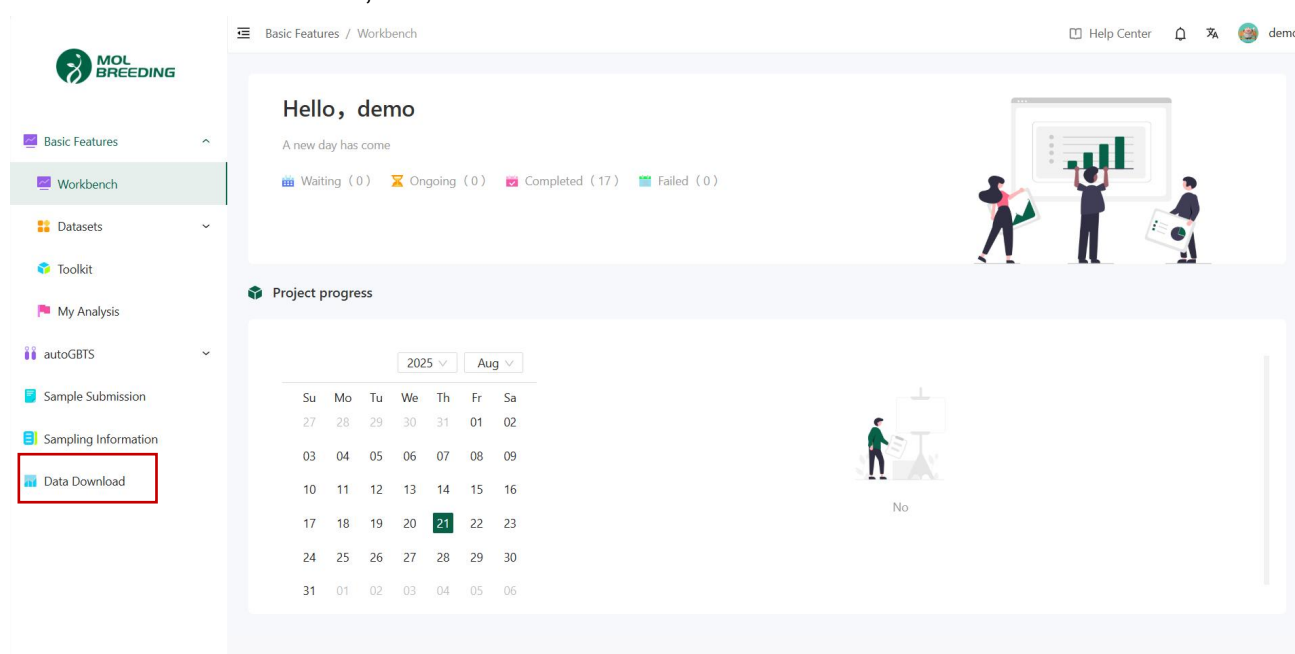


MolBreeding Customer Portal Introductions

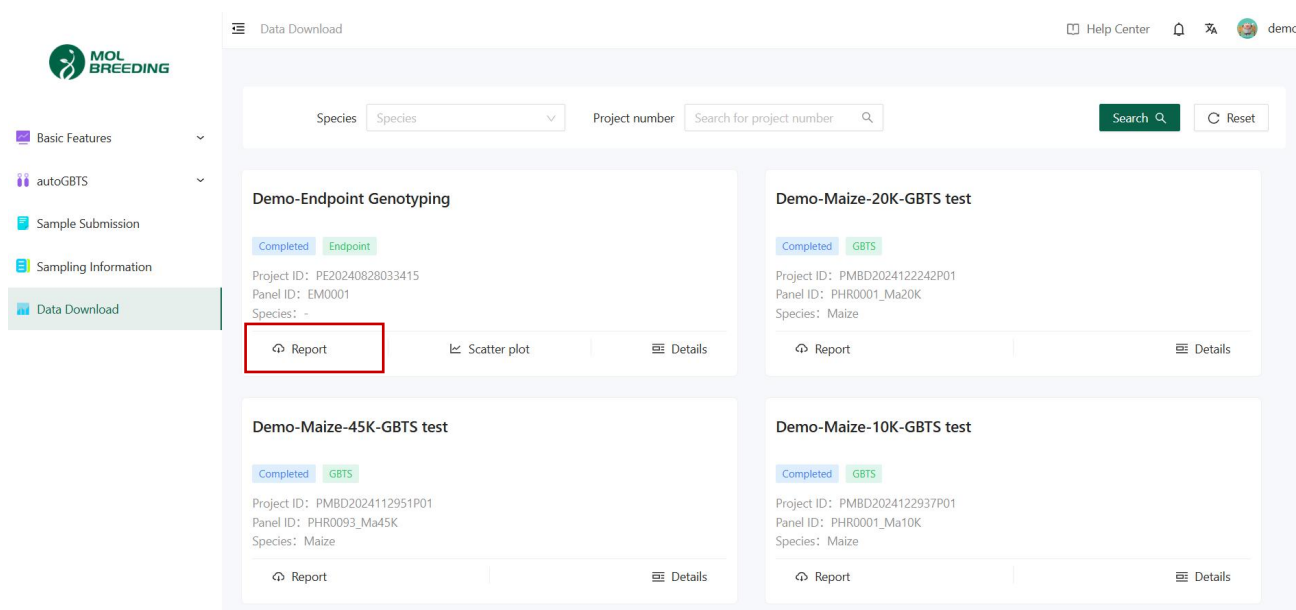
Once a project is confirmed, we will create a personalized account for you on our secure Customer Portal. Our portal offers comprehensive information management from sample to data analysis, allowing you to track your project's progress anytime and download your reports. Below is a quick guide to data download and analysis.

