NGDC

BioSample Submission Quick Start Guide
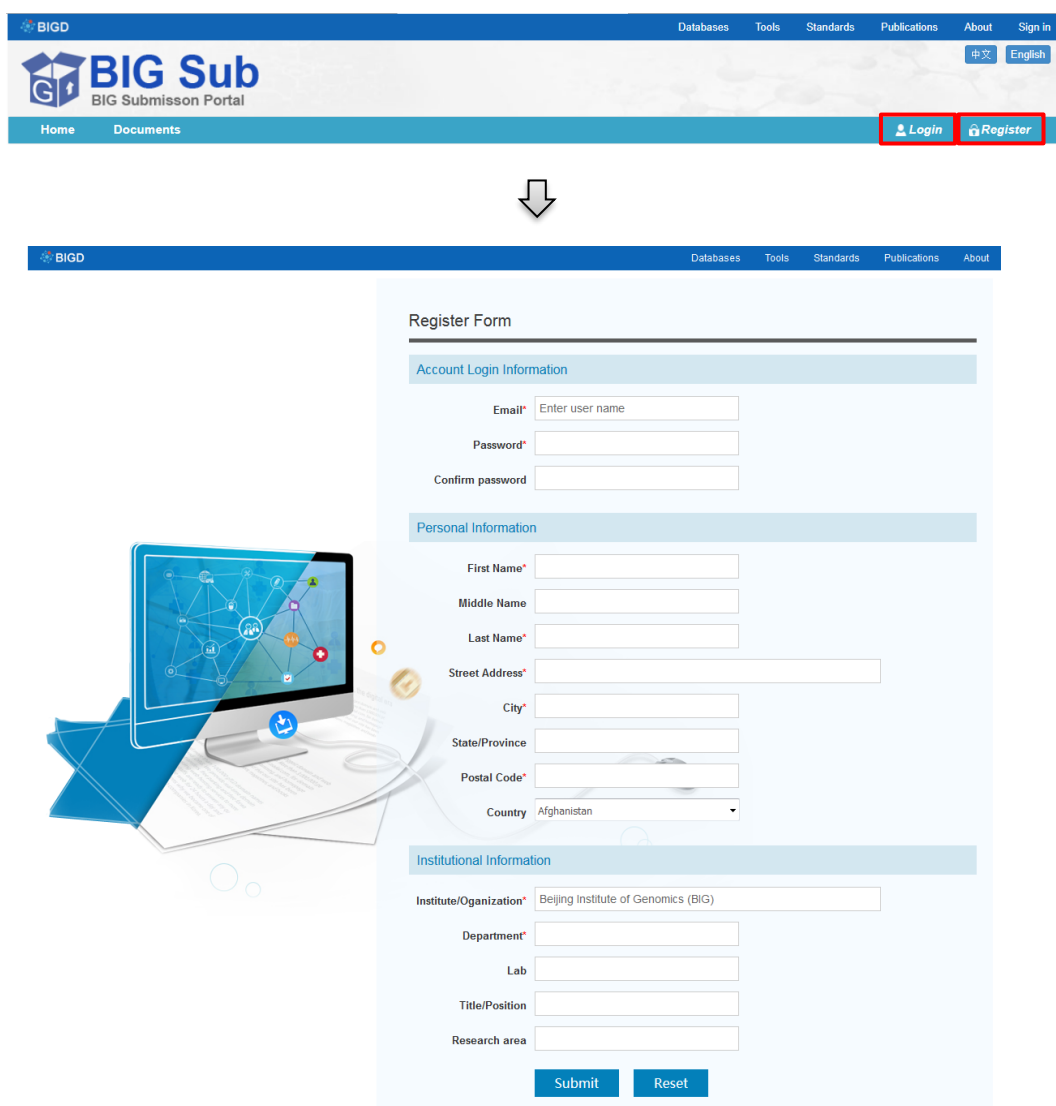
Introduction

BioSample contains descriptions of biological source materials used in studies that have data deposited in other BIG Data Center databases such as Genome Warehouse, Gene Expression Nebulas, Genome Variation Map, BioCode, etc.

Login to the BIG Submission Portal

Login to the BIG Submission Portal (BIG Sub, https://bigd.big.ac.cn/gsub/): Click the '**login**' button, then login. If you do not have an account yet, click the '**Register**' button to create one. If you have any problems about your account usage, please contact bigd-admin@big.ac.cn for assistance.

