

CNSA Handbook

Introduction

China Nucleotide Sequence Archive (CNSA) is a convenient and fast online submission system for biological research projects, samples, experiments and other information data. Based on the International Nucleotide Sequence Database Collaboration (INSDC) standard and DataCite standard, following the international data open protocol such as Fort Lauderdale Agreement, NHGRI Rapid Data Release Policies, Joint Data Archiving Policy, CCO-No Rights Reserved, accepting the submission of global scientific research sequencing data (including raw data and other support data), its data submission service can be used as a supplement to the literature publishing process to support early data sharing. CNSA is committed to the storage and sharing of biological sequencing information and data, and is designed to provide global researchers with the most comprehensive data and information resources, enabling researchers to access and use data easily and deeply.

Submission flow

1. Database login

There is a unified user registration and login platform for all databases in CNGB, and the registered account can be used for all CNGB databases. Users can access CNSA database by visiting the website <http://db.cngb.org/cnsa/> (Figure 1). Please click User Instructions at the top of homepage and read it carefully before you agree with it. Then click “LOGIN/SIGNUP” at the top right of homepage to enter the registration and login page (Figure 2). Note: register and login first, then submit data.

CHINA NATIONAL GENE BANK DATA CENTER PROJECTS

ENGLISH LOGIN/SIGNUP

CNSA

HOME MY SUBMISSION PROJECT SAMPLE EXPERIMENT/RUN ASSEMBLY HELP

CNSA: China Nucleotide Sequence Archive

China Nucleotide Sequence Archive (CNSA) is a convenient and fast online submission system for biological research projects, samples, experiments and other information data. Based on the International Nucleotide Sequence Database Collaboration (INSDC) standard, following the international data open protocol such as Fort Lauderdale Agreement, NHGRI Rapid Data Release Policies, Joint Data Archiving Policy, CCO-No Rights Reserved, accepting the submission of global scientific research sequencing data (including raw data and other support data), its data submission service can be used as a supplement to the literature publishing process to support early data sharing. CNSA is committed to the storage and sharing of biological sequencing information and data, and is designed to provide global researchers with the most comprehensive data and information resources, enabling researchers to access and use data easily and deeply.

Search

Global retrieval is available. All published Project/Sample/Experiment/Run/Assembly can be retrieved in CNSA. Retrieval results with GigaDB are not supplied. To retrieve in GigaDB, please click <http://gigadb.org/>.

Type your keywords here. Please refer to the examples below for available options. **Search**

Biological diversity

- 1KITE
- B10k
- Fish T1K
- Millet
- MLGD
- MT10K
- 1KP

Health & Disease

- BDDb
- DHGV
- DISSECT
- GDRD
- GeMap
- HMD
- ICGC
- PIRD

Figure 1 Home page



Language ▼

Login

 Account

 Password

 Captcha 

Log in

[Sign up an account.](#)

[Forget password?](#)

Log in with:       

Figure 2 Login page

2. Homepage

2.1 CNSA introduction

It briefly summarizes the purpose and significance of CNSA.

2.2 Global retrieval

All published information about Project/Sample/Experiment/Assembly/Run can be retrieved in CNSA (see Figure 3).

2.3 Data submission entrance

There are two ways to submit: one is ENA broker interface, the other is DOI (GigaDB) interface, providing raw data submission and other support data submission respectively (see Figure 3).

Search

Global retrieval is available. All published Project/Sample/Experiment/Run/Assembly can be retrieved in CNSA. Retrieval results with GigaDB are not supplied. To retrieve in GigaDB, please click <http://gigadb.org/>.

Type your keywords here. Please refer to the examples below for available options.

 Search

Example: Accession `CNP000001/CNS00001/CNX000001/CNR00001/CNA000001`, Project title, Sample name, Experiment title, Organism, Data type, Sample type, Description.

Submit flow

For both two workflows below, any questions can report to datasubs@cngb.org.



Raw sequence data submission

Raw sequence data without any filtering that needs to be published and conforms to the Human Genetic Resources Regulations and Ethics is automatically synchronized to the EBI-ENA through this service process. If the submitted data requires permission control, or needs to be uploaded to NCBI SRA or DDBJ DRA, please click [HELP](#).