Data Download:

1. Log onto MolBreeding's Customer Portal (<https://cloud.molbreedinglab.com>) for data access.
2. On the left-hand side, click on the "Data Download" tab.



3. Click on "Report" to download the compressed file containing the report of the project.



Data Download

Species: Project number:

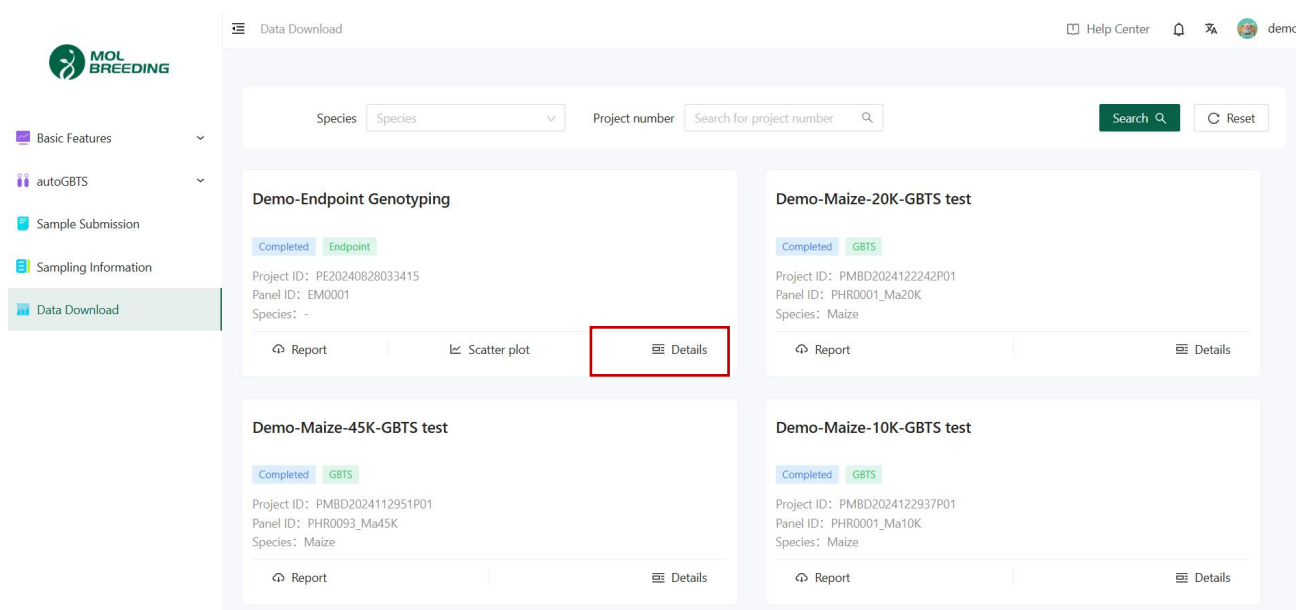
Demo-Endpoint Genotyping
Completed Endpoint
Project ID: PE20240828033415
Panel ID: EM0001
Species: -

