

GSA Submission Quick Start Guide

Steps for GSA Submission:

- Register a username on GSA web site (<http://gsa.big.ac.cn>). If you have already a username, please use that for your GSA submission as well.



Notes:

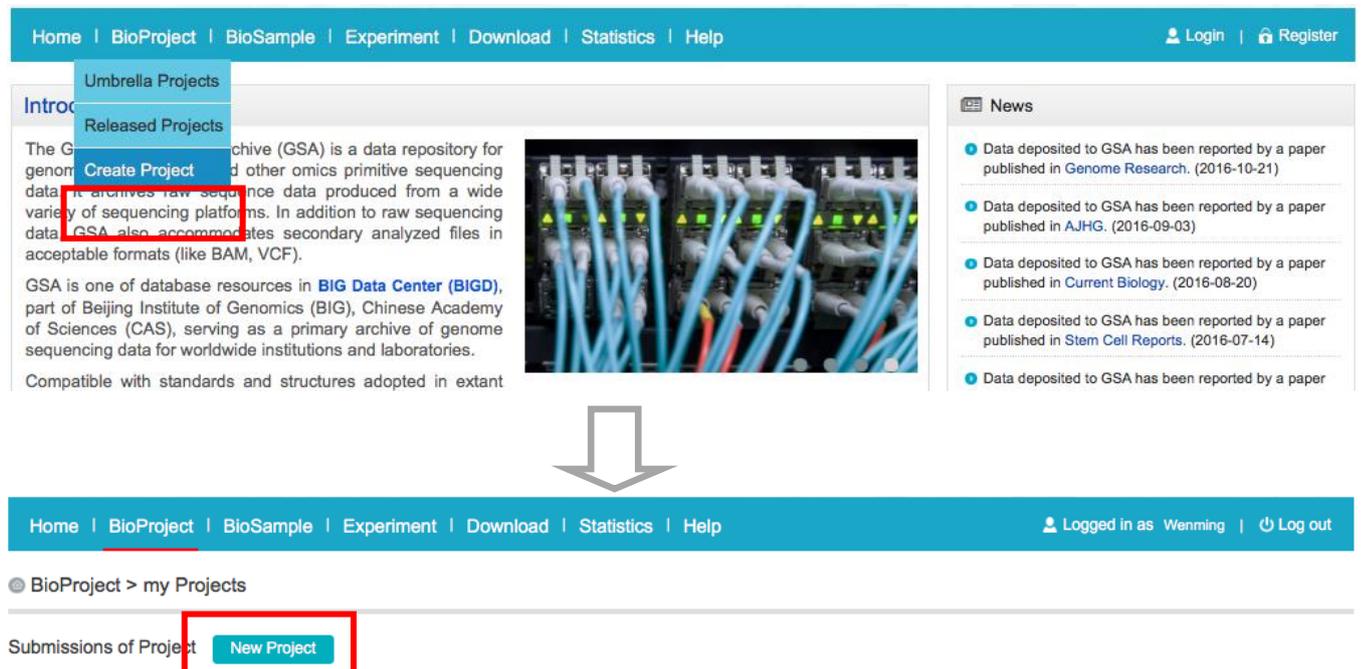
[1] Do NOT suggest using the Win10 operating system;

[2] Recommend the use of Firefox browser Chinese version, other browsers may have bugs.

- After the activation of the login system, you can follow those steps to finish the submission.

BioProject→BioSample→Experiment→Run→Data Upload→Quality Control and Feedback by GSA system

Step 1: Create a BioProject for this research





Submitter

* First name: Wenming

Middle name:

* Last name: Zhao

* Email (primary): zhaowm@big.ac.cn

Email (secondary):

* Submitting organization: BIG

Submitting organization URL:

* Department: IMC

Phone:

Fax:

* Street: #1, Beichen West Road,

* City: Beijing

State/Province:

* Postal code: 100101

* Country/Region: China

[Save and forward](#)



Project Type

* Project data type: Transcriptome or Gene expression

* Sample scope: Multiisolate

* Methodology: Sequencing

Project type only support single selection, that means that every Project ID only include single type of data. Consider to many missions will generate various types of sequencing data, such as include both genome sequencing data and transcriptome sequencing data, we suggest to **divide to several Project ID** to provide data information if in this situation.

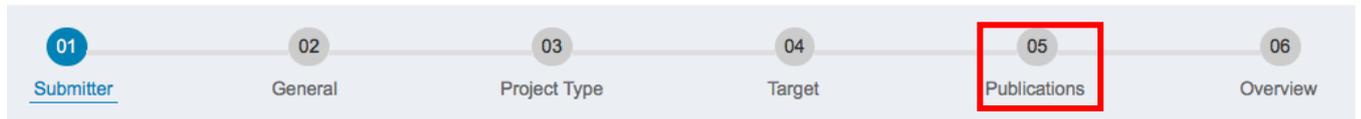


Target

* Organism Name (You must select from the hint list which will be displayed after at least 3 letters are provided)

rice

Strain, breed, cultivar OR Isolate name or label



Publications

PubMed ID OR DOI



My unpublished projects

Accession	Title	Organism	Data Type	Related Data	Submitter	Release Date
PRJCA000092	Analysis of molecular module systems for grain shape in rice	Oryza sativa	Transcriptome or Gene expression	Samples: Experiments:	wu shuangyang, Beijing Institute of Genomics	2020-12-01

Please remember this Accession number, this is the bridge for next step of BioSample.

Notes:

- [1] Release Date is the date your submission can be public access, so if your submitted information need to be **protected** for some times, please set this date one or two years later.
- [2] You can revise your information in any step before you submit in Overview page. However, you are **NOT** able to revise your information after submitting. In this way, please check carefully before clicking the 'Submit' button.