Other support data submission

Other support data except the raw reads includes but not limited to process and result data, analysis methods, software programs, image files, audio files, video files, imaging files, electronic charts and word documents. CNSA cooperates with Gigascience GigaDB to review and archive the support data. With a link to DataCite, each dataset will be assigned with a DOI which can be quickly referenced. For more information, please click [HELP](#).

Figure 3 Global retrieval and data submission entrance

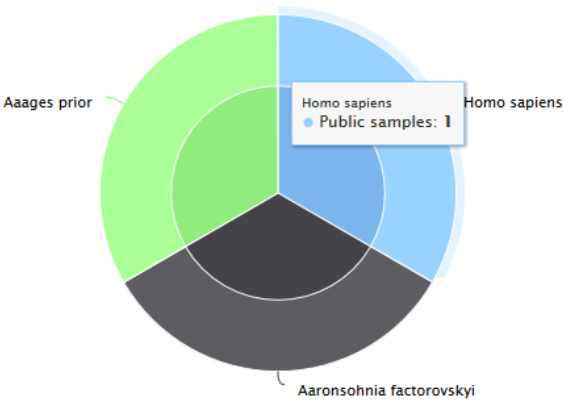
2.4 Statistics

The distribution of organisms is derived from all samples submitted by users (see Figure 4).

Statistics

Organism distribution in the sample

In the chart below, each color represents an organism. Each colored pie consists of inner and outer rings. The inner ring represents the number of sample for current organism. The outer ring can be divided into two pieces with two shades of specific color. The dark one represents the number of published sample for current organism, and the light one represents the number of unpublished sample. The two shades may not be available according to the sample disclosure.



Top 10 Organisms

Organism	Samples	Controlled	Public
Homo sapiens	1	0	1
Aaronsohnia factorovskiy	1	0	1
Aaages prior	1	0	1

Figure 4 Statistics

3. My submission

3.1 Submission flow

First fill in the project information, then submit sample, and then select Experiment/Run submission or Assembly submission (see Figure 5).

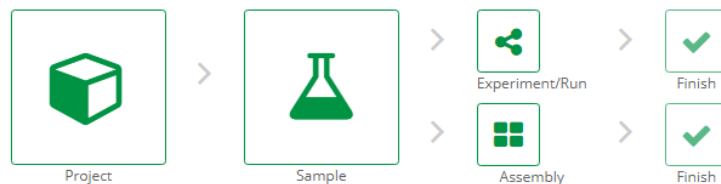
3.2 Submit progress

All submitted Project/Sample/Experiment/Run/Assembly information counts for current user (see Figure 5).

Submission Submitter

Submit flow

Note: The submission is beginning with Project, then Sample, then select Experiment/Run, or Assembly. If it is not the first time to submit, you can click directly on the following modules to start.



Submit progress

	Number	Meta data status	Update		Number	File data status	Update
Project	1		2017-10-23 12:42:40	Experiment/Run	1/1		2017-10-23 14:20:25
Sample	4		2017-10-25 06:51:13	Assembly	1		2017-10-24 16:12:32

● Successful submissions ● Processing submissions
● Uploaded ● Uploading ● Upload failed ● Not uploaded

Figure 5 Submission flow and progress

3.3 Submitter registration

Fill in the submitter information that will be associated with the subsequent Project/Sample/Experiment/Run/Assembly information to submit. It's allowed that the registered user is not the same as the registered submitter (see Figure 6).

Submission Submitter

Information

* First name ? Lorraine	Middle name ? Please input	* Last name ? Lee
* Primary E-mail ? llzq_350139456@163.com	Secondary E-mail ? Please input	

Organization

* Department ? Data Center	* Submitting organization ? CNGB	Submitting organization URL ? Please input
* Postal code ? 518000	Phone ? Please input	Fax ? Please input

Address

* Street ? Jinsha	* City ? Shenzhen	State/Province ? Please input
* Country ? China		

Save

Figure 6 Submitter information input

4. Project Submission

4.1 Project page visit

4.1.1 Public project information browsing

Click “PROJECT” on the navigation bar to enter the project page, which lists all public projects for current user. Click the accession ID to browse the public project details page, as shown in Figure 7-8.