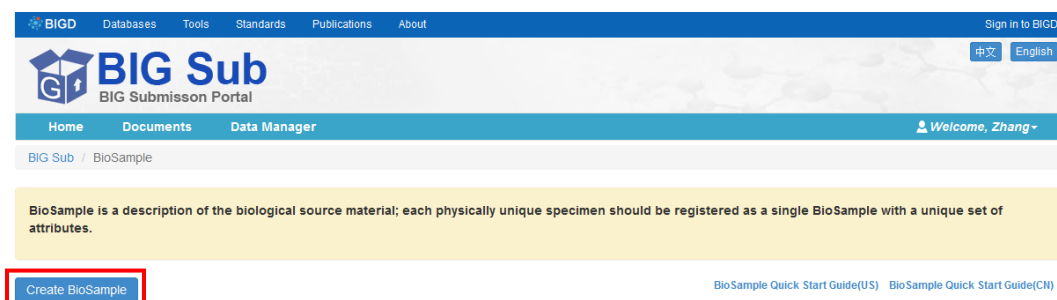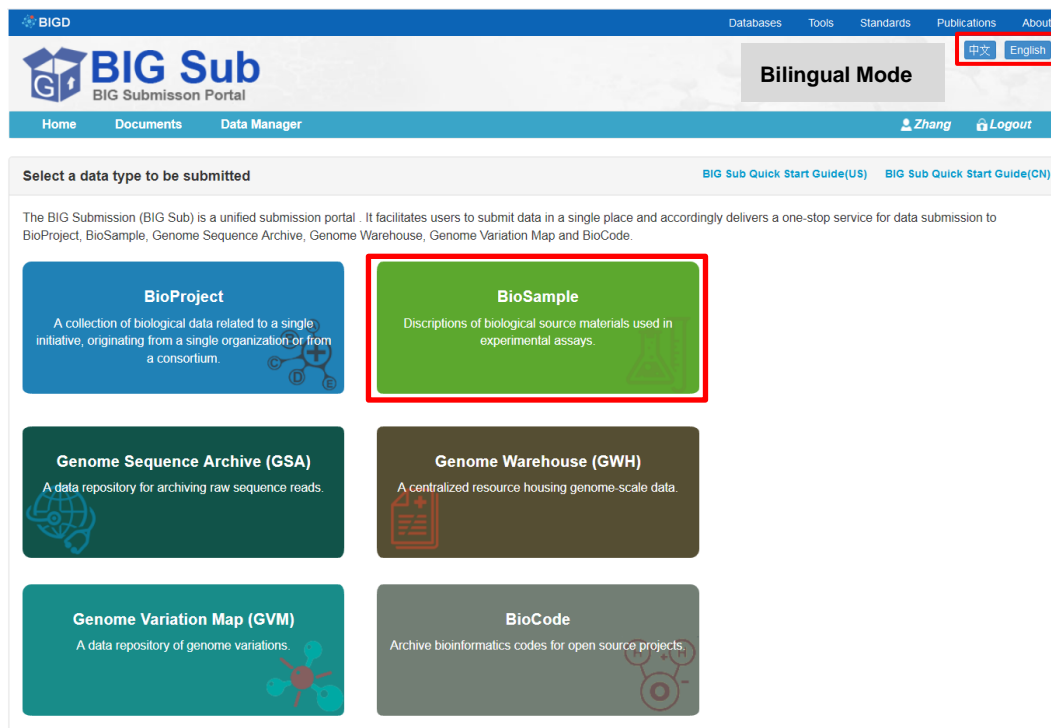# Create the BioSample Submission for Biological Sample(s)

The BioSample database provides structured and indexed descriptive information on

biological materials. A BioSample record clarifies context to the derived data, with reciprocal links to BioProject as well as other relevant database resources. The BioSample database supports two Submission types: **Batch BioSamples** and **Single BioSample.**

Notice: The majority of BioSample submissions contain more than one sample. Make sure that every organism/metagenome, tissue type or treatment type has their own sample.

Batch BioSamples (Recommend)

Batch BioSamples submission allows you to submit information about multiple samples in a single table. To submit batch BioSamples, click the '**Create BioSample**' button to initiate the submission wizard:

- *Submitter* – the name and email information are auto-filled if you have logged in, and in this case, the system is able to identify the person who is entering the data in the form.

- *General information* – this page collects general descriptive information about the **Release Date**, **Submission type** and **General Information**.

Notice: If you select '**Release immediately following curation**', the records will be released after the approval passed. If you select '**Release on a specified date**', the

BioSamples will be released on the date you specify or upon the release of any data that reference those BioSample accessions, whichever is first.

- *Sample Type* – this page provides a preview of the sample type that submitter is asked to supply during the submission process.

Notice: If you determined that your human data must be submitted via **GSA Human database**, please delete your current submission and contact us at gsa@big.ac.cn.

- *Attributes* –this page allows you to upload attributes information about multiple samples in a single table. To finish **Batch submission steps**, you should:

  1) Download the BioSample submission template table Human.us.xlsx. For column explanations and examples, please see the e.g.Human.us.xlsx. For more information, please see the Help.

