

Species Taxonomy Quick Start Guide

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Home

① Global Species Search

Enter the taxonomy ID or species name of the species and click the "Search" button to quickly access the detailed information page of the species.

② Species Classification Search

Provide direct entry points for Taxonomy List Search, Structured Tree Search, and Tree Level Search. Click to jump to the corresponding page.

③ Species Evolution Module

Supports four mainstream algorithms: Clustal Omega, MAFFT, Kalign, and MUSCLE. Click "Enter Construction Module" to enter the multi sequence alignment page.

④ Auxiliary Search Tool

Taxonomy Changelog Search retrieves historical iteration records of specific species; Lowest Common Ancestor Calculation supports inputting multiple species to quickly calculate and locate their lowest common ancestor node in the lineage relationship.

⑤ Platform Information Area

Popular Species: A popular species card that provides frequent access to the platform, click to quickly enter its details page.

News & Updates: Display the latest system announcements, update logs, and related dynamic information of the platform.

Species Taxonomy

classification and nomenclature for Species, with species search, lineage retrieval, taxonomy updates and phylogenetic analysis in a cleaner research-oriented workflow.

Search

e.g., "9606" or "Homo sapiens"

① Global Species Search

Species Classification ② Species Classification Search

Taxonomy List Search

Supports species list search by species ID or species name.

Tree Level Search

Build a taxonomic tree with a specified depth, using a selected species as the root node.

Structured Tree Search

Supports building taxonomic trees from Newick-formatted structured data, for example, (A,B,(C,D)E)F;.

Species Evolution ③ Species Evolution Module

Phylogenetic Tree Construction

Supports phylogenetic tree construction based on multiple sequence alignment using four types of algorithms: HMM-based methods, FFT-based methods, sequence embedding strategies, and iterative methods.

Clustal Omega

MAFFT

Kalign

MUSCLE

Enter Construction Module

Taxonomy Changelog Search

Retrieves species update records to help track changes in classification and nomenclature.

④ Auxiliary Search Tool

Lowest Common Ancestor Calculation

Calculates the lowest common ancestor of multiple query species to quickly assess lineage relationships.

⑤ Platform Information Area

Popular Species

Provides quick access to popular species, with one-click navigation to the details page.

Archaea

ID: 2157

domain

Homo sapiens

ID: 9606

species

Fructilactobacillus fructivorans

ID: 1014

species

News & Updates

Provides news and updates related to the platform.

The taxonomy is now unavailable online.

2026-04-09

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Species Classification Search

Taxonomy List Search

① Species Search

Enter the Taxonomy ID or species name, and click the "Search" button on the right to search; Below the search box, quick tags for "related species" will be automatically recommended. Click on any tag to perform a search with just one click.

② Search Result List

Display the search results in a paginated table format, and click on the Taxonomy ID to jump to the detailed information page of the species.

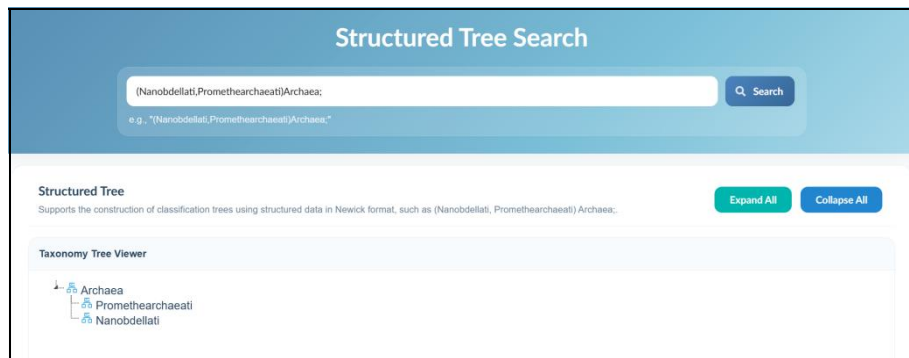
The screenshot displays the 'Taxonomy List Search' interface. At the top, there is a search bar containing the text '9606' and a 'Search' button. Below the search bar, a section titled 'related species:' contains several tags: 'Homo', 'Homo sapiens neanderthalensis', 'Homo sapiens subsp. 'Denisova'', 'Homo heidelbergensis', 'environmental samples', and 'unclassified Homo'. A red box highlights the search bar and the 'related species' section. Below this, a section titled '9606 in Taxonomy Resources' contains a 'Search Result List' link. The search results are displayed in a table with the following columns: 'Taxonomy ID', 'Scientific Name', 'Common Name', 'Rank', and 'Lineage'. The table shows one entry for 'Homo sapiens' with a rank of 'species'. The 'Lineage' column contains a detailed list of taxonomic groups: 'cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcoplerygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo;'. The table is paginated, showing 'Showing 1 to 1 of 1 entries' and 'Previous 1 Next' buttons.