HOME	MY SUBMISSION	PROJECT	SAMPLE	EXPERIMENT/RUN	ASSEMBLY	HELP
------	---------------	---------	--------	----------------	----------	------

Project ▶ All released projects My projects New project

Accession	Project title	Submitter	Organism	Data type	Release date
CNP0000003	Single cells Genome Se...	lijin you	Homo sapiens	Raw sequence reads	2017-10-23
CNP0000002	search algorithm	nancy guo	Aaages prior	Exome	2017-10-23
CNP0000001	proejct title testing	fan yang	Abarema microcalyx	Genome sequencing an...	2017-10-22

First Previous 1 Next Last Go to page Go

Figure 7 Project page



HOME	MY SUBMISSION	PROJECT	SAMPLE	EXPERIMENT/RUN	ASSEMBLY	HELP
------	---------------	---------	--------	----------------	----------	------

Project: CNP0000003

Summary

Title:	Single cells Genome Sequencing-1
Submitter:	lijin you; BGI
Public description:	The pilot study on single cell CNV detection in BGI-Shenzhen. Single cells isolated from blood or embryos.
Organism:	Homo sapiens
Data type:	Raw sequence reads
ENA ID:	-

Data

Samples:	1
Experiments:	1
Runs:	1
Assemblies:	-
Download:	-

Figure 8 Public project details page

4.1.2 My project

Click “My project” to view the projects submitted by the user (Figure 9), including committed and uncommitted projects. It supports query with project title or organism. Clicking “Edit” will automatically jump to the step where the user has not yet completed last time. For submitted project, it will jump to the overview page.

The project submission page will show the forms by clicking “New project”.

Project > Submissions

Filter fields: Submission, Accession, Proje

Submission	Accession	Project title	Organism	Status	Update	Operation
sub000003	CNP0000003	Single cells Geno...	Homo sapiens	finished	2017-10-23 12:42:40	View Edit

First Previous 1 Next Last Go to page Go

Figure 9 My project page

4.2 Project general information

The general page of project (see Figure 10) requires the basic information of project, for example, project name, relevance, public description. It is encouraged to provide the information such as external links, related projects, grants, consortiums, data providers. The release date is also needed. It should be noticed that the fields with asterisk (*) are mandatory and the other fields are optional.

Project > Submissions > New project

General Specific Overview

Basic information

* Project title ? Please input

Project name ? Please input

Relevance ? Please input or select

* Public description ? Please input

Function annotation ?
☐ Yes ☒ No

External links ? [+ Add](#)

URL	Link description	Operation
No entries.		

Related projects ? [+ Add](#)

Figure 10 The general page of project

4.3 Project specific information

After having completed the general information of project, click “Save and Continue” to enter the specific page of project (Figure 11). This page requires the information such as project data type, sample scope, etc. It also should be noticed that the fields with asterisk (*) are mandatory and the other fields are optional.

General

Specific

Overview

1

2

3

Project type

*** Project data type** ?

☐ Assembly ☐ Clone ends ☐ Epigenomics ☐ Exome ☐ Genome sequencing and assembly ☐ Genome sequencing ☐ Map ☐ Metagenome ☐ Metagenomic assembly ☐ Other ☐ Phenotype or Genotype ☐ Proteome ☐ Random survey ☒ Raw sequence reads ☐ Targeted loci cultured ☐ Targeted loci environmental ☐ Targeted Locus (Loci) ☐ Transcriptome or Gene expression ☐ Variation

*** Sample scope** ?

Other

Target

* Taxonomy ID ?	* Organism ?	
9606	Homo sapiens	
Strain ?	Breed ?	Cultivar ?
Please input	Please input	Please input
Isolate name ?	Label ?	
Please input	Please input	

Figure 11 The specific page of project

4.4 Project overview

After having completed the specific information of project, click “Save and Continue” to enter the overview page of project (Figure 12). This page summarizes the previous two pages. If you find any error, you can enter any page to modify. Click “Submit” if correct. It will automatically generate an accession number (e.g. CNP0000001) with which to view detailed information after project submission. It can also be modified after submission completed. During the process of project information input, halfway withdraw from the system will retain the information last filled in.

General

Specific

Overview

1

2

3

General information

* **Project title:**
Single cells Genome Sequencing-1

* **Relevance:**
-

* **Public description:**
The pilot study on single cell CNV detection in BGI-Shenzhen. Single cells isolated from blood or embryos.

* **Function annotation:**
No

Project type

* **Project data type:**
Raw sequence reads

* **Sample scope:**
Other

* **Organism:**
Homo sapiens

Accessions in other databases

After a project submitted successfully, it will take a few days to review and upload the project to ENA, and an ENA Accession number will be available.

