your data should be submitted under, you can safely create a new study for yourself.

## 9 Describe the study

Fill in the form with the details of the study. Fields marked with (\*) are mandatory. You can edit this information later.

Please specify the release date of your study:  
This is when your study will be made public.

Please provide a short name for the study:

Please provide a short descriptive title for the study: (\*)

Please provide an abstract to describe the study in detail: (\*)

Please provide attributes to add a deeper description of the study:

Tag	FieldType

Add

Please provide PubMed IDs of publications you want to associate with the study:  
(numeric value)

PubMed IDs

Add

For genome assembly projects only: In this study, will you provide functional genome annotation? (\*)  
PLEASE ANSWER WITH YES IF YOU HAVE ANNOTATION: Locus tag prefixes are only associated to studies providing functional genome annotation.

☐ Yes  
☒ No

<< Previous Submit

Registering a study form

Once you have submitted the form, you should see a receipt like this:

Congratulations! You successfully completed a TEST submission, please go to [this page](#) to perform your

Dear Colleague,

Thank you for your recent submission to the European Nucleotide Archive with your account 'Webin-55756'.

We are pleased to advise you that the metadata has passed validation and the following accession numbers have been assigned:

Your study accession number is: PRJEB39067  
Your study unique name is: ena-STUDY-test-25-06-2020-12:58:02:313-6

Your study will be held private until '25-Aug-2020'.

Before the study has been made public, you can edit the release date if you wish to extend this date or release the study; do this see here: <http://www.ebi.ac.uk/ena/about/data-release-mechanism>.

Release is mandatory once the data is published in a journal.

Note that citations are added only on Study level. Therefore, once your study is published, please add the PubMed ID (if any).

Please DO NOT reply to this email. If you need further assistance, contact ENA helpdesk <https://www.ebi.ac.uk/ena/browse>

Accession Summary

Type Accession Unique Name  
Study PRJEB39067 ena-STUDY-test-25-06-2020-12:58:02:313-6

Kind regards,  
European Nucleotide Archive (ENA)

Your accession summary is also available as a downloadable .tsv spreadsheet. [Download Accession Summary](#)

Study registered success receipt

If you complete this on the production submission site, You can cite the study accession number in your publication.

You can see the new study when you go back the "Studies". You can also edit the details and release date here.

Search by: Accession / Unique name: ENA...

Show: ☒ accession ☐ unique name

Primary Accession	Secondary Accession	Title	Submission Date	Status	Release Date	Reset	Edit
PRJEB39067	ERP122535	test	25-Jun-2020	Confidential	25-Aug-2020		Edit

Uploading sequencing data 1w

## 10 Uploading sequencing data

It is recommended that read data is submitted via one of the Webin clients. The easiest method to get started with *Webin File Uploader* but there may be a better approach depending on your environment. There is extensive documentation here <https://ena-docs.readthedocs.io/en/latest/submit/fileprep/upload.html>

Registering samples and submitting sequencing metadata (Part 1) 1w

## 11

### Samples and metadata

This is by far the most complicated step in the submissions process. This is where you must format your rich metadata according to the EBI data submission requirements. For SARSCov2 submission, they ask that the metadata comply with Checklist ERC000033: <https://www.ebi.ac.uk/ena/browser/view/ERC000033>.

There is a detailed protocol for filling out the sample sheet here.  
<https://www.protocols.io/private/AC87DEE56E44C12B5F731895CC821F65>

There is extended guidance available at the **PHA4GE SARS-CoV-2 metadata specification**:  
<https://github.com/pha4ge/SARS-CoV-2-Contextual-Data-Specification>

You should start formatting your metadata according these specifications before you begin.

## 11.1 Preparing the sample spreadsheet

Skip this step, if you already have a spreadsheet completed.

If your metadata is in order, starting from the new submissions page, select "*Submit sequence reads and experiments*" and click Next.