Taxonomy ID	Scientific Name	Common Name	Rank	Lineage
9606	Homo sapiens	-	species	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcoplerygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Euarchontoglires; Primates; Haplorhini; Simiiformes; Catarrhini; Hominoidea; Hominidae; Homininae; Homo;

Structured Tree Search

Enter string text in Newick format (e.g. (Nanobdellati, Promethearchaeati) Archaea;), Click the "Search" button on the right, and the system will automatically parse the input data format and generate the corresponding tree structure.

Click the "Expand All / Collapse All" button to expand and collapse the tree, and click on a node in the tree to jump to the detailed information page of the corresponding species.



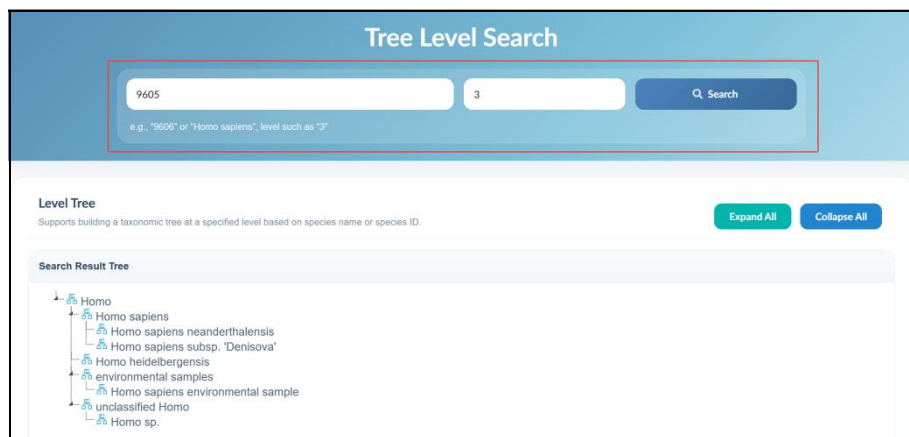
Tree Level Search

① Search Settings

Enter the Taxonomy ID or species name, specify the level to query, click the "Search" button, and the corresponding taxonomy tree will be displayed below.

② Taxonomy Tree Operation

Click the icon next to the node to manually expand/collapse the branches step by step. Click the "Expand All/Collapse All" button to control the tree with one click. Click on the node of the tree to jump to the detailed information page of the corresponding species.



Taxonomy Changelog

Enter the species taxonomy ID or species name, click the "Search" button, and display the update iteration records of the species in a paginated table format, including update time, update content, etc.

Taxonomy Changelog Search

Q Search

e.g., "9606" or "Homo sapiens"

Taxonomy changelog for Archaea

Changelog Table

Show **10** entries
Search:

Taxonomy ID	Version	Change type	Change value	Name	Taxonomy Rank	Lineage	Lineage Taxids
2157	2025-04-01	CHANGE_RANK	-	Archaea	domain	cellular organisms; Archaea	131567; 2157
2157	2014-08-01	NEW	-	Archaea	superkingdom	cellular organisms; Archaea	131567; 2157

Showing 1 to 2 of 2 entries

Previous
1
Next

Lowest Common Ancestor Calculation

Enter at least two species taxonomy IDs (e.g. 9606; 10090; 7955, separated by semicolons in English), click the "Search" button, and the system will perform a comparison calculation and display the lowest common ancestor information in the "Search Results" panel in the middle:

- ① Click on the taxonomy ID to view more species information
- ② Click on the genetic code to jump to the genetic code page
- ③ Click on the species lineage to jump to the species details page
- ④ Click on the reference to jump to OpenLB and view the specific content

The bottom of the page provides quick input sample cards for four typical biological groups, including primates, marine organisms, crops, and pathogens.

Calculation of the Lowest Common Ancestor

Q Search

Enter at least two species IDs, separated by semicolons, for example: 9606;10090;7965

Search result

Lowest common ancestor: Euarchontoglires (Taxonomy ID: 314146)

Euarchontoglires

Taxonomy ID: 314146

Click to view more species information

Basic Information

Current Name

Euarchontoglires

Rank

superorder

Genetic Code

Genetic Code

Translation table 1 (Standard)

Atx = FFLSSSTT**CCWLLLLLFFPPBBQRERIIINNTTTNNKESRRVVVYAAAGDEGGG
Startx = ————+—————+—————+—————+

Mitochondrial Genetic Code

Tranlation table 2 (Vertebrate Mitochondrial)