If you do not want the data to be transmitted to EBI-ENA, please e-mail the accession id to datasub@cngb.org after submitting.

ENA:
-

Previous step

Submit

Figure 12 Project overview page

5. Sample submission

5.1 Sample page visit

5.1.1 Public sample information browsing

Click “SAMPLE” on the navigation bar to enter the sample page, which lists all public samples for current user. Click the accession ID to browse the public sample details page, as shown in Figure 13-14.

Sample ▶ All released samples

[My samples](#)
[New sample](#)

Accession	Sample name	Submitter	Organism	Project	Release date
CNS0000002	Typographic variants	nancy guo	Aaages prior	CNP0000002	2017-10-23
CNS0000001	BGI_Single_Cell	lijin you	Homo sapiens	CNP0000003	2017-10-23

[First](#)
[Previous](#)
[1](#)
[Next](#)
[Last](#)
 Go to page [Go](#)

Figure 13 Sample page

Sample: CNS0000001

Summary

Name: BGI_Single_Cell
Submitter: lijin you
Organism: Homo sapiens
ENA ID: -

Attributes

Sample name: BGI_Single_Cell
Sample title: -
Taxonomy ID: 9606
Organism: Homo sapiens
Common name: man
Isolate: Homo sapiens
Public description: -
Age: 20
Biomaterial provider: bgi
Sex: female
Tissue: blood
Cell line: -
Cell subtype: -
Cell type: -
Culture collection: -
Development stage: -

Figure 14 Public sample details page

5.1.2 My Sample

Click “My sample” to view the samples submitted by the user (Figure 15), including committed and uncommitted samples. It supports query with sample title or organism. Clicking “Edit” will automatically jump to the step where the user has not yet completed last time. For submitted sample, it will jump to the overview page.

The sample submission page will show the forms by clicking “New sample”.

HOME	MY SUBMISSION	PROJECT	SAMPLE	EXPERIMENT/RUN	ASSEMBLY	HELP
------	---------------	---------	--------	----------------	----------	------

Sample ▶ Submissions

My samplesNew sample

Filter fields: Submission, Accession, Sample name, Taxonomy ID, Orgar

Submission	Accession	Sample name	Taxonomy ID	Organism	Status	Update	Operation
sub000005	-	-	-	-	processing, a...	2017-10-23 14:54:55	View Edit Delete
sub000004	CN50000001	BGI_Single_Cell	9606	Homo sapiens	finished	2017-10-23 14:03:07	View Edit
sub000003	-	-	-	-	processing, a...	2017-10-23 12:01:46	View Edit Delete

FirstPrevious1NextLast
Go to pageGo

Figure 15 My sample page

5.2 Sample general information

The general page of sample (see Figure 16) requires the general information of sample, for example, related project accession, release date. It should be noticed that the fields with asterisk (*) are mandatory and the other fields are optional.

HOME	MY SUBMISSION	PROJECT	SAMPLE	EXPERIMENT/RUN	ASSEMBLY	HELP
------	---------------	---------	--------	----------------	----------	------

Sample ▶ Submissions ▶ New sample

General

Sample type

Attributes

Overview

General information

* Project accession

Please input then select.

Sample release

* Release date(Beijing time)

2017-10-23

Save and continue

Figure 16 The general page of sample

5.3 Sample type

After having completed the general information of sample, click “Save and Continue” to enter the sample type page (Figure 17). This page requires user to choose the type of sample.

HOME
MY SUBMISSION
PROJECT
SAMPLE
EXPERIMENT/RUN
ASSEMBLY
HELP

Sample
Submissions
New sample

General
Sample type
Attributes
Overview

Sample type

☐ Pathogen affecting public health
☐ Clinical or host-associated pathogen(v1)
☐ Environmental, food or other pathogen(v1)
☐ Microbial sample(v1)
☐ Model organism or animal sample(v1)
☐ Metagenome or environmental sample(v1)
☐ Invertebrate(v1)
☒ Human sample(v1)
☐ Plant sample(v1)

Figure 17 The sample type page

5.4 Sample attributes

After the sample type selected, click the “Save and Continue” button to enter the sample attributes page (see Figure 18). Different sample types require to fill in different attributes. Take human sample for example, the sample attributes page requires to fill in the information such as sample name, isolate, age, biomaterial provider, sex, tissue. It is encouraged to provide more attributes to describe sample better. It should be noticed that the fields with asterisk (*) are mandatory and the other fields are optional.

