

Jpred 4

Incorporating Jnet

How to make a prediction
from a single sequence and
what the output means



Contents

1. Short Guide (two pages)
2. Detailed step-by-step tutorial with results overview

1. Short Guide (two pages)

How to run JPred

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1. Paste protein sequence

Input sequence(?)

Advanced options (click to show/hide)

- Make Prediction
- Reset Form

2. Push to submit...

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



Short Guide

- Submitting a single sequence for prediction is very easy:
 - Cut-paste the query sequence into the “Input sequence” field on the main page
 - Push “Make Prediction” button
- For more details on the format, process and results – see the more detailed tutorial below, as well as other tutorials and the Help/F.A.Q. JPred pages

2. Detailed step-by-step tutorial

Submission

www.compbio.dundee.ac.uk/jpred4/index.html

1. Jpred home page URL

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Input sequence^(?)

```
MQVWPIEGIKKFETLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKVG FVYRENHRSPGYDGRY  
WTMWKLPFMFGCTDATQVLKELEEAKKAYPDAFVRIIGFDNVRQVQLISFIAYKPPGC
```

Advanced options (click to show/hide)

Make Prediction

Reset Form

3. Push the "Make Prediction" button

2. Cut-paste the input sequence into the window.

Jpred requires input as either a single sequence, cut and pasted into the text box, or a multiple sequence alignment uploaded as a file (see the following pages). It is important not to cut and paste a multiple sequence alignment as the formatting can get messed up. When pasting in a sequence, do not add any comment or description lines, but spaces and carriage returns are allowed. You can also upload single sequences as files.

The upload option takes precedence if both inputs have been filled.

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

Please cite JPred if you use it in your work.



Searching the PDB

www.compbio.dundee.ac.uk/jpred4/cgi-bin/jpred_form

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1. By default Jpred searches the PDB before doing a prediction. If your sequence has sequence similarity to a protein of known 3D structure you should reconsider the utility of making a prediction.

The PDB is never searched with alignment or batch queries so this option is ignored for those input types.

Match found in PDB

You might want to reconsider the accuracy and what you might gain from secondary structure prediction, if close sequence homologues exist in the structural database.

If you still want to carry out a Jpred prediction click

2. Even if a PDB search yielded results you can force JPred to continue by pushing the button

Hits found

PDB	Chain	Description	Blast E-value
3axm	Z	Ribulose biphosphate carboxylase...	4e-70
3axm	Y	Ribulose biphosphate carboxylase...	4e-70
3axm	X	Ribulose biphosphate carboxylase...	4e-70
3axm	W	Ribulose biphosphate carboxylase...	4e-70

Advanced options

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Input sequence^(?)

MQVWPIEGIKKFKETLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKVGfVYRENHRSPGYDGRY
WTMWWKLPFMFGCTDATQVLKELEEAKKAYPDAFVRIIGFDNVRQVQLISFIAYKPPGC

Advanced options (click to show/hide)

...or upload a file^(?)

Choose File No file chosen

Select type of input^(?)

Single Sequence (click to select format): Raw/Fasta Batch Mode
Multiple Alignment (click to select format):

Skip searching PDB before prediction^(?)

Check to skip

Email address (optional)^(?)

a.drozdetskiy@dundee.ac.uk

Query name (optional)^(?)

TestName_17

Make Prediction

Reset Form

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



1. Click to show advanced options

2. Click to select input format (default is "Raw/Fasta" which is suitable for submission of single sequences)

3. Select this to skip the PDB search (see the previous page.)

4. Providing an (optional) e-mail address means you will be notified of the fate of your job. A simple summary of the result will be emailed to you when the prediction is complete. Please make sure your e-mail is valid and correct as the Jpred server will not check the validity of it.

5. Provide a (optional) name with which to identify your prediction. If no name is provided a randomly generated one will be used. Query names can only be made up of alphanumeric and '_' characters. Invalid characters will throw up an error. This option is probably not very useful if not used in conjunction with an e-mail address.

Tool-tips

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Input sequence(?)

```
MQVWPIEGIKKFETLSYLPLTVEDLLKQIEYLLRSKWVPCLEFSKVGfVYRENHRSPGYDGRY  
WTMWWKLPFMFGCTDATQVLKELEEAKKAYPDAFVRIIGFDNVRQVQLISFIAYKPPGC
```

Advanced options (click to show/hide)

...or upload a file (?) No file chosen

Select type of input (?) Single Sequence (click to select format): Raw/Fasta Batch Mode

Skip searching PDB before prediction (?)