Atx = FFLSSSSTT**CCWLLLLLFFPPBBQRERIIINNTTTNNKES**YYVYAAAGAAGEGGG
Startx = ——++-----+-----+---+-----+

Click to jump to the genetic code page

Other Names

Scientific Name

Euarchontoglires

Lineage

Metazoa

Chordata

Mammalia

Click to jump to the detailed information page of species

Full Lineage

cellular organisms

Eukaryota

Opisthokonta

Metazoa

Eumetazoa

Bilateria

Deuterostomia

Chordata

Cranialta

Vertebrata

Gnathostomata

Teleostomi

Euteleostomi

Sarcopterygii

Dipnotetrapodomorpha

Tetrapoda

Amniota

Mammalia

Theria

Eutheria

Boreoeutheria

Comments and Reference

A new phylogenetic marker, apolloprotein B, provides compelling evidence for eutherian relationships (2003).

Rabbits, if anything, are likely Glires (2004).

Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear gene

Molecular phylogenetics and the origins of placental mammals (2001).

Click to jump to OpenLB

Examples → Quick Input Sample

Primates

Humans, Chimpanzees, Macaques

TaxID: 9606;9598;9544

Marine life

Zebrafish, Pufferfish, Flounder

TaxID: 7955;31033;8267

Crops

Wheat, Rice, Soybeans

TaxID: 4565;4530;3847

Pathogen

COVID-19, Influenza, HIV

TaxID: 2697049;11320;11676

Species Detailed Information Page

① Basic Information and Lineage

The left side of the page provides a hierarchical tree structure of the species, which can be quickly browsed through its upper and lower categories by "Expand All/Collapse all";

Intuitively display the current scientific name, rank, taxonomy ID, common name, and complete taxonomic evolution path of the species, and the lineage tags can be searched by clicking.

② Genetic Code and Online Analysis

Provide the standard amino acid translation table and mitochondrial genetic code table for the species, click to jump to the genetic code page; Click the "BLAST all sequences" button in the upper right corner to quickly perform sequence similarity search.

The screenshot displays the 'Species Detailed Information Page' for *Homo sapiens*. The page is divided into two main sections: 'Taxonomy Tree' on the left and 'Taxonomy Detail' on the right.

Taxonomy Tree: This section shows a hierarchical tree structure. It includes buttons for 'Expand All' and 'Collapse All'. The tree lists 'Homo sapiens', 'Homo sapiens neanderthalensis', and 'Homo sapiens subsp. 'Denisova''.

Taxonomy Detail: This section provides detailed information about the species.

- Header:** Displays 'Homo sapiens' with a star icon and a 'Click to jump to BLAST' link. A 'BLAST all sequences' button is also present.
- Basic Information:** Includes 'Current Name' (Homo sapiens), 'Rank' (species), and 'GenBank Common Name' (human).
- Genetic Code:** Contains 'Genetic Code' and 'Translation table 1 (Standard)'. A red box highlights this section with the text 'Click to jump to the genetic code page'.
- Other Names:** Includes 'Scientific Name' (Homo sapiens) and 'Authority Name' (Homo sapiens Linnaeus, 1758).
- Lineage:** A red box highlights the lineage path: Metazoa > Chordata > Mammalia > Primates > Hominidae > Homo.
- Full Lineage:** A list of taxonomic levels: cellular organisms, Eukaryota, Opisthokonta, Metazoa, Eumetazoa, Bilateria, Deuterostomia, Chordata, Craniata, Vertebrata, Gnathostomata, Teleostomi, Euteleostomi, Sarcopterygii, Dipnotetrapodomorpha, Tetrapoda, Amniota, Mammalia, Theria, Eutheria, Boreoeutheria, Euarchontoglires, Primates, Haplorhini, Simiiformes, Catarrhini, Hominoidea, Hominidae, Hominoidea, Homo.

③ User evaluation interaction

After logging in, there is an asterisk next to the species name at the top of the page (★) Icon, click to expand interactive menu:

Taxonomy Detail

Homo sapiens ★

Taxonomy ID: 9606

Basic Information

Current Name: *Homo sapiens*

Rank: species

GenBank Common Name: human

BLAST all sequences

Comment

View comments

Comment: Rate the species with a star rating (1-5 stars) in the pop-up window, and support detailed comments of up to 500 words.

Comment Species ×

Taxonomy Name

Homo sapiens

Taxonomy ID

9606

Select star rating

★ ★ ★ ★ ★

Comment Content

Please enter your review, up to 500 characters

0/500

Cancel Submit Commit

View comments: Open the comment list panel and browse other users' comments and rating records for this species.