Demo-Maize-20K-GBTS test
Completed GBTS
Project ID: PMBD2024122242P01
Panel ID: PHR0001_Ma20K
Species: Maize

Demo-Maize-45K-GBTS test
Completed GBTS
Project ID: PMBD2024112951P01
Panel ID: PHR0093_Ma45K
Species: Maize

Demo-Maize-10K-GBTS test
Completed GBTS
Project ID: PMBD2024122937P01
Panel ID: PHR0001_Ma10K
Species: Maize

4. Click on “Details” to see the batch info, product info, and results reports for the project.



Data Download

Species: Project number:

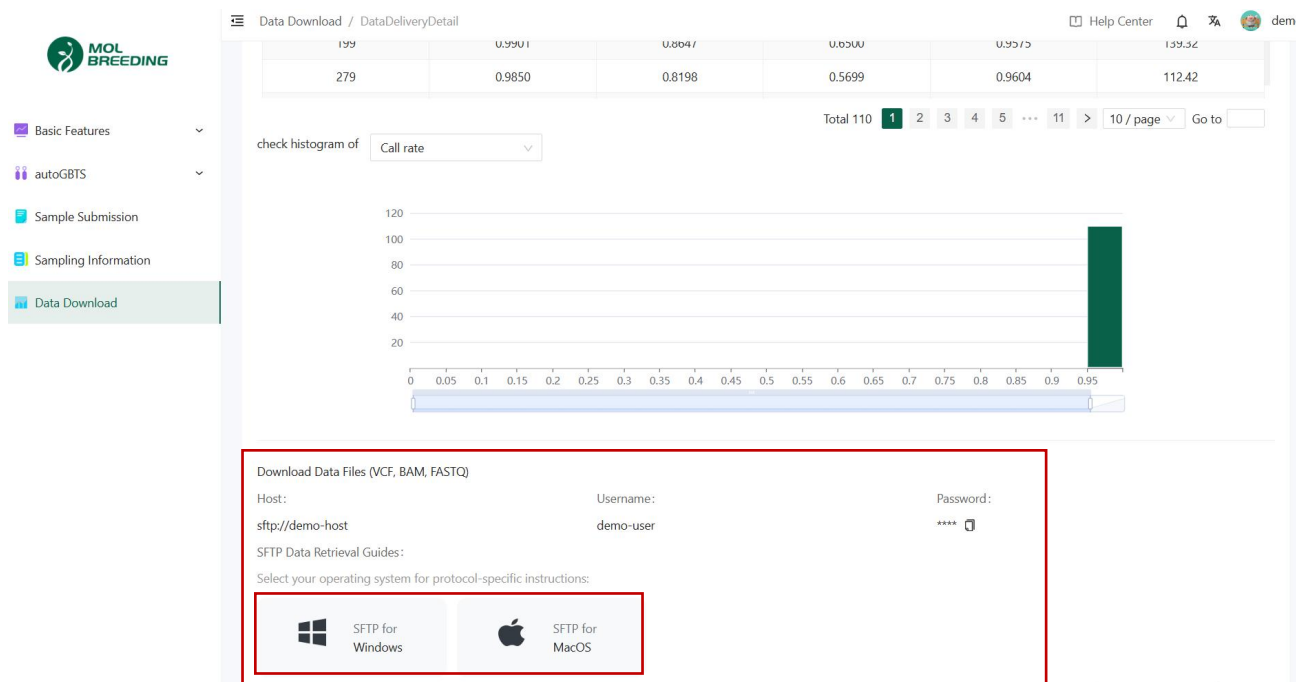
Demo-Endpoint Genotyping
Completed Endpoint
Project ID: PE20240828033415
Panel ID: EM0001
Species: -