Email address (optional) (?)

Query name (optional) (?)

Primary citation: Drozdetskiy et al. (2005) [\[link\]](#)
Previous: Cole C, Barber JD & Barton GJ (2008) [\[link\]](#)

Input Format Help

Jpred accepts four types of input (links to examples of each): [Show/hide more...](#)

[Raw](#) | [Fasta](#) | [MSF](#) | [BLC](#) | [Batch](#)

Batch submission of multiple sequences for individual secondary structure prediction is now possible via file upload. The file must be in Fasta format and each sequence must be given a unique name (up to 25 characters with no spaces). Additional words or descriptions on the define will be ignored. Batch jobs cannot be run interactively and results will be provided via e-mail only.

A limit of 200 sequences are allowed per batch submission. You may submit several batch jobs, but there is a hard limit of 4,000 sequence predictions in total per user per day. Please let us [know](#) if this limit is a problem for you and we'll look at temporarily changing it.

Wherever on the site you see “(?)” – if you hover/click on it – a tool-tip help will appear.

When the text of the help is long – you may see “show/hide more...” clicking on this will toggle the display of more text.

The tool-tip will disappear shortly after moving the cursor off the tool-tip field.



Job URL, submission/progress

www.compbio.dundee.ac.uk/jpred4/cgi-bin/chklog?jp_E_ntW2T

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Job Status

Your job is next to be submitted.

The current load on the server is: **Low**

If the job is taking too long it may be worth deleting and resubmitting it using an e-mail address: [delete job](#)

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



1. URL once job has started. Note the format: it is JPred main URL, followed by /cgi-bin/chklog?NAME, where 'NAME' – is the JPred generated random name for your job.

You can **bookmark** the URL and come back to it within two days (the time the JPred server stores results for you).

If you keep the page open – it will automatically reload showing **the job progress** and eventually – results.

2. JPred estimates how busy is the computer cluster and informs you on where your job is in the list.

3. At any stage of submission/running of the job, if you realize that a mistake was made and you like to cancel (re-submit) a job – you may delete the current job.

Job URL, submission/progress

www.compbio.dundee.ac.uk/jpred4/cgi-bin/chklog?keywords=jp_E_ntW2T

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Job Status

Your job (**jp_E_ntW2T**) started at 10:20 on 18/12/2014, the current time is 10:23 on 18/12/2014.

40% complete...



See below for a more detailed log of progress (use your back button to return):

[Log file](#)

If the job is taking too long it may be worth deleting and resubmitting it using an e-mail address: [delete job](#)



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

Summary email

If you provide an (optional) email address, you will receive an email with a short results summary and a link to all the results and files produced.

From www-jpred@compbio.dundee.ac.uk★

Subject Jpred job jp_E_ntW2T completed

To Alexey Drozdetskiy★

Your job has completed successfully and the prediction is summarised below:

Query: MQVWPIEGIKKFETLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKVGFBVYRENHRSPGY
Jpred: -----EEEE-----HHHHHHHHHHHHHH---EEEEEE-----
Conf: 885355677523211777776278999999998745872667743677765456677777

Query: YDGRYWTMWKLPFMFGCTDATQVLKELEEAKKAYPDAFVRIIGFDNVRQVQLISFIAKPP
Jpred: -----HHHHHHHHHHHHHH---EEEEEE-----EEEEEEEEEE---
Conf: 77766533567656776278999999998625885089987157631688999872588

Query: GC
Jpred: --
Conf: 99

The complete set of outputs can be viewed at:
http://www.compbio.dundee.ac.uk/jpred4/cgi-bin/chklog?jp_E_ntW2T

Results summary page

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- REST API
- About
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- Monitoring
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- Publications

1. Clicking on the link in the summary email, or using the URL from the job status/progress – see previous pages, or simply keeping the job status/progress page open – will provide you with the results summary page.