Sample
Submissions
New sample

General
Sample type
Attributes
Overview

General

* Sample name
Please input

Sample title
Please input

* Taxonomy ID
Please select

* Organism
Please select

Common name
Please select

* Isolate
Please input

Public description

Collection

Figure 18 The attributes page of sample

5.5 Sample overview

After having completed the sample attributes, click “Save and Continue” to enter the overview page of sample (Figure 19). This page summarizes the previous three pages. If

you find any error, you can enter any page to modify. Click “Submit” if correct. It will automatically generate an accession number (e.g. CNS0000001) with which to view detailed information after sample submission. It can also be modified after submission completed. During the process of sample information input, halfway withdraw from the system will retain the information last filled in.

Sample ▶ Submissions ▶ New sample

General Sample type Attributes Overview

1
2
3
4

General information

* **Project Accession ID:**
CNP0000003

Release date:
2017-10-23

Sample type

* **Sample type:**
Human sample

Attributes

* **Sample name:**
BGI_Single_Cell

Sample title:
-

* **Taxonomy ID:**
9606

* **Organism:**
Homo sapiens

Common name:
-

Ethnicity:
-

Health state:
-

Karyotype:
-

Phenotype:
-

Population:
-

Race:
-

Sample type:
-

Treatment:
-

Accessions in other databases

After a sample submitted successfully, it will take a few days to review and upload the sample to ENA, and an ENA Accession number will be available.
If you do not want the data to be transmitted to EBI-ENA, please e-mail the accession id to datasubs@cngb.org after submitting.

ENA:
-

Previous step
Submit

Figure 19 Sample overview page

6. Experiment/Run Submission

6.1 Experiment/Run page visit

Click “EXPERIMENT/RUN” on the navigation bar to enter the experiment/run page after logged in (see Figure 20). Click “Run” to enter the run lists page (see Figure 21) which lists all public submitted runs. Click the accession ID with the prefix CNR to view its detailed information, related project, sample, experiment, and downloadable data (see Figure 22).

Experiment/Run ▶ All released experiments/runs

[My experiments/runs](#)
[New experiment/run](#)

Accession	Experiment title	Submitter	Platform	Project	Release date	Operation
CNX0000006	ANTS_EXP	nancy guo	454 GS 20	CNP0000004	2017-10-24	Run
CNX0000005	start_guo	nancy guo	454 GS 20	CNP0000002	2017-10-24	Run
CNX0000004	data_sync_test	nancy guo	454 GS 20	CNP0000002	2017-10-24	Run
CNX0000003	nancy.guo	nancy guo	454 GS 20	CNP0000002	2017-10-24	Run
CNX0000002	test guo	nancy guo	454 GS 20	CNP0000002	2017-10-23	Run
CNX0000001	Illumina HiSeq 2000 seq...	lijin you	Illumina HiSeq 2000	CNP0000003	2017-10-23	Run

[First](#)
[Previous](#)
[1](#)
[Next](#)
[Last](#)
 Go to page [Go](#)

Figure 20 Experiment/Run page

Run of CNX0000006

×

Accession	File Type
CNR0000006	bam

[First](#)
[Previous](#)
[1](#)
[Next](#)
[Last](#)
 Go to page [Go](#)

Figure 21 Run lists page

Run: CNR0000006

Summary

File type bam
ENA ID -

Data

Project CNP0000004
Sample CNS0000003
Experiment CNX0000006
Release date -

Filename	Filesize	Status	Accession	Download
ANT_TEST.bam	711	uploaded	CND0000007	download

Figure 22 Run details page

Click the button “My experiments/runs” as shown in Figure 23 will show all

experiments/runs for current user. Click “New experiment/run” to enter experiment/run submission page. Click “Run” to enter the individual run lists page (see Figure 24) to view the detailed information and data upload progress. The submitted information can be viewed by clicking “view” button (see Figure 25).