The screenshot shows the EBI ENA submission interface. At the top, there is a progress bar with steps: Start, Study, Sample, and Run. The 'Start' step is currently active. Below the progress bar, there is a text box explaining the service and a link to the ENA helpdesk. Below this, there is a section titled 'Please select the type of submission you would like to make:'. There are four radio button options: 'Submit sequence reads and experiments' (which is selected), 'Register study (project)', 'Taxonomy Check/Request', and 'Register samples'. Below these options, there is a text box explaining the first step of the submission process and a link to the 'Fair Use Policy'.

Specify a checklist for the metadata. In this case, it is the ENA VIRUS PATHOGEN REPORTING STANDARD CHECKLIST, under *Select Checklist > Pathogens Checklist*.

The screenshot shows the EBI ENA submission interface at the 'Select Checklist' step. At the top, there is a progress bar with steps: Home, New Submission, Studies, Samples, Runs, and Analyses. The 'New Submission' step is currently active. Below the progress bar, there is a section titled 'Start building your submission'. It contains a text box explaining the checklist process and a 'Select Checklist' button. Below this, there is a section titled 'Upload a submission completed using a template spreadsheet'. It contains a text box explaining the upload process and a 'Submit Completed Spreadsheet' button.

Start >> Sample >> Finish

Please select the most appropriate checklist from the list below then click the **Next >>** button.

This group currently includes Genomic Standards Consortium (GSC) Mix5 sample checklists

**Marine Checklists**  
This group currently includes Micro B3 and Tara Oceans sample checklists

**Pathogens Checklists**  
This group currently includes several prokaryote and virus pathogen sample checklists

- ☐ ENA Global Microbial Identifier reporting standard checklist GMI\_MDM1.1  
Minimum Data for Matching (MDM). A checklist for reporting metadata of pathogen samples for the Global Microbial Identifier (GMI) reporting system. More about GMI can be found here <http://www.g-m-i.org/>
- ☐ COMPARE-ECDC-EFSA pilot food-associated reporting standard  
A checklist for reporting metadata of food-borne pathogen samples for the COMPARE-ECDC-EFSA reporting system.
- ☐ COMPARE-ECDC-EFSA pilot human-associated reporting standard  
A checklist for reporting metadata of human-associated pathogen samples for the COMPARE-ECDC-EFSA reporting system.
- ☐ ENA parasite sample checklist  
Minimum information about parasite samples. A checklist for reporting metadata of parasite samples associated with molecular data. This standard was developed by the COMPARE platform and can be used for submission of sample metadata derived from protozoan parasites (e.g. Cryptosporidium) and also multicellular eukaryotic parasites (e.g. Platyhelminthes and Nematoda).
- ☐ ENA prokaryotic pathogen minimal sample checklist  
Minimum information required for a prokaryotic pathogen sample
- ☒ ENA virus pathogen reporting standard checklist  
Minimum information about a virus pathogen. A checklist for reporting metadata of virus pathogen samples associated with genomic data. This minimum metadata standard was developed by the COMPARE platform for submission of virus surveillance and outbreak data (such as Ebola) as well as virus isolate information.
- ☐ ENA influenza virus reporting standard checklist  
Minimum information about an influenza virus sample. A checklist for reporting metadata of influenza virus samples associated with genomic data. This minimum metadata standard supports submission of avian, human and mammalian surveillance data as well as serology and virus isolate information (where available). The ENA influenza sample checklist is based on standards in use at the Influenza Research Database.

**Other Checklists**  
This group currently includes the ENA default sample checklist and a few project specific checklists

<< Previous Next >>

Clicking Next at this point will show you the details of the various fields. You can check or uncheck different fields to add or remove them. Once this is complete, click *Download template spreadsheet*

Filter fields...