List of Species Comment

Taxonomy Name

Archaea

Taxonomy ID

2157

Show 10 entries

Search:

Rating	Comment Content	Comment Time
★★★★★	测试	2026-04-20 07:01:20

Showing 1 to 1 of 1 entries

Previous

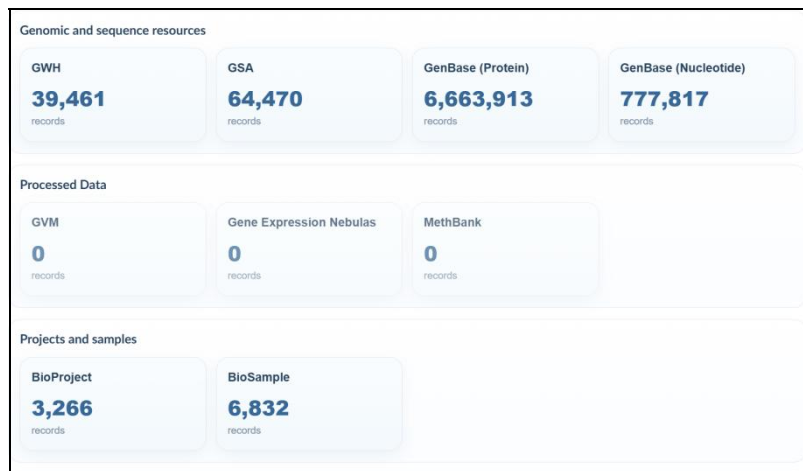
1

Next

Close

④ Linking data resources and literature

NGDC Resource Statistics Dashboard: The data volume of this species in various databases of the platform has been classified and summarized, including but not limited to genome and sequence resources (GWH, GSA, GenBase), processed data (GVM, MethBank, etc.), and project/sample libraries (BioProject, BioSample). Click on the blue number on the card to jump to the corresponding database and view detailed records.



Other data links

Show entries Search:

Database	Records	Description
OpenLB	22431	Publication, education and data
DMS_BV_BRC_bacteria	9680	The Bacterial and Viral Bioinformatics Resource Center (BV-BRC) is an information system designed to support research on bacterial and viral infectious diseases. BV-BRC combines two long-running BRCs: PATRIC, DMS_BV_BRC_bacteria is the bacterial system, and IRD/VIIPR
Database Commons	285	a curated catalogue of biological databases.
NODE	279	The National Omics Data Encyclopedia
DMS_MeSH	85	MeSH (Medical Subject Headings) is the NLM controlled vocabulary thesaurus used for indexing articles for PubMed.
DMS_Ontobee	45	Ontobee is a linked ontology data server that stores ontology information using RDF triple store technology and supports query, visualization and linkage of ontology terms and is also the default linked data server for publishing and browsing biomedical ontologies in the Open Biological Ontology (OBO) Foundry (OBO) library.
BioCode	22	a repository archiving codes for bioinformatics tools
eLMSG	13	An eLibrary of Microbial Systematics and Genomics
DMS_Chemical Entities of Biological Interest Ontology	6	Chemical Entities of Biological Interest (ChEBI) is a freely available dictionary of molecular entities focused on 'small' chemical compounds.
DMS_PMO	6	a standardized ontology for human precision medicine with consistent, reusable and sustainable descriptions of human disease terms, genomic molecular, phenotype characteristics and related medical vocabulary disease concepts through collaborative efforts of researchers at Institute of Medical Information, Chinese Academy of Medical Sciences.

Showing 1 to 10 of 17 entries

Previous [1](#) [2](#) Next

External and Extended Data Links: integrated external authoritative databases such as Wikipedia and UCSC Genome Browser with jump links in a table format.

External Information Resources for *Archaea*

Show entries Search:

LinkOut	Subject	LinkOut Provider
Wikipedia	taxonomy/phylogenetic	iPhylo
UCMP	taxonomy/phylogenetic	UCMP phylogeny exhibit
ToL	taxonomy/phylogenetic	Tree of Life
The Prokaryotes	taxonomy/phylogenetic	NCBI taxonomy bookmarks
SILVA rRNA database	taxonomy/phylogenetic	NCBI taxonomy bookmarks
Show Biotic Interactions	taxonomy/phylogenetic	Global Biotic Interactions
RDP II	taxonomy/phylogenetic	NCBI taxonomy bookmarks
OMA	taxonomy/phylogenetic	OMA Browser: Orthologous MATrix
Monera	taxonomy/phylogenetic	Integrated Taxonomic Information System
IJSEM	taxonomy/phylogenetic	NCBI taxonomy bookmarks

Showing 1 to 10 of 39 entries

Previous [1](#) [2](#) [3](#) [4](#) Next

References: A list of key academic literature supporting the current taxonomic status and naming of the species has been compiled.