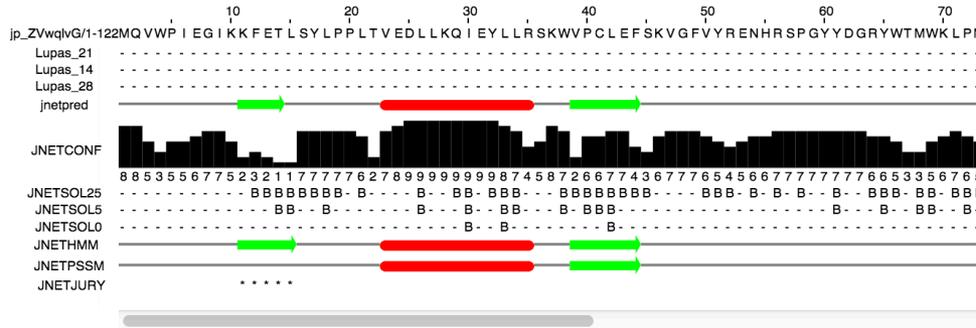
2. One of the new additions in JPred4 – is the SVG image of results summary generated using Jalview (see jalview.org).
Let's go through results JPred produces one by one.
NOTE: the screenshots shown are only parts of the results.

3. You may download all (but *.PS) results files using the link to the *.TAR.GZ archive for your job

Results

After much trouble and strife, Bob the scheduling penguin has retrieved your results! Rejoice. For your pleasure the following viewing options are available. You may bookmark this page for future reference although data is not kept on the server for more than two days.

- View results summary in SVG - displayed below (details on acronyms used):



- Get all (but PS) files in TAR.GZ archive
- View results using in-browser Jalview Java applet (light version, limited functionality w.r.t. Jalview Desktop version linked above)

This Jpred prediction was made with following.

Jnet version: 2.3.1
 UniRef90 release: 2014_07, 09-Jul-2014

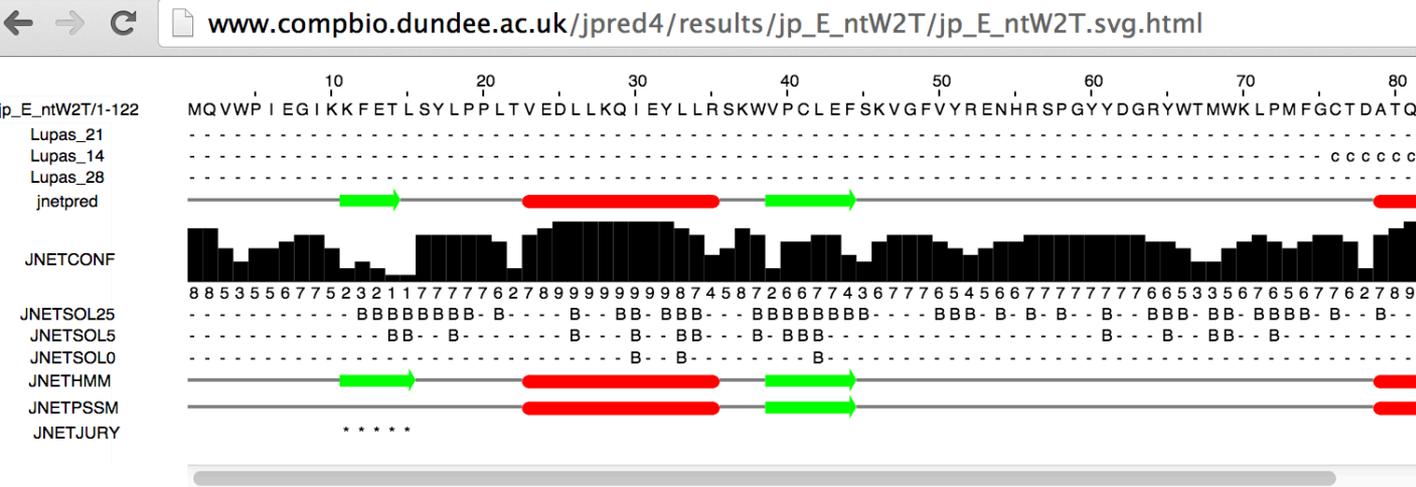


- View full results in HTML
- View simple results in HTML
- View results in PDF
- View results in Jalview (Link to a separate page with the Jalview Java Desktop application)
- View everything in a results directory (details on data each file contains are available through README file)

Primary citation: Drozdetskiy A, Cole C, Procter J & Barton GJ. Nucl. Acids Res. (first published online April 16, 2015) doi: 10.1093/nar/gkv332 [link]
 More citations: link.