Demo-Maize-20K-GBTS test
Completed GBTS
Project ID: PMBD2024122242P01
Panel ID: PHR0001_Ma20K
Species: Maize

Demo-Maize-45K-GBTS test
Completed GBTS
Project ID: PMBD2024112951P01
Panel ID: PHR0093_Ma45K
Species: Maize

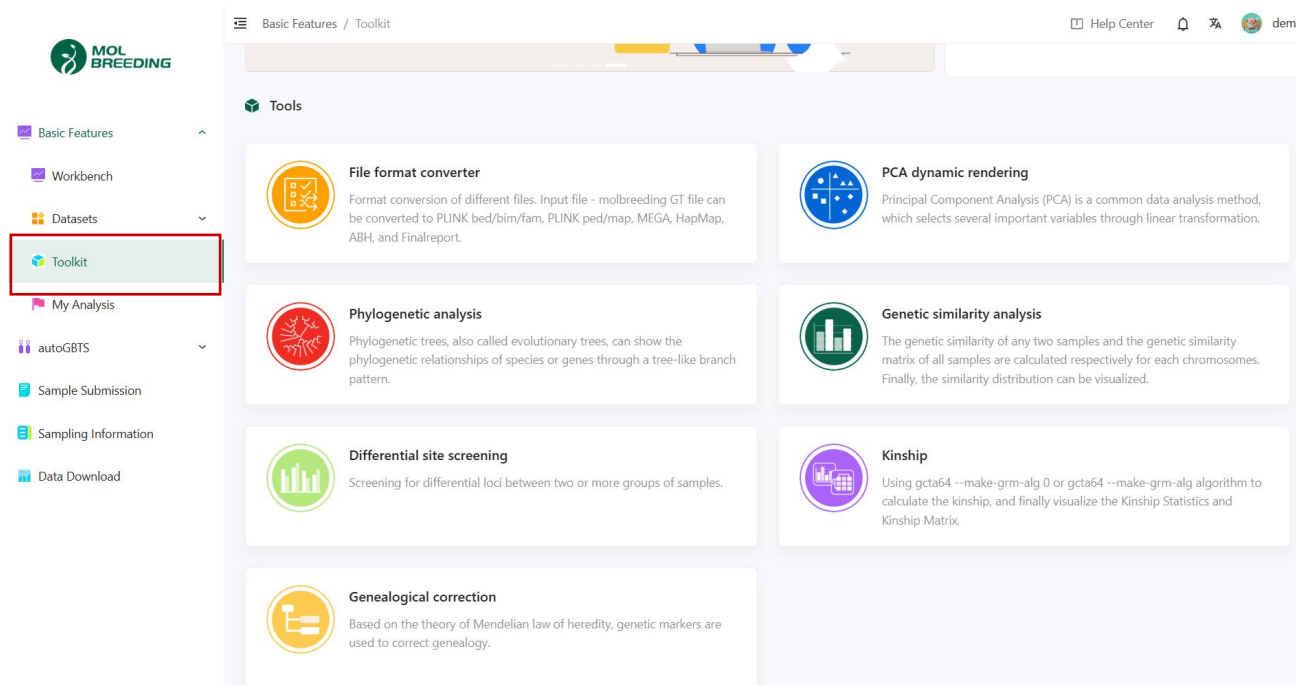
Demo-Maize-10K-GBTS test
Completed GBTS
Project ID: PMBD2024122937P01
Panel ID: PHR0001_Ma10K
Species: Maize