Comments and Reference

[Woese CR & Fox GE \(1977\)](#)

[Click to jump to OpenLB](#)

Woese, C.R., and Fox, G.E. "Phylogenetic structure of the prokaryotic domain: the primary kingdoms." *Proc. Natl. Acad. Sci. U S A* (1977) 74:5088-5090.

[Murray RG & Schleifer KH \(1994\)](#)

Murray, R.G., and Schleifer, K.H. "Taxonomic notes: a proposal for recording the properties of putative taxa of procaryotes." *Int. J. Syst. Bacteriol.* (1994) 44(1):174-176.

[Clayton RA et al. \(1995\)](#)

Clayton, R.A., Sutton, G., Hinkle, P.S. Jr, Bult, C., and Fields, C. "Intraspecific variation in small-subunit rRNA sequences in GenBank: why single sequences may not adequately represent prokaryotic taxa." *Int. J. Syst. Bacteriol.* (1995) 45:595-599.

[Palys T et al. \(1997\)](#)

Palys, T., Nakamura, L.K., and Cohan, F.M. "Discovery and classification of ecological diversity in the bacterial world: the role of DNA sequence data." *Int. J. Syst. Bacteriol.* (1997) 47:1145-1156.

[Euzéby JP \(1997b\)](#)

Euzéby, J.P. "List of Bacterial Names with Standing in Nomenclature: a folder available on the Internet." *Int. J. Syst. Bacteriol.* (1997) 47:590-592.

[Tindall BJ \(1999e\)](#)

Except for the display and click operation of the taxonomy tree, the rest of the content in this module is consistent with the corresponding content on the Species Details page. The complete classification tree displays all species by default, and clicking on a node can view its detailed information. Double click a node to expand or collapse its child nodes.

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Phylogenetic Tree

Clustal Omega

- ① Choose the type of sequence to input
- ② Choose the method of sequence input

Input sequences: Click on the sample to quickly fill in the test sequence, click on clear sequence to clear with one click;

Upload a file: Click to open the file and upload the local sequence file.

Note: The sequence format only supports fasta format.

- ③ Select the corresponding parameters based on the actual situation
- ④ Fill in the title and valid email address
- ⑤ After confirming that the sequence and parameters are correct, submit the task

The screenshot displays the Clustal Omega web interface. At the top, the title 'Clustal Omega' is followed by a brief description: 'Clustal Omega is a multiple sequence alignment program that uses seeded guide trees and HMM profile-profile techniques to generate alignments for three or more sequences. This tool can align up to 4000 sequences or a maximum file size of 4 MB.' Below this, the 'Input sequences' section is expanded, showing options for 'Sequence type' (Protein, DNA, RNA) and 'Input type' (Input sequences, Upload a file). A large text area for 'Input sequences' is provided, with 'Example' and 'Clear Sequences' buttons. The 'Parameters' section is also expanded, showing various settings: 'OUTPUT FORMAT' (ClustalW with character counts), 'DEALIGN INPUT' (No), 'MBED-LIKE CLUSTERING GUIDE-TREE' (No), 'MBED-LIKE CLUSTERING ITERATION' (No), 'COMBINED ITERATIONS' (default(0)), 'MAX GUIDE TREE' (default), 'MAX HMM ITERATIONS' (default), 'ORDER' (aligned), 'DISTANCE MATRIX' (No), and 'OUTPUT GUIDE TREE' (Yes). The 'Submit' section is expanded, showing fields for 'Input Title' and 'Email', with a 'Submit' button and a 'Submit task' link.

MAFFT

- ① Choose the type of sequence to input
- ② Choose the method of sequence input

Input sequences: Click on the sample to quickly fill in the test sequence, click on clear sequence to clear with one click;

Upload a file: Click to open the file and upload the local sequence file.

Note: The sequence format only supports fasta format.

- ③ Select the corresponding parameters based on the actual situation
- ④ Fill in the title and valid email address
- ⑤ After confirming that the sequence and parameters are correct, submit the task

The screenshot shows the MAFFT web interface. At the top, there's a header with the MAFFT logo and a brief description. Below this, there are two main sections: 'Input sequences' and 'Parameters'. The 'Input sequences' section has a dropdown for 'Sequence type' (Automatic, Protein, DNA) and a dropdown for 'Input type' (Input sequences, Upload a file). There's a text area for 'Input sequences' with 'Example' and 'Clear Sequences' buttons. The 'Parameters' section has several dropdown menus for 'OUTPUT FORMAT', 'MATRIX (PROTEIN ONLY)', 'GAP OPEN PENALTY', 'GAP EXTENSION PENALTY', 'ORDER', 'TREE REBUILDING NUMBER', 'GUIDE TREE OUTPUT', 'MAX ITERATE', and 'PERFORM FFTS'. At the bottom, there's a 'Submit' section with 'Input Title' and 'Email' fields, and a 'Submit' button.

