BioProject Help Document

Version 2.1, 2018

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Submitter

* First name

First name of submitter.

Middle name

Middle name of submitter.

* Last name

Last name of submitter.

* Email (primary)

Primary Email address of submitter.

Email (secondary)

Secondary Email address of submitter.

* Organization

Full name of organization

Submitting organization URL

The URL of submitter's organization.

* Department

The department of submitter.

Phone

The phone number of submitter.

Fax

The Fax of submitter.

* Street

The Street.

* City

The City.

State/Province

The State/Province.

* Postal code

The Postal code.

* Country/Region

The Country/Region of submitter.

General Information

* Release date

Select "Release immediately following curation" or "Release on specified date". If select "Release on specified date", you should select or give release data in correct format (yyyy-MM-dd)

Umbrella project

If your project is belonged to some umbrella project, choose correct one.

1) eGPS: evolutionary Genotype-Phenotype Systems biology;

2) MMDB: Molecule Model Design & Breeding

Project

* Project title

Provide a brief title, as a phrase or short sentence for public display.

* Relevance

Select or provide the primary general relevance of the project.

Relevance
Agricultural
Medical
Industrial
Environmental
Evolution
Model Organism

* Description

Provide a description (a paragraph) of the study goals and relevance.

Grants

* Agency

The name of the funding source, please select one from the dropdown list, or fill in to the box if it

is not collected.

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Ministry of Science and Technology of the People's Republic of China (MOST)

National Natural Science Foundation of China (NSFC)

Chinese Academy of Sciences (CAS)

Other

No funding support

Program

The name of the program.

* Grant ID

Grant ID information is collected to support searches. Fill in "N/A" if your Grant do not have an ID number.

Grant title:

Grant title may also support searches.

External Links

Link description

Display name of web site that is related to this project.

URL

URL of web site that is related to this project.

Related projects

Accession

Related project accession in GSA (e.g. PRJCA000001).

Description

Short description of relationship of the two projects.

Accessions in other database

Accession

Accession of the project in another database.

Database name

The name of the database where the project is also available, such as NCBI, DDBJ etc.

Consortium

Consortium name

If study is carried out as part of a consortium, provide the consortium name.

Consortium URL

If the consortium maintains a web site, provide the URT.

Data provider

Indicate the data provider (data submitter) if it is someone other than the submitting organization or consortium. For example, a sequencing center or a DACC.

Data provider URL

If you would like use to present a link to the data provider then please provide the URL.

Biomaterial provider

Provide the information of the center and lab, or a culture collection identifier.

Project Type

* Project data type

Indicate the general label of the primary study goal. Select appropriate types.

Project Data type	Description
Whole Genome sequencing	whole, or partial, genome sequencing project (with or without
	a genome assembly)
Clone ends	clone-end sequencing project
Epigenomics	DNA methylation, histone modification, chromatin access-
	ibility datasets
Exome	exome resequencing project
Мар	project that results in non-sequence map data such as
	genetic map, radiation hybrid map, cytogenetic map, optical
	map, and etc.
Metagenome	sequence analysis of environmental samples
Phenotype/Genotype	project correlating phenotype and genotype

Random Survey	Sequence generated from a random sampling of the
	collected sample; not intended to be comprehensive
	sampling of the material.
Targeted Locus (Loci)	project to sequence specific loci, such as a 16S rRNA
	sequencing
Targeted loci cultured	targeted loci cultured: targeted locus from cultured sample
Targeted loci environmental	targeted loci environmental: targeted locus from environ-
	mental sample (uncultured)
Transcriptome or Gene Expression	Large-scale RNA sequencing or expression analysis.
	Includes cDNA, EST, RNA-seq, and microarray.
Variation	Project with a primary goal of identifying large or small
	sequence variation across populations.
Genome sequencing and assembly	whole, or partial, genome sequencing project with a genome
	assembly
Raw sequence reads	Raw sequence reads
Genome sequencing	whole, or partial, genome sequencing project without a
	genome assembly
Assembly	genome assembly project utilizing already existing sequence
	data including data that was submitted by a different group
Metagenomic assembly	a genome assembly generated from sequenced environ-
	mental samples
Proteome	large scale proteomics experiment including mass spec.
	analysis
Other	a free text description is provided to indicate Other data type

* Sample scope

The scope and purity of the biological sample used for the study.

Sample scope	Description
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Monoisolate	A single animal, cultured cell-line, inbred population or possibly a heterogeneous
	population (a single genome assembly is generated from the pooled sample; not
	preferred).
Multisolate	Multiple individuals, a population (representation of a species).
Multi-species	Sample represents multiple species.
Environment	Species content of the sample is not known. Nucleic acid is directly isolated from
	an environmental sample for analysis. This is used for metagenome studies.
Synthetic	Sample is synthetically created in a laboratory.
Single cell	Single cell sequencing examines the sequence information from individual cells
Other	Specify the sample scope that was used.

Publications

PubMed ID

Provide a PubMed ID.

DOI

Provide a DOI if a PubMed ID is not available.

Journal name

Provide the journal name.

Article title

Provide the article title.

Year

Provide publication year.

Volume

Provide publication volume.

Issue

Provide publication issue.

• Page from

Provide publication page from.

• Page to

Provide publication page to.

Author list

Provide the author list