Add your own custom field Add

**Collection event information**

- ☒ collection date - recommended  
The date of sampling, either as an instance (single point in time) or interval. In case no exact time is available, the date/time can be right truncated (i.e. all of these are valid ISO8601 compliant times: 2008-01-23, 2008-01-23T00:00:00, 2008-01-23T19:23:10+00:00, 2008-01-23T19:23:10+00:00).
- ☒ geographic location (country and/or sea) - mandatory  
The geographical origin of the sample as defined by the country or sea. Country or sea names should be chosen from the INSDC country list (<http://insdc.org/country.html>).
- ☐ geographic location (latitude) - recommended  
The geographical origin of the sample as defined by latitude and longitude. The values should be reported in decimal degrees and in WGS84 system
- ☐ geographic location (longitude) - recommended  
The geographical origin of the sample as defined by latitude and longitude. The values should be reported in decimal degrees and in WGS84 system
- ☒ geographic location (region and locality) - recommended

22 of 35 fields selected

Expand Collapse

When you have selected the fields click the **Next >>** button to begin entering your data. Alternatively, download a template spreadsheet using the **Download Template Spreadsheet** button. Once you have filled the spreadsheet please restart the submission process and upload the spreadsheet using the **Upload Completed Spreadsheet** button.

Download Template Spreadsheet

<< Previous Next >>

The download will be a tab separated table which you can open in your favourite spreadsheet program (Excel).

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
1	#checklist	ERC000033														
2	#unique_name_prefix															
3	sample_accession_id	scientific	common	sample_id	sample_d	collection	geographi	geographi	host_disea	host_comr	host_subje	host_age	host_health	host_sex	host_sci	
4	#template															
5	#units												centuries			
6																
7																
8																
9																
10																
11																
12																
13																
14																
15																
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34																
35																

Check the [PH4GE guidance for how to fill out this table with your metadata](#). There is also a separate protocol with informations about the various fields, see [SOP for populating EBI submission templates](#)

- You may need to change "centuries" (host age units) to "years".
- The scientific name for SARSCov2 is "Severe acute respiratory syndrome coronavirus 2"
- The correct taxon id for SARSCov2 is "2697049"

Click *Previous* twice to go back to the first part of the submission process and click *Submit complete*



*spreadsheet* to submit your completed spreadsheet (Continued on the next step). If there are any problems just restart the submission (click restart submission at the bottom).

## 11.2 Uploading the sample spreadsheet

Start ✓ >> Sample >> Finish

**Start building your submission**

We use checklists to help provide required information in a standard format. You will be guided through the following steps:

- Selecting a checklist
- Selecting optional fields in addition to mandatory ones
- Entering your data directly into this application

Alternatively, after selecting the checklist and fields you will be able to download a template spreadsheet. You can then enter your data in the spreadsheet and upload it.

Select Checklist >

**Upload a submission completed using a template spreadsheet**

If you have downloaded and filled a template spreadsheet please upload it using the **Submit Completed Spreadsheet** button.

Please note that only spreadsheets in tab-delimited text format are supported (with either .tsv or .txt extensions). If you edited the spreadsheet in Microsoft Excel (or equivalent) please save the spreadsheet as Text (Tab delimited). To do this please see [these instructions](#).

Submit Completed Spreadsheet

<< Previous

From this page, click Submit completed spreadsheet, which will allow you to upload your prepared spreadsheet. If successful, you will see this dashboard with all the sample names on the left and the details of the selected sample on the right.

Start ✓ >> Sample >> Finish

Please add samples to the submission. Multiple samples can be created by increasing the number by the add button.

+ Add 1 samples

Sample ID	Status	Errors
NORW-EB469	✓	
NORW-EB46F	✗	(i) ✗
NORW-EB46E	✗	(i) ✗
NORW-EBB28	✗	(i) ✗
NORW-EBB46	✗	(i) ✗
NORW-EBB70	✗	(i) ✗
NORW-EBB8F	✗	(i) ✗
NORW-EBD22	✗	(i) ✗
NORW-EBD6E	✗	(i) ✗
NORW-EBD8C	✗	(i) ✗

1-10 of 296

Please submit by clicking the **Submit** button. Alternatively, download your data as a spreadsheet using the **Download Spreadsheet** button. Once you have filled the spreadsheet please restart the submission process and upload the spreadsheet using the **Upload Completed Spreadsheet** button.