Kalign

- ① Choose the type of sequence to input
- ② Choose the method of sequence input

Input sequences: Click on the sample to quickly fill in the test sequence, click on clear sequence to clear with one click;

Upload a file: Click to open the file and upload the local sequence file.

Note: The sequence format only supports fasta format.

- ③ Select the corresponding parameters based on the actual situation
- ④ Fill in the title and valid email address
- ⑤ After confirming that the sequence and parameters are correct, submit the task

Kalign
Kalign is a fast and accurate multiple sequence alignment algorithm. This tool can align up to 2000 sequences or a maximum file size of 2 MB.

▼ Input sequences ①

Sequence type: ☒ Protein ☐ DNA ☐ RNA ① Choose sequence type

Input type: ☒ Input sequences ☐ Upload a file ② Choose input type

Input sequences: Example Clear Sequences

Enter sequences here...

▼ Parameters ③ Select parameters

OUTPUT FORMAT: ClustalW

GAP OPEN PENALTY: 11

GAP EXTENSION PENALTY: 0.85

TERMINAL GAP PENALTIES: 0.45

▼ Submit ④ Fill in title and email

Input Title: Please input a title

Email: Please input email

Submit ⑤ Submit task

MUSCLE

- ① Choose the method of sequence input

Input sequences: Click on the sample to quickly fill in the test sequence, click on clear sequence to clear with one click;

Upload a file: Click to open the file and upload the local sequence file.

Note: The sequence format only supports fasta format.

- ② Select the corresponding parameters based on the actual situation
- ③ Fill in the title and valid email address
- ④ After confirming that the sequence and parameters are correct, submit the task

MUSCLE
MUSCLE stands for Multiple Sequence Comparison by Log-Expectation. MUSCLE is designed to provide both strong average accuracy and high speed compared with older multiple sequence alignment tools. This tool can align up to 500 sequences or a maximum file size of 1 MB.

▼ Input sequences ①

Input type: ☒ Input sequences ☐ Upload a file ① Choose input type

Input sequences: Example Clear Sequences

Enter sequences here...

▼ Parameters ② Select parameters

OUTPUT FORMAT: ClustalW

OUTPUT TREE: none

▼ Submit ③ Fill in title and email

Input Title: Please input a title

Email: Please input email

Submit ④ Submit task

Recent Tasks

① Task Search

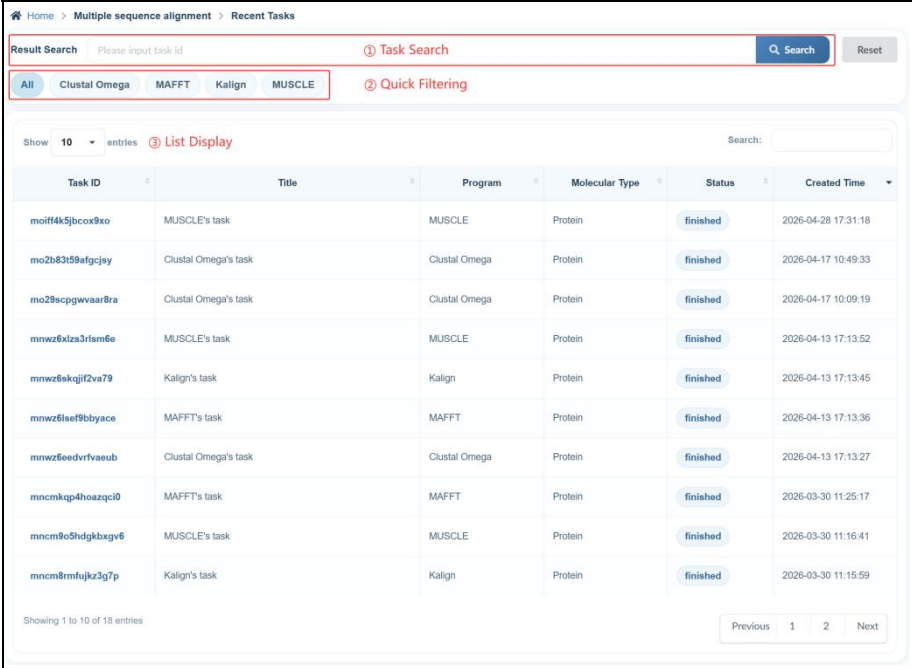
Enter the specific task ID in the "Result Search" input box at the top, and click the "Search" button to accurately locate the task. Click 'Reset' to clear the current input.

② Quick Filtering

Use the program tags below (All, Clustal Omega, MAFFT, Kalign, MUSCLE) to quickly filter tasks generated by specific alignment tools.

