

# BioSample Submission Quick Start Guide

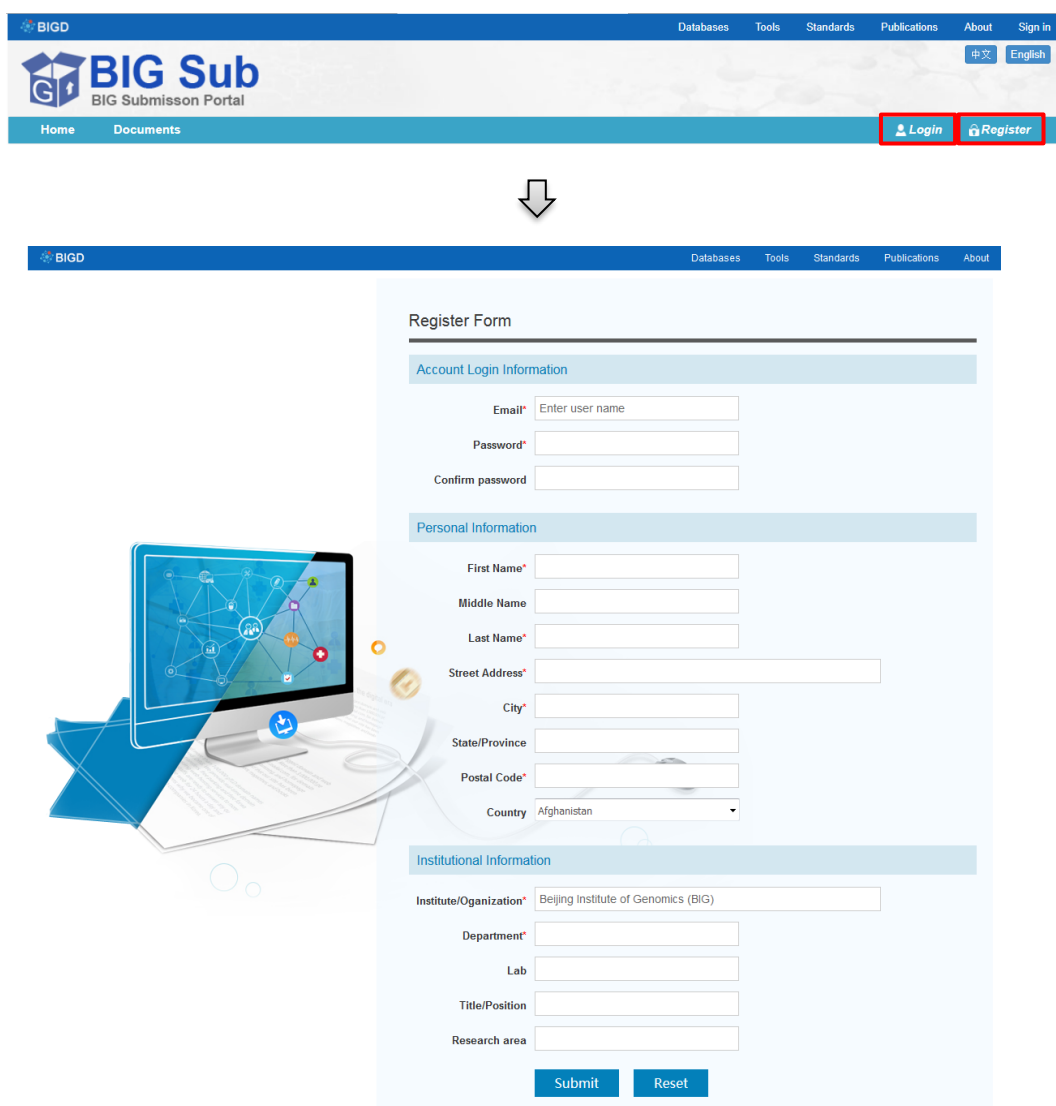
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## Introduction