Step 2: Create BioSample for a BioProject

Introduction

Released Samples

Create Sample

The Genome Sequencing Archive (GSA) is a data repository for genome, transcriptome and other omics primitive sequencing data. It archives raw sequence data produced from a wide variety of sequencing platforms. In addition to raw sequencing data, GSA also accommodates secondary analyzed files in acceptable formats (like BAM, VCF).

GSA is one of database resources in **BIG Data Center (BIGD)**, part of Beijing Institute of Genomics (BIG), Chinese Academy of Sciences (CAS), serving as a primary archive of genome sequencing data for worldwide institutions and laboratories.

Compatible with standards and structures adopted in extant archives in International Nucleotide Sequence Database Collaboration, GSA covers the spectrum of raw sequencing



News

- Data deposited to GSA has been reported by a paper published in *Genome Research*. (2016-10-21)
- Data deposited to GSA has been reported by a paper published in *AJHG*. (2016-09-03)
- Data deposited to GSA has been reported by a paper published in *Current Biology*. (2016-08-20)
- Data deposited to GSA has been reported by a paper published in *Stem Cell Reports*. (2016-07-14)
- Data deposited to GSA has been reported by a paper published in *Journal of Cell Science*. (2016-05-17)



Sample Submitter

01 Submitter 02 General 03 Sample Type 04 Attributes 05 Overview

Submitter

* First name <input type="text" value="Wenming"/>	Middle name <input type="text"/>	* Last name <input type="text" value="Zhao"/>
* Email (primary) <input type="text" value="zhaowm@big.ac.cn"/>	Email (secondary) <input type="text"/>	
* Submitting organization <input type="text" value="BIG"/>	Submitting organization URL <input type="text"/>	* Department <input type="text" value="IMC"/>
Phone <input type="text"/>	Fax <input type="text"/>	
* Street <input type="text" value="#1, Beichen West Road,"/>	* City <input type="text" value="Beijing"/>	State/Province <input type="text"/>
* Postal code <input type="text" value="100101"/>	* Country/Region <input type="text" value="China"/>	

Save and forward



General Info

*** Release date**

Release immediately following curation (**recommended**)

Release on specified date:

*** Project accession**

*** Sample title**

Public description

Save and forward



Sample type

Clinical or host-associated pathogen

Environmental, food or other pathogen

Microbe

Virus sample

Human sample

Model organism or animal sample

Plant sample

Select the type of your Sample, for example 'Plant sample'



Attributes

Plant Sample

*** Sample Name**

*** Organism** (You must select from the hint list)

*** cultivar**

*** biomaterial provider**

*** tissue** (You must select from the hint list)



Submissions ID	Title	Status	Updated
subSAM00892	rice endosperm	checked-K SAMC000204	2016-01-29 17:41:59

Please remember this Accession number, this is the bridge for next step of experiment.

Step 3: Create Experiment

Meta information

* Platform

* Alias

* Title

* Project accession

* Sample accession

Library Construction/Experiment design

Library

Library name * Strategy * Source * Selection

* Layout

Processing

Release date (YYYY-MM-DD)

Fill in with corresponding platform of sequencing.

The Project ID and Sample ID

Same function as BioProject and BioSample

Step 4: Generate New Run

Generate New Run in My Experiment, and fill in the information of run data, include file name and MD5 code.

Accession	Alias	Submit Date	Release Date	Files
- CRX000205	Analysis of molecular module systems for grain shape in rice	2016-01-29	2020-12-01	



New Run

General info

* Alias

Run data file type

Data blocks

File name	MD5 checksum	Delete
<input type="text"/>	<input type="text"/>	<input type="button" value="Delete"/>

Support zip and gz format of compressed files.

Release date: (YYYY-MM-DD)

File name	MD5 checksum	Delete
G32QM2-27_S70_L005_R1_001.fastq	201acde10efb23899143dd436d65b8	<input type="button" value="Delete"/>

Generation method of MD5 code: we suggest to use md5sum + file command with Linux users, and use md5sums.exe or WinMD5Free tools with windows users.

Step 5:Date Upload

Use FTP client software (such as FileZilla Client) to log in FTP serve. Serve's address and username is gsa, password is gsa@big. Pay attention to use submit.big.ac.cn as hostname when you log in FTP.

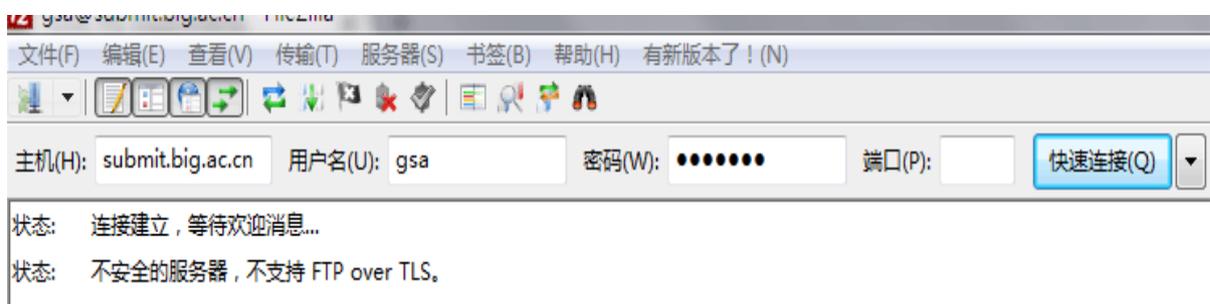
Transmitting your data files to the GSA FTP site

using the following credentials:

Address: **ftp://submit.big.ac.cn**

User: **gsa**

Password: **ycQ5QtaF1bDi**



Step 6:Quality Control and Feedback

After finished all above tasks, GSA system will check your information and files, and give your feedback.