Jalview generated SVG



For more details on Jalview, and Jalview tutorials,
please visit: <http://www.jalview.org/>

```

QUERY      : MQVWPIEGIKKFETLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKVG FVYRENHRSPGYDGRYWTMWKLPFMFGCTDATQVLKELEF
UniRef90_Q40250 : MKVWPPIGLKKYETLSYLPPLSDEALSKEIDYLIRNKWIPCLEFEEHGFVYREHHHSPGYDGRYWTMWKLPYMGCTDSTAQVMKEVGE
UniRef90_A7YVW5 : MQVWPPLGKRKFETLSYLPPLPVDALLKQIDYLRSGWIPCI EFTVEG FVYREHHHSPGYDGRYWTMWKLPYMGCTDSTQVLAEVEA
UniRef90_P04714 : MQVWPPYGKKKYETLSYLPDLTDEQLL...SPRYDGRYWTMWKLPFMFGCTDATQVLGELQF
UniRef90_K9SEV4 : -----EVAEQVRQDVRNHRVGVIEVVD-----EKKFRTSWNCATLDTARPEEALAALEN
UniRef90_K9XQK7 : -----DAIAQQVRSLLNQCGDIGIEHANQ-----RRFKTSWLTAGQFSGNTNQVISQVEK
UniRef90_M1X366 : -----DTAVVDRVRYLLQQGYKIATEHVDE-----RRFRTGWSW--SCTPIEARSLEQVIVSVEI
UniRef90_UPI00031FCDA6 : -----AETVDQVQQLLAGGYKIGMEHVD-----ERRFRTSWQCQPIEATSTKEVVAALEI
UniRef90_UPI00031FCDA6 : -----AQTVDQVRYLLDQGYKIGTEHVD-----ERRFRTSWQCTPIEARSVGEAIAALEK

OrigSeq    : 1-----11-----21-----31-----41-----51-----61-----71-----81-----
            : MQVWPIEGIKKFETLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKVG FVYRENHRSPGYDGRYWTMWKLPFMFGCTDATQVLKELEI

Jnet       : -----EEEE-----HHHHHHHHHHHH-----EEEEEE-----HHHHHHHHHH
jhmm       : -----EEEE-----HHHHHHHHHHHH-----EEEEEE-----HHHHHHHHHH
jpssm      : -----HHHHHHHHHHHH-----EEEEEE-----HHHHHHHHHH

Lupas 14   : -----cccccccccccc
Lupas 21   : -----
Lupas 28   : -----

Jnet_25    : -----BBBBBBBB-B---B--BB-BBB---BBBBBBBB---BBB-B-B-B-B---BBB-BB-BBBB-B-B--BB-BB--
Jnet_5     : -----BB-B---B--B--BB---B-BBB---B---B---B---BB-B-B---B---B---
Jnet_0     : -----B-B---B---B---B---B---B---B---B---B---B---B---B---
Jnet Rel   : 8853556775232117777762789999999874587266774367776545667777665335676567762789999999
    
```

Notes

Key:

- Colour code for alignment:
 - Blue - Complete identity at a position
 - Shades of red - The more red a position is, the higher the level of conservation of chemical properties of the amino acids
- Jnet - Final secondary structure prediction for query
- jalign - Jnet alignment prediction
- jhmm - Jnet hmm profile prediction
- jpssm - Jnet PSIBLAST pssm profile prediction
- Lupas - Lupas Coil prediction (window size of 14, 21 and 28)
- Note on coiled coil predictions
 - = less than 50% probability
 - c = between 50% and 90% probability
 - C = greater than 90% probability

1. Characters 'E', 'H', 'B' and '-' represent extended (E), helical (H) and other (-) types of secondary structure respectively. In the solvent accessibility predictions they represent buried (B) and exposed (-) for each of the 0%, 5% and 25% solvent accessibility cut-offs.

- Jnet_25 - Jnet prediction of burial, less than 25% solvent accesibility
- Jnet_5 - Jnet prediction of burial, less than 5% exposure
- Jnet_0 - Jnet prediction of burial, 0% exposure
- Jnet Rel - Jnet reliability of prediction accuracy, ranges from 0 to 9, bigger is better.