5. You can download and access the project’s report and its data files (VCF, BAM, FASTQ) via FileZilla by following the SFTP Data Retrieval Guide



Data Analysis:

1. On the left-hand side, click the “Toolkit” tab to access automated bioinformatics tools for further data analysis.




Basic Features / Toolkit

Tools

- File format converter**
Format conversion of different files. Input file - molbreeding GT file can be converted to PLINK bed/bim/fam, PLINK ped/map, MEGA, HapMap, ABH, and Finalreport.
- PCA dynamic rendering**
Principal Component Analysis (PCA) is a common data analysis method, which selects several important variables through linear transformation.
- Phylogenetic analysis**
Phylogenetic trees, also called evolutionary trees, can show the phylogenetic relationships of species or genes through a tree-like branch pattern.
- Genetic similarity analysis**
The genetic similarity of any two samples and the genetic similarity matrix of all samples are calculated respectively for each chromosomes. Finally, the similarity distribution can be visualized.
- Differential site screening**
Screening for differential loci between two or more groups of samples.
- Kinship**
Using gcta64 --make-grm-alg 0 or gcta64 --make-grm-alg algorithm to calculate the kinship, and finally visualize the Kinship Statistics and Kinship Matrix.
- Genealogical correction**
Based on the theory of Mendelian law of heredity, genetic markers are used to correct genealogy.

2. Select the analysis tool you want to use, name the analysis task, click "Dataset", select the data you want to analyze, submit the data, and the data will enter the automatic analysis process.

**MOL
BREEDING**

Basic Features

Workbench

Datasets

Toolkit

My Analysis

autoGBTS

Sample Submission

Sampling Information

Data Download

Basic Features / Toolkit / Phylogenetic analysis

Help Center

demo

Phylogenetic analysis

Instructions

* Task name

Please enter the task name

* Dataset

Please select your dataset

Submission

Back

Introduction

Description

Results

Tool name: Phylogenetic analysis

Online time: 2021-12-30 08:08:00

Software version: 1.0

Software description:
Phylogenetic trees, also called evolutionary trees, can show the phylogenetic relationships of species or genes through a tree-like branch pattern.

Task Wizard Overview

User guide for Phylogenetic Anal...

1. Phylogenetic Analysis

2. Getting started

2.1 Create a task

3.1 Input

3.2 My projects

3.3 Task details

4. Embellish your tree

4.1 Turn to iTOL


4.2 Introduction of iTOL

User guide for Phylogenetic Analysis tool

By reading this instruction, you can learn how to use the Phylogenetic Analysis of molbreeding cloud.

1. Phylogenetic Analysis

Phylogenetic trees, also called evolutionary trees, can show the phylogenetic relationships of species or genes through a tree-like branch pattern. By using this analytical tool you can manage and visualize your trees direct



Basic Features

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Basic Features / My Analysis / Details