[HOME](#)
[MY SUBMISSION](#)
[PROJECT](#)
[SAMPLE](#)
[EXPERIMENT/RUN](#)
[ASSEMBLY](#)
[HELP](#)

Experiment/Run ▶ Submissions
My experiments/runs
New experiment/run

Filter fields: Accession, Experimen

Accession	Experiment title	Project	Update	Release date	Datafile submission	Operation
CNX0000001	Illumina HiSeq 2000 sequencin...	CNP0000003	2017-10-23 14:20:25	2017-10-23	Uncompleted	Run

First Previous 1 Next Last
Go to page Go

Figure 23 My experiments/runs page

Run of CNX0000001 ✕

Accession	File type	Update	Is released	Status	Operation
CNR0000001	fastq	2017-10-23 14:10:25	Yes		View Edit

● Uploaded
● Uploading
● Upload failed
● Not uploaded

Previous Next
Go to page Go

Figure 24 The individual run lists page

Experiment/Run detail: CNR0000001

Files

- * **File type:** fastq
- * **File name:** BGI_Single_Cell_HUMafrRHYDFAAPEI-1_110812.gz
- * **MD5:** 38b8c2c1093dd0fec383a9d9ac940515
- * **Status:** not upload
- Is this an experiment you ever submitted?:** Yes --

General information

- * **Project accession:** CNP0000003
- * **Sample accession:** CNS0000001
- * **Title:** Illumina HiSeq 2000 sequencing: Single cell CNV
- * **Platform:** Illumina HiSeq 2000

Library

- * **Library name:** HUMafrRHYDFAAPEI-1
- * **Strategy:** WGS
- * **Source:** GENOMIC
- * **Selection:** PCR

Figure 25 Experiment/Run view page

6.2 Experiment/Run submission page

The experiment/run submission page (Figure 26) requires file type, file name and md5 value with which the data integrity can be guaranteed. Secondly, the relevant experiment information such as the metadata, including platform, title, project accession, sample accession, the library, including library name, strategy, source, selection, design description, and the pipeline, including program and version is required. The release date is also needed. It should be noticed that the project and sample should be submitted first to acquire the project accession ID and sample accession ID before experiment/run submission. Users can use the account and password given by CNSA to upload data to FTP server for data submission. The uploaded data will be checked via md5 to make sure the data integrity. Click “Submit” after information input and error check. It will automatically generate two accession numbers (e.g. CNX0000006/CNR0000001) with which the detailed information of experiment/run can be checked. It also should be noticed that the fields with asterisk (*) are mandatory and the other fields are optional. It can be modified after submission completed. During the process of experiment/run information input, halfway withdraw from the system will retain the information last filled in.

HOME
MY SUBMISSION
PROJECT
SAMPLE
EXPERIMENT/RUN
ASSEMBLY
HELP

Experiment/Run
Submissions
New experiment/run

* File type

Please select

* Files

+ Add

File name	MD5	Status	Operation
No entries.			

* Is this an experiment you ever submitted?

☐ Yes
☒ No

General information

* Project accession

Please input then select

* Sample accession

Please input then select

* Platform

Please select

* Title

Please input

Library

Library name

* Strategy

* Source

Figure 26 Experiment/Run submission page

7. Assembly Submission

7.1 Assembly page visit

Click “ASSEMBLY” on the navigation bar to enter the assembly page, which lists all public assemblies for current user. Click the accession ID to browse the public assembly details page, as shown in Figure 27-28.



CNSA

HOME
MY SUBMISSION
PROJECT
SAMPLE
EXPERIMENT/RUN
ASSEMBLY
HELP

Assemblies
All released assemblies

My assemblies
New assembly

Accession	Title	Submitter	Assembly method	Release date
CNA0000001	single cell scaffold	lijin you	SOAPdenovo	2017-10-24

First
Previous
1
Next
Last

Go to page
Go

Figure 27 Assembly page

[HOME](#)
[MY SUBMISSION](#)
[PROJECT](#)
[SAMPLE](#)
[EXPERIMENT/RUN](#)
[ASSEMBLY](#)
[HELP](#)

Assemblies: CNA0000001

Summary

Title:
Assembly name:
Molecule type:
Sequencing technology:
Assembly method:
ENA ID:

Assembly
single cell scaffold assembly
genomic DNA
Illumina HiSeq
SOAPdenovo(1.0)
-

Data

Project: CNP0000003
Sample: CNS0000001
Release date: 2017-10-24

File name	File type	Status	File size	Accession	Download
No data available.					

