

# Jpred 4

Incorporating Jnet

## Submitting multiple sequence alignment



# Submitting MSA to JPred

## Jpred 4 Incorporating Jnet

A Protein Secondary Structure Prediction Server

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**Input sequence** [\(?\)](#)

MQVWPPIEGIKKFETLSYLPLTVEDLLKQIEYLLRSKWVPCLEFSKVGFWRENHRSPGYYDGRYWT  
MWKLPFMFGCTDATQVLKELEEAKKAYPDAFVRIIGFDNVRQVQLISFIAYKPPGC

[Advanced options \(click to show/hide\)](#)

1. Click to show advanced options

**...or upload a file** [\(?\)](#)

[Choose File](#)

2. Upload file (see tool-tip help for details and example)

**Select type of input** [\(?\)](#)

Single Sequence (click to select format):

Multiple Alignment (click to select format):  MSF  BLC  Fasta

3. Click to show format options

**Skip searching PDB before prediction** [\(?\)](#)

Check to skip

4. Select format (MSA in FASTA format used in this example)

**Email address (optional)** [\(?\)](#)

5. Provide email optional in non-batch mode

**Query name (optional)** [\(?\)](#)

[Make Prediction](#)

[Reset Form](#)

6. Push to submit...

Primary citation: Drozdetskiy A, Cole C, Procter J & Barton GJ. Paper in preparation  
Previous: Cole C, Barber JD & Barton GJ. Nucleic Acids Res. 2008. 35 (suppl. 2) W197-W201 [\[link\]](#)  
More citations: [\[link\]](#)

# Input MSA file example

```
>QUERY
MQVWPIEGIKKFETLSYLPLTVEDLLKQIEYLLRSKWVPCLEFSKVGTVYRENHRSPGYYDGRYWTMWKLP
MFGCTDATQVLKELEEAKKAYPDAFVRIIGFDNVRQQLISFIAYKPPGC
>UniRef90_Q40250_2
MKVWPPIGLKKYETLSYLPLSDEALSKEIDYLIRNKWIPCLEFEEHGFVYREHHHSPGYYDGRYWTMWKLP
MFGCTDSAQMKEVGECKKEYPNAFIRVIGFDNIRQVQCISFIAKPPGV
>UniRef90_A7VW5_3
MQVWPPLGKRKFETLSYLPLPVDAALLKQIDYLIRSGWIPCIETVEGFVYREHHHSPGYYDGRYWTMWKLP
MYGCTDSTQVLAEVANEANKKEYPSYIRIIGFDNKRQVQCVSFIVHTPPS-
>UniRef90_P04714_4
MQVWPPYGKKYETLSYLPDLTDEQLLKEIEYLLNKGWVPCLEFTEHGFVYREYHASPRYYDGRYWTMWKLP
MFGCTDATQVLGELQEAKKAYPNAWIRIIGFDNVRQVQCISFIAYKPPG-
>UniRef90_W9RUU9_5
MQVWPPRGKLKFETLSYLPDLTDEQLLKEIDYLLRSNWIPCLEFEVKAHIYRENNRSPGYYDGRYWTMWKLP
MFGCTDATQVLAEVQETKKAYPDAHVRIIGFDNNRQVQCISFIAYKPPA-
>UniRef90_K3ZA66_6
MQVW-PIGGKKFETLSYLPLSTDLLKQIDYLIRKNWIPCLEFSKVGTVYRENNRSPGYYDGRYWTMWKLP
MFGCTEATQVYAELEECKKAYPDAYIRILGFDNVRQVQCIMFIAYKPPGC
>UniRef90_V4UWB0_7
MKVWPPTGLKKFETLSYLPLSDEALLKEISYLIIRSGWIPCLEFEEKGWVYREHHRSPGYYDGRYWTMWKLP
MYGCTDATQVLKEVGEVQKEYPHSFVRIIGFDNKRQVQCISFIAKPPGV
>UniRef90_A9PFS6_8
MQVWPPTGLKKFETLSYLPDLTEEEELAKEIDYLLRSKWVPCLEFEEKGWVYREHHSSPGYYDGRYWTMWKLP
MFGCTEASQVLLLEEAKKAYPNAFIRIIGFDNTRQVQCISFIAKPKGV
>UniRef90_Q9ZP07_9
MQVWPPIGKKFETLSYLPLTTEEQLLKEVEYLLRKGWVPCLEFEEKGFVYREHNNSPGYYDGRYWTMWKLP
LFGCTEAVQVLKELQEVVKAYPNAFVRIIGFDNVRQVQCISFIATHPK--
>UniRef90_Q96542_10
MQVWPPLGLKKFETLSYLPLSSEQLAKEVDYLLRKNLIPCLEFEEHGFVYREHNHRSPGYYDGRYWTMWKLP
MFGCNDSSQVLKELEECKKAYPSAFIRIIGFDNKRQVQIISFIAYKPPGV
>UniRef90_P08474_11
MKVWPPLGLRKFETLSYLPDMSNEQLSKEDCYLLRNNGWVPCVEFDISGFVYRENHRSPGFYDGRYWTMWKLP
MFGCTDSSQVIQEIEEAKKEYPDAFIRVIGFDNVRQVQCISFIAYKP--
```

Example of multiple sequence alignment input file (in FASTA format).