Help Center



Task number: brdcloud-treetoolkit78r9

submission time: 2025-08-21 10:27

Analysis tool: treetoolkit

Task name: testing

Estimated time of end: 2025-08-21 11:27

Resubmit

Task number
brdcloud-
treetoolkit78r9

Ongoing

Waiting

2025-08-21 10:27

Ongoing


Completed

2025-08-21 11:27

Output file

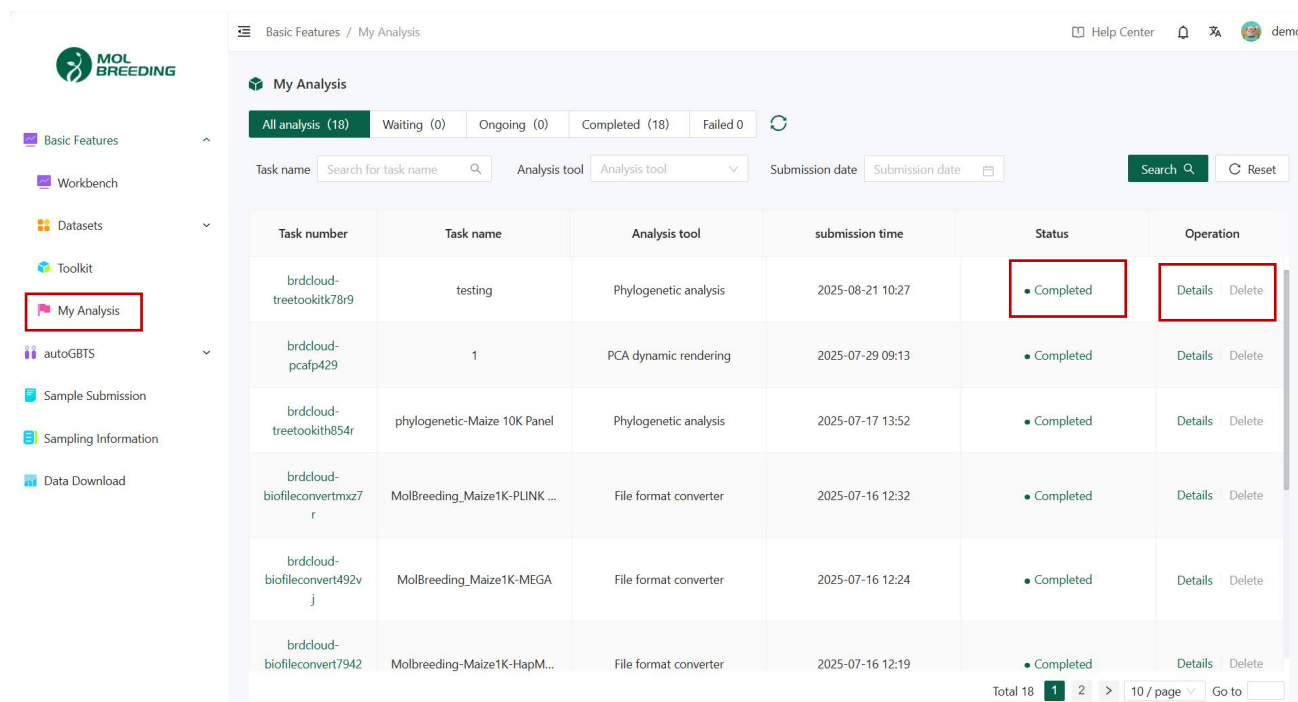
Input file

FAQs



NoOutput file

- Click the “My Analysis” tab on the left to open all completed analyses. When a workflow shows “Completed”, click “Details” to refine your charts or download them directly.



