

The BLAST-Like Alignment Tool

BLAT is the BLAST-like alignment tool, designed to find regions of similarity between query and target sequences, which is characterized by its high speed.

Usage:

1. Select the sequence type.
2. Paste the sequence to be queried in the sequence box or upload the sequence file.
3. Select the species, database type and output format. Click "Submit" to submit.

Enter Query Sequence

Please select the sequence type: DNA ▼ **← Select the sequence type**

Paste the sequence

Example

Sequence File (in FASTA): 选择文件 未选择任何文件 **← Upload the sequence file**

Choose Search Set

Choose species : MSU7 ▼ The Database Type: genome ▼

Output format : Tab separated format, no sequence ▼ **← Select the species, database type and output format**

Submit Reset

↑
Click to submit

Results:

1. The blat result. Click the link to download the result file.

The Blat Result :

Loaded 373245519 letters in 12 sequences Searched 2011 bases in 3 sequences



[Click here to download the blast results.](#)

← Click here to download