  Notice: Downloading new template ensures that you get the most current and correct version.

2) Fill in the template table and double-check it before uploading. Use the Selection box to select your completed table.

3) Then click the '**Check**' button to verify the submitted batch information online.

4) If the file has passed the examination, please click the '**Save and forward**' button to complete your submission. If not, please click the '**Delete**' button. You should edit and re-upload the file until it is correct.

Attributes of human

* Uploaded BioSample batch submission file using Excel format that includes the attributes for each of Samples

5.Human.cn.test4.xlsx   54KB   [Delete]   [Check]   ✖ ERROR:

Please download the error file: error.txt

Error in Sample sheet
row 11, column 1: "sample_name" ("scRNA-seq of WJMSC21") already exist in this project
row 12, column 1: "sample_name" ("scRNA-seq of WJMSC22") already exist in this project
row 13, column 1: "sample_name" ("scRNA-seq of WJMSC23") already exist in this project
row 14, column 1: "sample_name" ("scRNA-seq of WJMSC24") already exist in this project
row 15, column 1: "sample_name" ("scRNA-seq of WJMSC25") already exist in this project
row 16, column 1: "sample_name" ("scRNA-seq of WJMSC26") already exist in this project

ⓘ Please click the "**Check**" button to verify the submitted batch information online. If the file checked OK, please click the "**Save and forward**" to complete your submission. If not, please delete the file first, then modify and reload until it passed the examination.

[Save and forward]

⬇

Attributes of human

* Uploaded BioSample batch submission file using Excel format that includes the attributes for each of Samples

5.Human.cn.test5.xlsx   50KB   [Delete]   [Check]   ✔ Checked OK.

ⓘ Please click the "**Check**" button to verify the submitted batch information online. If the file checked OK, please click the "**Save and forward**" to complete your submission. If not, please delete the file first, then modify and reload until it passed the examination.

[Save and forward]

- *Overview* – this page presents a summary of the provided information. On this step, please be careful to check the details of your submission. If you need to make changes, go back by clicking the relevant tab then edit. If everything is correct, click the '**Submit**' button to complete the submission.

Notice: After the completion of the submission, you will no longer be able to change the associated **BioProject accession**, **Submission Type** and **Sample Type**.

Notice: After the submission, you will get the **BioSample Accession** numbers in the form of SAMC#, like SAMC021054. Please use this number in [BIG Search](). Any new submission receives a temporary **submission ID** in the form of sub#, like subSAM023451. Please provide this ID when contacting GSA Working Team. Do not use the temporary **Submission ID** in [BIG Search]().

Single BioSample

Single BioSample submission allows you to submit only one sample. To submit a single BioSample, click the '**New submission**' button to initiate the BioSample wizard.

- *Submitter* – the name and email information are auto-filled if you have logged in, and in this case, the system is able to identify the person who is entering the data in the form.

- *General information* – this page collects general descriptive information about the **Release Date**, **Submission type** and **General Information**.

General information

Release date

○ After the approval is passed, release immediately following curation (recommended)
● Release on specified date

2019-05-15

(yyyy-mm-dd)

> **Release Date** is the date your submission can be publicly accessed. If your submitted information need to be protected for some time, you should set this date to a future date within two years.

Submission type

○ Batch BioSamples
● Single BioSample

General information

* Project accession

[   ] OR Go to create **BioProject**

* Sample title

[   ]
Sample title is required

* Public description

[   ]
You should give some description

Save and forward

- *Sample Type* – this page collects information about Sample Type.

Sample type

○ **Pathogen**
Used for pathogen samples that are relevant to public health. Required attributes include those considered useful for the rapid analysis and trace back of pathogens.

  ○ **Clinical or host-associated**

  ○ **Environmental, food or other**

○ **Microbe**
Used for bacteria or other microbes when it is not appropriate or advantageous to use for Pathogen or Virus packages.

○ **Animal**
Used for multicellular samples or cell lines derived from common laboratory model organisms, e.g., mouse, rat, Drosophila, worm, fish, frog, or large mammals including zoo and farm animals.

○ **Human** ⚠
WARNING: Only used for human samples or cell lines that have no privacy concerns. If there are human data requiring controlled access, please contact gsa@big.ac.cn and submit them to the GSA for Human database.

○ **Plant**
Used for any plant sample or cell line.

○ **Virus**
Used for all virus samples not directly associated with disease. Viral pathogens should be submitted using the Pathogen: Clinical or host-associated pathogen package.

○ **Metagenome/Environmental Sample (GSC MIMS unsupported)**
Use for metagenome/environmental samples when it is not appropriate or advantageous to use the GSC (Genome Standards Consortium) MIMS (Minimum Information about a MetaGenome Sequence) standards.