Figure 28 Assembly details page

Click “My assembly” to view the assemblies submitted by the user (Figure 29), including committed and uncommitted assemblies. Clicking “View” will automatically jump to the assembly details page (Figure 30). Click “Edit” to fill in or update the assembly information (Figure 31). The assembly submission page will show the forms by clicking “New assembly” (Figure 32).



CNSA

[HOME](#)
[MY SUBMISSION](#)
[PROJECT](#)
[SAMPLE](#)
[EXPERIMENT/RUN](#)
[ASSEMBLY](#)
[HELP](#)

Assemblies ▸ Submissions

My assemblies
New assembly

Filter field: Accession, Title

Accession	Title	Update	Status	Operation
CNA0000001	single cell scaffold	2017-10-24 16:12:32		View Edit

First
Previous
1
Next
Last
Go to page

● Uploaded
● Uploading
● Upload failed
● Not uploaded

Figure 29 My Assembly page

HOME
MY SUBMISSION
PROJECT
SAMPLE
EXPERIMENT/RUN
ASSEMBLY
HELP

Assembly detail: CNA0000001

General

- * **Project accession:** CNP0000003
- * **Sample accession:** CNS0000001

Files

- * **File type:** scaffold_fasta
- * **File name:** HUMAN_SCAFFOLD.fasta.gz
- * **MD5:** e3b5dd475c449300dd11f258538ff493
- * **Status:** not upload

Assembly metadata

- * **Title:** single cell scaffold
- * **Assembly name:** -
- * **Molecule type:** genomic DNA
- * **Coverage:** 120
- * **Sequencing technology:** Illumina HiSeq

Figure 30 Assembly view page

HOME
MY SUBMISSION
PROJECT
SAMPLE
EXPERIMENT/RUN
ASSEMBLY
HELP

Assemblies > Submissions > Update assembly

General information

* **Project accession** ⓘ

CNP0000003

* **Sample accession** ⓘ

CNS0000001

* **Files** ⓘ

+ Add

contig_fasta and contig_flatfile CANNOT be submitted at the same time.
scaffold_fasta and scaffold_agp CANNOT be submitted at the same time.
chromosome_fasta and chromosome_agp CANNOT be submitted at the same time.
unlocalised_contig_list requires contig_fasta or contig_flatfile file to be submitted together.
unlocalised_scaffold_list requires scaffold_fasta, scaffold_flatfile or scaffold_agp file to be submitted together.
Every file type can only appear once at most.

File type	File name	MD5	Status	Operation
scaffold_fasta	HUMAN_SCAFFOLD.fasta.gz	e3b5dd475c449300dd11f258538ff493	Not upload	

Figure 31 Assembly update page

7.2 Assembly submission page

The assembly submission page (Figure 32) requires the relevant information such as

project accession, sample accession, file type, file name, status, and metadata which includes title, assembly name, molecular type, coverage, sequencing technology, assembly method. It should be noticed that the project and sample should be submitted first to acquire the project accession ID and sample accession ID before assembly submission. Users can use the account and password given by CNSA to upload data to FTP server for data submission. The uploaded data will be checked via md5 to make sure the data integrity. Click “Submit” after information input and error check. It will automatically generate an accession number (e.g. CNA00000006) with which the detailed information of assembly can be checked. It also should be noticed that the fields with asterisk (*) are mandatory and the other fields are optional. It can be modified after submission completed. During the process of assembly information input, halfway withdraw from the system will not retain the information last filled in.

HOME
MY SUBMISSION
PROJECT
SAMPLE
EXPERIMENT/RUN
ASSEMBLY
HELP

Assemblies
Submissions
New assembly

General information

* Project accession
Please input then select

* Sample accession
Please input then select

* Files
Add

contig_fasta and contig_flatfile CANNOT be submitted at the same time.
scaffold_fasta and scaffold_agp CANNOT be submitted at the same time.
chromosome_fasta and chromosome_agp CANNOT be submitted at the same time.
unlocalised_contig_list requires contig_fasta or contig_flatfile file to be submitted together.
unlocalised_scaffold_list requires scaffold_fasta, scaffold_flatfile or scaffold_agp file to be submitted together.
Every file type can only appear once at most.

File type	File name	MD5	Status	Operation
No entries.				

Assembly metadata

* Title
Please input

Figure 32 Assembly submission page

Help

Please refer to the FAQ on the Help page(<https://db.cngb.org/cnsa/help/>) for more assistance.