**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](mailto:bigd-admin@big.ac.cn) for assistance.



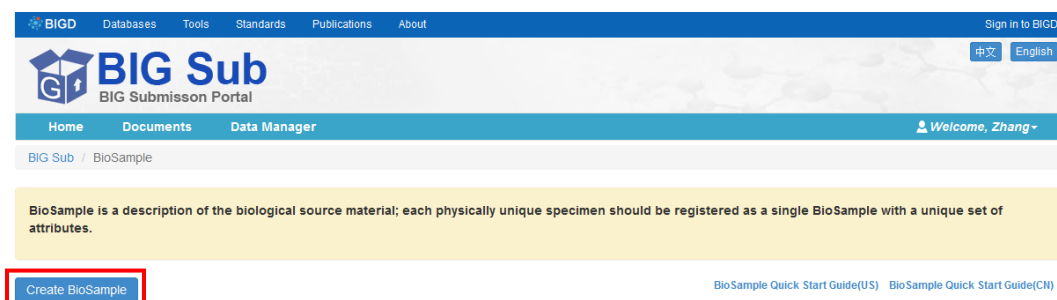
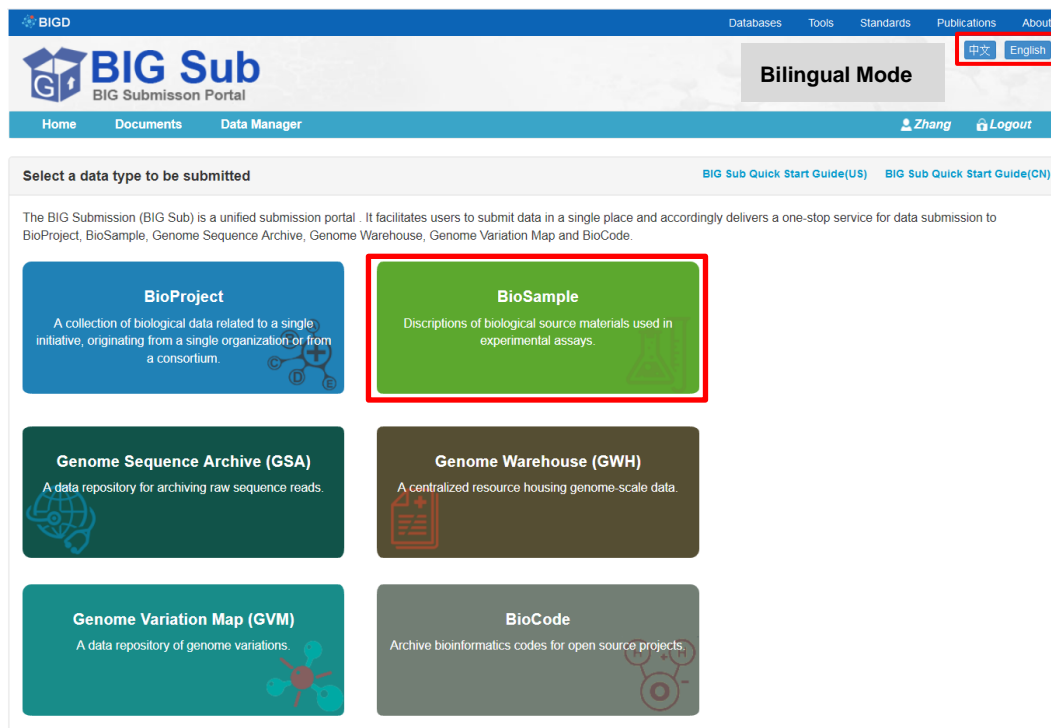
The image shows two screenshots of the BIG Submission Portal. The top screenshot displays the portal's header with navigation links (Databases, Tools, Standards, Publications, About, Sign in) and language options (中文, English). The 'Login' and 'Register' buttons are highlighted with red boxes. A downward arrow points to the second screenshot, which shows the 'Register Form'. The form is divided into three sections: 'Account Login Information' (Email, Password, Confirm password), 'Personal Information' (First Name, Middle Name, Last Name, Street Address, City, State/Province, Postal Code, Country), and 'Institutional Information' (Institute/Organization, Department, Lab, Title/Position, Research area). The 'Institute/Organization' field is pre-filled with 'Beijing Institute of Genomics (BIG)'. The 'Country' dropdown is set to 'Afghanistan'. 'Submit' and 'Reset' buttons are at the bottom of the form.

## 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.

BIG Sub / BioSample / New BioSample

01 Submitter 02 General 03 Sample Type 04 Attributes 05 Overview

Submitter

\* First name: Zhang Middle name: middle name \* Last name: Sisi

\* Email: zhangss@big.ac.cn Email (secondary): secondary email

\* Organization: Beijing Institute of Genomics, Ch Organization website: http://www.big.ac.cn \* Department: BIG Data Center

Phone: Fax:

\* Street: Beichen West Road \* City: Beijing State/Province:

\* Postal code: 100101 \* Country/Region: China

Save and forward

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

BIG Sub / BioSample / Submission: subSAM020681

01 Submitter 02 General 03 Sample Type 04 Attributes 05 Overview

General information

Release date

After the approval is passed, release immediately following curation (recommended)

Release on specified date

2019-05-15 (yyyy-mm-dd)