Download Spreadsheet

**Basic Details**

\* Unique Name: NORW-EB469

\* Title: NORW-EB469

Description:

**Organism Details**

If your organism is not found please go [here](#)

Search:

\* Tax Id: 2697049

\* Scientific Name: Severe acute respiratory syndrome coronavirus 2

Common Name:

**Collection event information**

collection date:

\* geographic location: United Kingdom

Restart Submission

Submit

Any record with errors will have the red exclamation warning. The columns with invalid values will be shown in the right hand pane. Mouse over the blue (i) to see what values the field expects.

< Previous Sample Next Sample >

\* Tax Id: 2697049

\* Scientific Name: Severe acute respiratory syndrome coronavirus 2

Common Name:

**Collection event information**

collection date:

\* geographic location (country and/or sea): United Kingdom

The date of sampling, either as an instance (single point in time) or interval. In case no exact time is available, the date/time can be right truncated i.e. all of these are valid  
ISO8601 compliant times: 2008-01-23T19:23:10+00:00; 2008-01-23T19:23:10; 2008-01-23; 2008-01; 2008.

Once all the samples are green in the left hand pane, and everything looks OK, click submit. Any errors will appear below the form. If there are no errors, then there will be a final confirmation pop-up to

submit.

## 12 Submitting run & experiment metadata

This is a continuation of the previous section. By this point the raw sequencing data should have been uploaded and the sample information should have been completed. Select a file format according to the directions.

Please select the file format. If you have files of different types please submit them in separate submissions.

☐ CRAM

☒ BAM  
One BAM file is submitted for each run.

☐ SFF

☐ One Fastq file (Single)

☐ Two Fastq files (Paired)

☐ Complete Genomics

☐ PacBio HDF5

☐ Oxford Nanopore

Mandatory fields are denoted by (\*)

Download Template Spreadsheet   Upload Completed Spreadsheet   Download Spreadsheet

[Sample reference suggestions]	Sample reference (*)	Instrument Model (*)	Library Name	Library Source (*)	Library Selection (*)	Library Strategy (*)	Description
test	test	Illumina HiSeq 4000		VIRAL RNA	PCR	AMPLICON	



You can only submit one type of file at once. If you have files of different types, these would need to be submitted through separate submissions.

Again, like the samples, download the template spreadsheet and fill in the information about your samples using your favourite spreadsheet program. You can then upload the sheet back, which will populate the table at the bottom. Review, correct any errors and then click Submit.

Check the [PH4GE guidance for how to fill out this table](#) with your metadata. There is also a separate protocol with informations about the various fields, see [SOP for populating EBI submission templates](#)

Errors on submission will be shown at the bottom.

If the submission is successful you will see a submission receipt. There is a downloadable table at the bottom that has all the accession codes, which can be included in your publication.



Congratulations! You successfully completed a TEST submission, please go to [this page](#) to perform your submission in PRODUCTION

Dear Colleague,

Thank you for your recent submission to the European Nucleotide Archive with your account 'Webin-55756'.

We are pleased to advise you that the metadata has passed validation and the following accession numbers have been assigned:

Please DO NOT reply to this email. If you need further assistance, contact ENA helpdesk <https://www.ebi.ac.uk/ena/browser/support>

#### Accession Summary

Type Accession Unique Name  
Sample ERS4783409 (SAMEA7015592) test  
Experiment ERX4244183 ena-EXPERIMENT-test-25-06-2020-15:19:22:337-1  
Run ERR4292371 ena-RUN-test-25-06-2020-15:19:22:337-1

Kind regards,

European Nucleotide Archive (ENA)

## 13 Epilogue

Congratulations! If you've made it this far you've successfully uploaded SARSCov2 data to ENA.

There are a few things to keep in mind.

- You can change the release date for your data under the studies page.  
<https://www.ebi.ac.uk/ena/submit/sra/#studies>
- You can review the submitted data under the various tables.
- If you want to download the accession or check if you have missed any samples, it is actually easier to view them on the Webin submission portal here <https://www.ebi.ac.uk/ena/submit/webin/>