○ **Metagenome/Environmental Sample (GSC MIMS compliant)**
Describe and standardize sample metadata, defined by the GSC (Genome Standards Consortium) MIMS (Minimum Information about a MetaGenome Sequence) standards for metagenome/environmental samples.

  ○ **human-gut**

  ○ **soil**

  ○ **water**

Save and forward

> Select the type of your Sample, for example 'Human sample'.

Notice: If you determined that your human data must be submitted via **GSA Human database**, please delete your current submission and contact us at gsa@big.ac.cn.

- *Attributes* –this page collects attributes information of the sample.

- *Overview* – this page presents a summary of the provided information. On this step, please be careful to check the details of your submission. If you need to make changes, go back by clicking the relevant tab and edit. If everything is correct, click the '**Submit**' button.

Notice: After the submission, you will no longer be able to change the associated **BioProject accession**, **Submission Type** and **Sample Type**.

Notice: After the completion of the submission, you will get the **BioSample Accession** numbers in the form of SAMC#, like SAMC021061. Please use this number in BIG Search. Any new submission receives a temporary **Submission ID** in the form of sub#, like subSAM023452. Please provide this ID when contacting GSA Working Team. Do not use the temporary **Submission ID** in BIG Search.
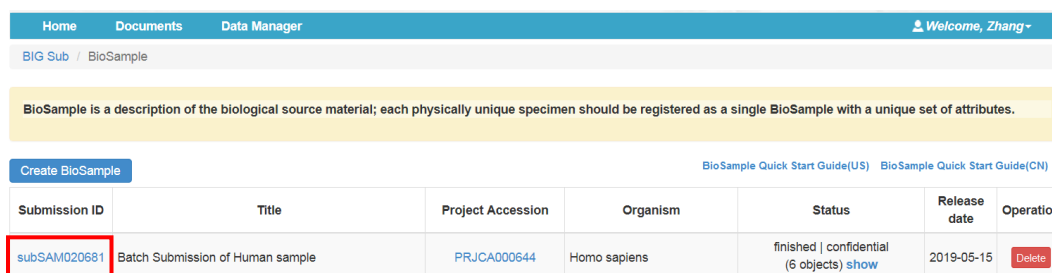
How to Edit or Delete BioSample(s)

Before the validation of the BioSample(s) by Administrators (Status is finished; confidential), you can click the '**Submission ID**' to enter the Overview page. On this page, you can 1) update the '**Release date**'; 2) Edit the '**Submitter information**' and 3) Edit or delete attributes for each submitted sample.

Notice:

1) When you submit a BioSample by the **Batch BioSamples submission type**, you can only edit the **Attributes** of the Sample. If you want to modify the **Sample title** or the **Public description**, please contact us at gsa@big.ac.cn.

2) When you submit a BioSample by the **Single BioSample submission type**, you can modify the **Submitter information**, the **General information (except the Submission type)** and all the **Attributes** of the Sample.

If you want to change your validated BioSample(s) (Status is Check OK; confidential), please contact us at gsa@big.ac.cn.

After the validation of the BioSample(s) by Administrators (Status is Checked OK; confidential), you can click the '**Submission ID**' to enter the Overview page. On the Overview page, you can update the '**Release date**' and edit the '**Submitter information**'. If you want to update the '**Release date**' or change the attributes for each submitted sample, please contact us at gsa@big.ac.cn.

General information

Project accession	PRJCA000618
Release date	2019-11-22 📅 **Update** Update the Release date
Sample count	3
Sample type	Plant sample
Status	3 Samples are checked ok
Metadata file	PRJCA000618-Plant.cn.test8.xlsx

✉ Contact us

Submitter Information

Submitter	Zhang Sisi
	zhangss@big.ac.cn
Organization	Beijing Institute of Genomics, Chinese Academy of Sciences
Department	BIG Data Center
Country/Region	China
Address	Beichen West Road Beijing
Postal code	100101

Edit Edit Submitter information

Attributes

Accession	Sample Name	Organism	Title	Status	Operation
SAMC016640	2	*Arabidopsis*	test	*Checked OK*	
SAMC018312	MS-1	*Cucumis melo subsp. agrestis*	MS-1	*Checked OK*	
SAMC018313	MS-2	*Cucumis melo subsp. agrestis*	MS-2	*Checked OK*	

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How to Release the BioSample(s)

We present two options for you to release your BioSample(s). One is to wait for the auto-releasing of the BioSample(s) on the date you specify or upon the release of any data that reference your BioSample accession(s), whichever is first. The other is to click on the '**Release Now**' button in the last column of the list to trigger the release as shown below.

After the BioSamples are released, you still can click the '**Submission ID**' to enter the Overview page to edit the '**Submitter information**'. If you want to edit your released BioSample(s), please contact us at gsa@big.ac.cn.