Submission type

Batch BioSamples

Single BioSample

General information

\* Project accession: PRJCA000644 OR Go to create [BioProject](#)

Save and forward

**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.

**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.

The screenshot shows a navigation bar with five buttons: 01 Submitter, 02 General, 03 Sample Type (active), 04 Attributes, and 05 Overview. Below the navigation bar is a form titled 'Sample type'. The form contains several radio button options:

- 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 ▲  
Only used for cell lines that have **no privacy concerns**. According to the latest [Regulations of the Peoples Republic of China on management of Human Genetic Resources](#), human genetic resources include both materials and information of human genetic resources. Hence, we suggest that any human genetic resources information, especially from international cooperation, special population cohort or large-scale population cohort projects, should be submitted to the controlled access database: GSA for Human. If you have any questions, please contact us at [gsa@big.ac.cn](mailto:gsa@big.ac.cn).
- 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

At the bottom of the form is a red button labeled 'Save and forward'.

Select the 'Human' package as an example.

**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](mailto: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.

01 Submitter   02 General   03 Sample Type   **04 Attributes**   05 Overview

Attributes of human

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

Please select file   Upload

1 Download BioSample batch submission template [Human.us.xlsx](#), then fill in and double-check it before uploading.  
For column explanations and examples, please see the [e.g.Human.us.xlsx](#).  
For more information, please see the [Help](#).

Save and forward

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

01 Submitter   02 General   03 Sample Type   **04 Attributes**   05 Overview

Attributes of human

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

Please select file   Upload

1 Download BioSample batch submission template [Human.us.xlsx](#), then fill in and double-check it before uploading.  
For column explanations and examples, please see the [e.g.Human.us.xlsx](#).  
For more information, please see the [Help](#).

Save and forward

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

01 Submitter   02 General   03 Sample Type   **04 Attributes**   05 Overview

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**

1 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

- 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 WJMISC21") already exist in this project

row 12, column 1: "sample\_name" ("scRNA-seq of WJMISC22") already exist in this project

row 13, column 1: "sample\_name" ("scRNA-seq of WJMISC23") already exist in this project

row 14, column 1: "sample\_name" ("scRNA-seq of WJMISC24") already exist in this project

row 15, column 1: "sample\_name" ("scRNA-seq of WJMISC25") already exist in this project

row 16, column 1: "sample\_name" ("scRNA-seq of WJMISC26") 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**.

01 Submitter 02 General 03 Sample Type 04 Attributes 05 Overview

Overview Relevant Tab

**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

**General Information**

Project accession: PRJCA000644  
 Sample type: Human sample  
 Sample count: 6  
 Create time: 2019-06-19  
 Release date: 2020-12-31  
 Modify time: 2019-06-21

**Attributes**

Sample Name	Organism	Title	Description
scRNA-seq of WJMISC27	<i>Homo sapiens</i>	scRNA-seq of WJMISC-1	whole-genome sequencing
scRNA-seq of WJMISC28	<i>Homo sapiens</i>	scRNA-seq of WJMISC-2	whole-genome sequencing
scRNA-seq of WJMISC29	<i>Homo sapiens</i>	scRNA-seq of BMISC BM-1-Hex	whole-genome sequencing
scRNA-seq of WJMISC30	<i>Homo sapiens</i>	Bulk-seq of WJMISC-1	whole-genome sequencing
scRNA-seq of WJMISC31	<i>Homo sapiens</i>	Bulk-seq of WJMISC-2	whole-genome sequencing
scRNA-seq of WJMISC32	<i>Homo sapiens</i>	Bulk-seq of BMISC BM-1-Hex	whole-genome sequencing

Total Items: 6 | Items of 1 - 6 | Page size: 20 | Page 1/1 | << First | Last >> | Jump To: 1 | GO

Download Property  
Files: 5.Human.cn.test5.xlsx

Contact us

**Submit**



BIG Sub / BioSample

BioSample is a description of the biological source material; each physically unique specimen should be registered as a single BioSample with a unique set of attributes.

Create BioSample

Submission ID	Title	Project Accession	Organism	Status	Release date	Operation
subSAM023451	Batch Submission of Human sample	PRJCA000644	<i>Homo sapiens</i>	finished   confidential (3 objects) hide SAMC021054:scRNA-seq of WJMISC1 SAMC021055:scRNA-seq of WJMISC2 SAMC021056:scRNA-seq of WJMISC3	2020-12-31	Delete

**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



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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.