③ List Display

Display task information in a paginated table format, including task number, title, program used, molecular type, running status, and creation time. Click on the corresponding task ID to jump to the detailed results page of the task.



The screenshot shows the 'Recent Tasks' interface. At the top, there is a 'Result Search' input field with a 'Search' button and a 'Reset' button. Below the search bar are filter tabs: 'All', 'Clustal Omega', 'MAFFT', 'Kalign', and 'MUSCLE'. The 'All' tab is selected. Below the filters, there is a 'Show 10 entries' dropdown and a 'List Display' link. The main table has columns: Task ID, Title, Program, Molecular Type, Status, and Created Time. The table contains 10 rows of task data, all with a 'finished' status. At the bottom, there is a pagination bar showing 'Showing 1 to 10 of 18 entries' and buttons for 'Previous', '1', '2', and 'Next'.

Task ID	Title	Program	Molecular Type	Status	Created Time
moiff4k5jbcox9xo	MUSCLE's task	MUSCLE	Protein	finished	2026-04-28 17:31:18
mo2b83t59afgcjey	Clustal Omega's task	Clustal Omega	Protein	finished	2026-04-17 10:49:33
mo29ecpgwvaar8ra	Clustal Omega's task	Clustal Omega	Protein	finished	2026-04-17 10:09:19
mnwz6xza3rlsm6e	MUSCLE's task	MUSCLE	Protein	finished	2026-04-13 17:13:52
mnwz6skqjlf2va79	Kalign's task	Kalign	Protein	finished	2026-04-13 17:13:45
mnwz6lsef9bbyace	MAFFT's task	MAFFT	Protein	finished	2026-04-13 17:13:36
mnwz6eedvrfvaeub	Clustal Omega's task	Clustal Omega	Protein	finished	2026-04-13 17:13:27
mncmkqp4hoazqc0	MAFFT's task	MAFFT	Protein	finished	2026-03-30 11:25:17
mncm9e5hdgkxbgv6	MUSCLE's task	MUSCLE	Protein	finished	2026-03-30 11:16:41
mncm8mfujkz3g7p	Kalign's task	Kalign	Protein	finished	2026-03-30 11:15:59

Task Results

① Basic information and parameters

Quick Navigation: The upper right corner provides a toolbar that allows for quick switching to submission pages for different comparison tools.

Task Overview: Display the unique identifier of the task (supports one click copying by clicking the icon next to it), title, user program, and specific running time. Provide quick viewing links for raw input data and

system standard output.

Execute Command: Recorded the complete command-line code for executing the comparison task in the background.

Operating Parameters: List all parameter configurations applied to the current task at the time of submission, such as molecular type, output format, iteration settings, etc.

Submission Details

Task ID

mkevjf2mvihoxp5g

Title

Clustal Omega's task

Program

Clustal Omega

Runtime

2026-01-15 11:12:37.540
2026-01-15 11:12:39.969

Input

[mkevjf2mvihoxp5g.input](#)

Output

[mkevjf2mvihoxp5g.output](#)

① Basic Submission Information

Command

```
#!/bin/sh
toolPath=D:/BioTools/clustalo
taskPath=D:/BioTools/task/clustalo
taskId=mkevjf2mvihoxp5g
cd ${toolPath}
./clustalo -i ${taskPath}/${taskId}/input.fasta --output-order=tree-order --guidetree-out=${taskPath}/${taskId}/guide_tree.dnd --outfmt=clustal --resno -o
${taskPath}/${taskId}/output.clustal --log ${taskPath}/${taskId}/clustalo.log -v
```

② Execute Command

Parameters

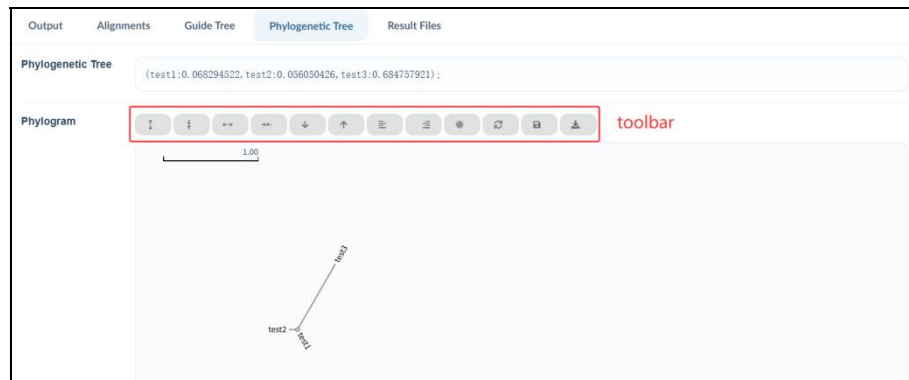
Molecular Type	Protein
OUTPUT FORMAT	ClustalW with character counts
DEALIGN INPUT	No
MBED-LIKE CLUSTERING GUIDE-TREE	No
MBED-LIKE CLUSTERING ITERATION	No
COMBINED ITERATIONS	default(0)
MAX GUIDE TREE	default
MAX HMM ITERATIONS	default
ORDER	aligned
DISTANCE MATRIX	No
OUTPUT GUIDE TREE	Yes