Basic Features / My Analysis

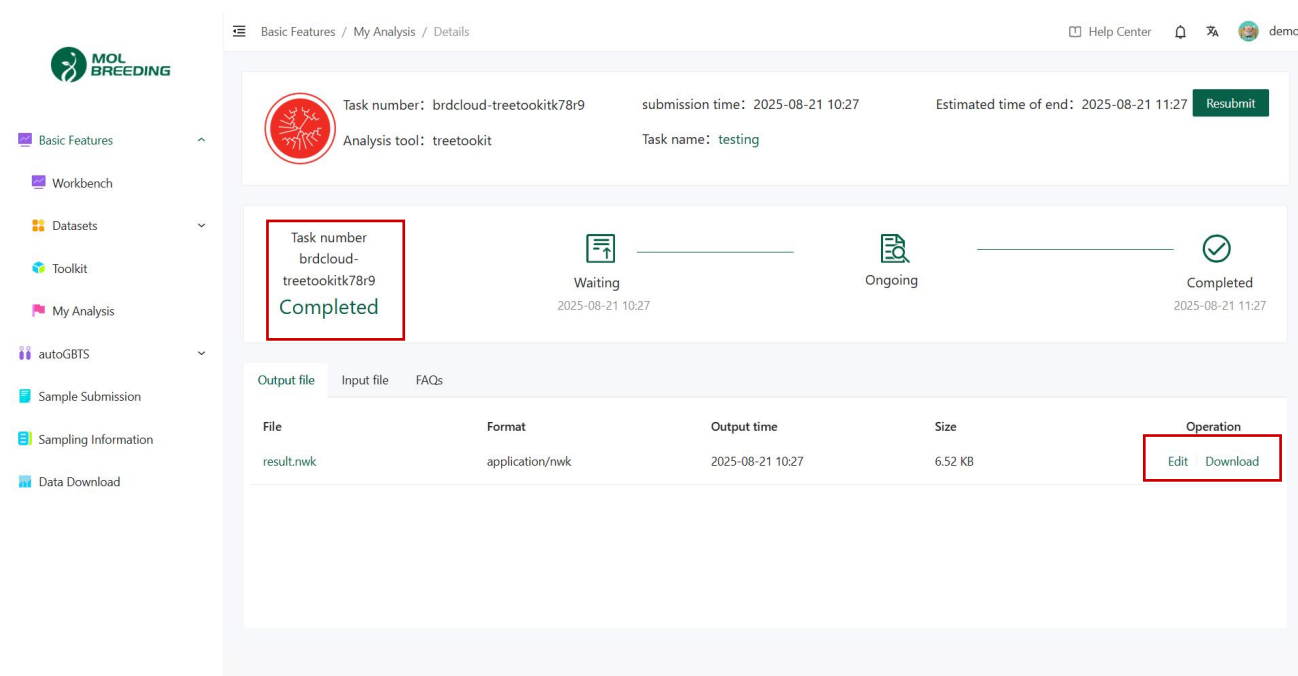
My Analysis

All analysis (18) Waiting (0) Ongoing (0) Completed (18) Failed 0

Task name: Search for task name Analysis tool: Analysis tool Submission date: Submission date Search Reset

| Task number | Task name | Analysis tool | submission time | Status | Operation |
|------------------------------|-------------------------------|-----------------------|------------------|-----------|----------------|
| brdcloud-treetookitk78r9 | testing | Phylogenetic analysis | 2025-08-21 10:27 | Completed | Details Delete |
| brdcloud-pcftp429 | 1 | PCA dynamic rendering | 2025-07-29 09:13 | Completed | Details Delete |
| brdcloud-treetookith854r | phylogenetic-Maize 10K Panel | Phylogenetic analysis | 2025-07-17 13:52 | Completed | Details Delete |
| brdcloud-biofileconvertmxz7r | MolBreeding_Maize1K-PLINK ... | File format converter | 2025-07-16 12:32 | Completed | Details Delete |
| brdcloud-biofileconvert492vj | MolBreeding_Maize1K-MEGA | File format converter | 2025-07-16 12:24 | Completed | Details Delete |
| brdcloud-biofileconvert7942 | Molbreeding-Maize1K-HapM... | File format converter | 2025-07-16 12:19 | Completed | Details Delete |

Total 18 1 2 > 10 / page Go to



Basic Features / My Analysis / Details

Task number: brdcloud-treetookitk78r9 submission time: 2025-08-21 10:27 Estimated time of end: 2025-08-21 11:27 Resubmit

Analysis tool: treetookit Task name: testing

Task number: brdcloud-treetookitk78r9 Completed

Waiting 2025-08-21 10:27 Ongoing Completed 2025-08-21 11:27

Output file Input file FAQs

| File | Format | Output time | Size | Operation |
|------------|-----------------|------------------|---------|---------------|
| result.nwk | application/nwk | 2025-08-21 10:27 | 6.52 KB | Edit Download |