BIG Sub / BioSample / New BioSample

01 Submitter    02 General    03 Sample Type    04 Attributes    05 Overview

Submitter

\* First name: Zhang  
Middle name: middle name  
\* Last name: Sisi

\* Email: zhangss@big.ac.cn  
Email (secondary): secondary email

\* Organization: Beijing Institute of Genomics, Ch  
Organization website: http://www.big.ac.cn  
\* Department: BIG Data Center

Phone:   
Fax:

\* Street: Beichen West Road  
\* City: Beijing  
State/Province:

\* Postal code: 100101  
\* Country/Region: China

Save and forward

- **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

(yyyy-mm-dd)

**Submission type**

Batch BioSamples  
 Single BioSample

**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.

**General information**

\* **Project accession**

OR [Go to create BioProject](#)

\* **Sample title**

Sample title is required

\* **Public description**

You should give some description

• **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](mailto: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

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](mailto:gsa@big.ac.cn).

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

BIG Sub / BioSample / Submission: subSAM020670

01 Submitter | 02 General | 03 Sample Type | **04 Attributes** | 05 Overview

Attributes of human

\* Sample name

\* Organism

\* Isolate

Age  Year

\* Biomaterial provider

\* Sex

\* Tissue

Disease

Cell line

Cell subtype

Cell type

Culture collection

Development stage

Disease stage

Ethnicity

Health State

Karyotype

Phenotype

Population

Race

Type

Treatment

e.g. Isolate: Prostate Cancer Cell Line from SAMN06642685 (NCBI)

- **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**.

Overview

**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

**General information**

Project accession: PRJCA000644  
 Sample title: Human sample  
 Public description: Human sample  
 Release date: 2019-08-07

**Attributes**

Sample name: scRNA-seq of BMMSC BM-1-Hex  
 Organism: Homo sapiens  
 Isolate: Han  
 Biomaterial provider: BIGD  
 Sex: not collected  
 Tissue: blood

Submit



BioSample is a description of the biological source material; each physically unique specimen should be registered as a single BioSample with a unique set of attributes.

Create BioSample

Submission ID	Title	Project Accession	Organism	Status	Release date	Operation
subSAM023452	Human sample	PRJCA000644	Homo sapiens	finished   confidential SAMC021061 scRNA-seq of BMMSC BM-1-Hex	2019-08-06	Delete

**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](#).

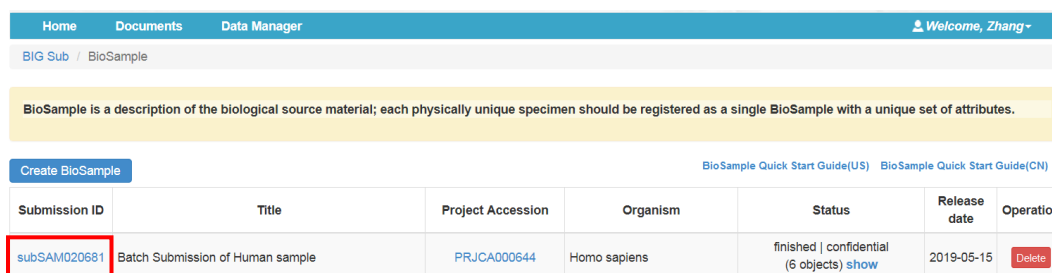
## How to Edit or Delete BioSample(s)

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](mailto: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](mailto:gsa@big.ac.cn).



Home Documents Data Manager Welcome, Zhang

BIG Sub / BioSample

BioSample is a description of the biological source material; each physically unique specimen should be registered as a single BioSample with a unique set of attributes.

Create BioSample BioSample Quick Start Guide(US) BioSample Quick Start Guide(CN)

Submission ID	Title	Project Accession	Organism	Status	Release date	Operation
subSAM020681	Batch Submission of Human sample	PRJCA000644	Homo sapiens	finished   confidential (6 objects) <a href="#">show</a>	2019-05-15	<a href="#">Delete</a>



BIG Sub / BioSample / Submission: subSAM020692

### General information

Project accession: PRJCA000644  
 Release date: 2019-05-15   Update Release date  
 Sample count: 6  
 Sample type: Human sample  
 Status: 6 Samples are waiting for check  
 Metadata file: 5.Human.cn.test4.xlsx