③ Operating Parameters

② Visualization Results Panel

Result output:

- Tool output: Display the native plain text comparison results generated by the comparison tool, supporting one click download.
- Alignment with colours: Provide simple highlight coloring comparison text based on the physicochemical properties of residues.



Result Files:

- Display all process files and final data generated by the comparison task, and click the download button on the right to download files in a specific format.

Output	Alignments	Guide Tree	Phylogenetic Tree	Result Files
Tool Output				mkgnlguh5286pu0.out Download
Input Sequences				mkgnlguh5286pu0.sequence Download
Alignment in CLUSTAL format				mkgnlguh5286pu0.aln-clustalw Download
Guide Tree				mkgnlguh5286pu0.tree Download
Phylogenetic Tree				mkgnlguh5286pu0.phylo tree Download
Percent Identity Matrix				mkgnlguh5286pu0.pim Download
The alignment in FASTA format				mkgnlguh5286pu0.fa Download
Tool outputs as a single compressed zip file				mkgnlguh5286pu0.zip Download

Sign in / Sign up

Sign in

Click the "Sign in" button in the upper right corner of the homepage, and the system will automatically redirect to the NGDC CAS unified authentication login page. Enter your email or username, password, and verification code in sequence, and click the login button to complete the login. After successful login, you can view your personal information.

The image displays three screenshots of the Species Taxonomy website and its authentication interface.

Top Screenshot: The homepage of the Species Taxonomy website. The header includes navigation links: Search, Taxonomic Tree, Phylogenetic Tree, Visualization, help, 中文 | English, and a Sign in button (highlighted with a red box). The main content area features a search bar and three search options: Taxonomy List Search, Tree Level Search, and Structured Tree Search.

Middle Screenshot: The NGDC CAS Central Authentication Service login page. It includes fields for Email or Username, Password, and Check Code (with a captcha). There are buttons for Login, Reset, and Sign up Personal Account. A sidebar on the right provides links to various services: BIG Sub, BioProject, BioSample, BioCloud, BioCode, GenBase, China BioBank, GSA for Human, Request Center, CNCB Cloud Platform, Database Commons, Genome Sequence Archive (GSA), Genome Warehouse (GWH), Genome Variation Map (GVM), Open Archive for Miscellaneous Data (OMIX), Scientific Data Archive System (SDAS), and The Immunity Deciphering Project (IDP).

Bottom Screenshot: The Species Taxonomy homepage after successful login. The Sign in button has been replaced by a user profile icon and a Sign out button (highlighted with a red box). The user's email address, zhengbo@big.ac.cn, is displayed next to the profile icon.

Sign up

Click the "Sign up" button in the upper right corner of the homepage to enter the NGDC unified registration page. Fill in the account login information, personal information, institution information, enter the characters displayed in the image on the right, confirm that all information is filled in correctly, and then click the submit button. If you need to clear the current form and fill it out again, you can click the reset button.

Welcome to Register for a Personal Account

[English](#)

Account Information

Email *
You can choose to use your email as the email address associated with your account. This email will be used to receive account-related information, updates, and notifications. If you don't choose the email address, please enter your phone number and select your preferred contact method.

User Name *
Username length should be between 4-16 characters. Only alphanumeric characters and underscores are allowed. The user cannot use the illegal symbols, and the password will contain uppercase and lowercase letters.

Password *
Minimum 8 characters, including uppercase letters, lowercase letters, numbers, and special characters, and must be different from the email address.

Confirm Password *

Personal Information

First Name *
(Required)

Last Name *
(Required)

Country / Region *
(Required)

Date of Birth *
(Required)

Address *
(Required)

Phone *
(Optional)

Postal Code *
(Optional)

Institution Information

Institution Name (Chinese) *
Please fill in the Chinese name of your institution. Do not use abbreviations or short names. Please make the name clear and use the official website or official introduction.

Institution Name (English) *
Please fill in the English name of your institution. Please use the English name of the institution. Please make the name clear and use the official website or official introduction.

Department / School *
(Optional)

Laboratory *
(Optional)

Professional Title *
(Optional)

Research Area *
(Optional)

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