### Submitter Information

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

### Attributes

Accession	Sample Name	Organism	Title	Status	Operation
SAMC018351	scRNA-seq of WJMISC21	<i>Homo sapiens</i>	scRNA-seq of WJMISC-1	Unchecked	<input type="button" value="Edit"/> <input type="button" value="Delete"/>
SAMC018352	scRNA-seq of WJMISC22	<i>Homo sapiens</i>	Edit or delete attributes for each submitted sample		<input type="button" value="Edit"/> <input type="button" value="Delete"/>
SAMC018353	scRNA-seq of WJMISC23	<i>Homo sapiens</i>			<input type="button" value="Edit"/> <input type="button" value="Delete"/>
SAMC018354	scRNA-seq of WJMISC24	<i>Homo sapiens</i>	Bulk-seq of WJMISC-1	Unchecked	<input type="button" value="Edit"/> <input type="button" value="Delete"/>
SAMC018355	scRNA-seq of WJMISC25	<i>Homo sapiens</i>	Bulk-seq of WJMISC-2	Unchecked	<input type="button" value="Edit"/> <input type="button" value="Delete"/>
SAMC018356	scRNA-seq of WJMISC26	<i>Homo sapiens</i>	Bulk-seq of BMMSC BM-1-Hex	Unchecked	<input type="button" value="Edit"/> <input type="button" value="Delete"/>

Total Items: 6 | Items of 1 - 6 | Page size: 20 | Page 1/1 | << First | Last >> | Jump To: 1 | GO

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](mailto:gsa@big.ac.cn).

BIG Sub / BioSample

BioSample is a description of the biological source material; each physically unique specimen should be registered as a single BioSample with a unique set of attributes.

BioSample Quick Start Guide(US) BioSample Quick Start Guide(CN)

Submission ID	Title	Project Accession	Organism	Status	Release date	Operation
subSAM018835	Batch Submission of Plant sample	PRJCA000618	Arabidopsis <a href="#">more</a>	checked OK   confidential (3 objects) <a href="#">show</a>	2019-11-22	<input type="button" value="ReleaseNow"/>



General information

**Project accession** [PRJCA000618](#)

**Release date**

**Sample count** 3

**Sample type** Plant sample

**Status** 3 Samples are checked ok

**Metadata file** [PRJCA000618-Plant.cn.test8.xlsx](#)

[Update](#) Update the Release date

[Contact us](#)

Submitter information

**Submitter** Zhang Sisi  
[zhangss@big.ac.cn](mailto: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
SAMC018640	2	<i>Arabidopsis</i>	test	<a href="#">Checked OK</a>	
SAMC018312	MS-1	<i>Cucumis melo subsp. agrestis</i>	MS-1	<a href="#">Checked OK</a>	
SAMC018313	MS-2	<i>Cucumis melo subsp. agrestis</i>	MS-2	<a href="#">Checked OK</a>	

Total Items: 3 | Items of 1 - 3 | Page size: 20 | Page 1/1 | [<< First](#) [Last >>](#) | Jump To:

## 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.

Create BioSample BioSample Quick Start Guide(US) BioSample Quick Start Guide(CN)

Submission ID	Title	Project Accession	Organism	Status	Release date	Operation
subSAM020681	Batch Submission of Human sample	PRJCA000644	Homo sapiens	finished   confidential (6 objects) <a href="#">show</a>	2019-11-22	<a href="#">Delete</a>
subSAM019239	Batch Submission of Model organism or animal sample	PRJCA000635	Canis lupus familiaris	checked OK   confidential	2019-11-15	<a href="#">ReleaseNow</a>



Create BioSample BioSample Quick Start Guide(US) BioSample Quick Start Guide(CN)

Submission ID	Title	Project Accession	Organism	Status	Release date	Operation
subSAM020681	Batch Submission of Human sample	PRJCA000644	Homo sapiens	finished   confidential (6 objects) <a href="#">show</a>	2019-11-22	<a href="#">Delete</a>
subSAM019239	Batch Submission of Model organism or animal sample	PRJCA000635	Canis lupus familiaris	checked OK   Public	2019-05-17	

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](mailto:gsa@big.ac.cn).

BIG Sub / BioSample / Submission: subSAM019239

**General information**

Project accession: [PRJCA000635](#)

Release date: 2019-05-17

Sample count: 2

Sample type: Model organism or animal sample

Status: Checked OK: 2

Metadata file: [4.Model\\_animal.cn.test4.xlsx](#)

[Contact us](#)

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**Submitter Information**

Submitter: Zhang Sisi  
[zhangss@big.ac.cn](mailto: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

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**Attributes**

Accession	Sample Name	Organism	Title	Description	Operation
SAMC016901	FAMBTAZ00004	<i>Canis lupus familiaris</i>	FAMBTAZ00004	whole-genome sequencing	
SAMC016902	FAMBTAZ00005	<i>Canis lupus familiaris</i>	FAMBTAZ00005	whole-genome sequencing	

Total Items: 2 | Items of 1 - 2 | Page size: 20 | Page 1/1 | << First | Last >> | Jump To: 1 | GO