Results: simple summary

← → ↻  www.compbio.dundee.ac.uk/jpred4/results/jp_E_ntW2T/jp_E_ntW2T.simple.html

MQVWPIEGIKKFETLSYLPPLTVEDLLKQIEYLLRSKWVPCLEFSKVG FVYRENHRSPGYDGRYWTMWKLPFGCTDATQVLKELEEAKKAYPDAFV
-----E E E E-----H H H H H H H H H H H H-----E E E E E E-----H H H H H H H H H H H H-----E E

Results summary in PDF

← → ↻ www.compbio.dundee.ac.uk/jpred4/results/jp_E_ntW2T/jp_E_ntW2T.concise.pdf

	1	10	20	30	40																																			
QUERY	M	Q	V	W	P	I	E	G	I	K	K	F	E	T	L	S	Y	L	P	P	L	T	V	E	D	L	L	K	Q	I	E	Y	L	L	R	S	K	W	V	P
UniRef90_Q40250	M	K	V	W	P	P	I	G	L	K	K	F	E	T	L	S	Y	L	P	P	L	S	D	E	A	L	S	K	E	I	D	Y	L	L	R	N	K	W	I	P
UniRef90_A7YVW5	M	Q	V	W	P	P	L	G	K	R	K	F	E	T	L	S	Y	L	P	P	L	P	V	D	A	L	L	K	Q	I	E	Y	L	L	R	S	G	W	I	P
UniRef90_P04714	M	Q	V	W	P	P	Y	G	K	K	K	F	E	T	L	S	Y	L	P	D	L	T	D	E	Q	L	L	K	E	I	E	Y	L	L	N	K	G	W	V	P
UniRef90_W9RUU9	M	Q	V	W	P	P	R	G	K	L	K	F	E	T	L	S	Y	L	P	D	L	T	D	E	Q	L	L	K	E	I	D	Y	L	L	R	S	N	W	I	P
UniRef90_K3ZA66	M	Q	V	W	P	P	G	G	K	K	F	E	T	L	S	Y	L	P	P	L	S	T	D	D	L	L	K	Q	I	D	Y	L	L	R	K	N	W	I	P	
UniRef90_V4UWB0	M	K	V	W	P	P	T	G	L	K	K	F	E	T	L	S	Y	L	P	P	L	S	D	E	A	L	L	K	E	I	S	Y	L	L	R	S	G	W	I	P
UniRef90_A9PFS6	M	Q	V	W	P	P	T	G	L	K	K	F	E	T	L	S	Y	L	P	D	L	T	E	E	E	L	A	K	E	I	D	Y	L	L	R	S	K	W	V	P
UniRef90_Q9ZP07	M	Q	V	W	P	P	I	G	K	K	K	F	E	T	L	S	Y	L	P	P	L	T	E	E	Q	L	L	K	E	V	E	Y	L	L	R	K	G	W	V	P
UniRef90_Q96542	M	Q	V	W	P	P	L	G	L	K	K	F	E	T	L	S	Y	L	P	P	L	S	S	E	Q	L	A	K	E	V	D	Y	L	L	R	K	N	L	I	P
UniRef90_P08474	M	K	V	W	P	P	L	G	L	R	K	F	E	T	L	S	Y	L	P	D	M	S	N	E	Q	L	S	K	E	V	D	Y	L	L	R	N	G	W	V	P
UniRef90_O48550	M	Q	V	W	P	P	E	G	K	K	K	F	E	T	L	S	Y	L	P	P	L	T	R	E	Q	L	G	Q	E	V	D	Y	L	L	R	N	G	W	I	P
UniRef90_P05348	M	Q	V	W	P	A	Y	G	N	K	K	F	E	T	L	S	Y	L	P	P	L	S	T	D	D	L	L	K	Q	V	D	Y	L	L	R	N	G	W	I	P

Results directory

<u>Name</u>	<u>Last modified</u>	<u>Size</u>
Parent Directory		-
LOG	15-Feb-2016 15:14	4.7K
README	15-Feb-2016 15:14	2.1K
README_more_details	15-Feb-2016 15:14	138
dlwdds_name	15-Feb-2016 15:14	0
jp_ZVwqlvG.align	15-Feb-2016 15:14	56K
jp_ZVwqlvG.als	15-Feb-2016 15:14	2.0K
jp_ZVwqlvG.blast.gz	15-Feb-2016 15:14	200K
jp_ZVwqlvG.coils.csv	15-Feb-2016 15:14	762
jp_ZVwqlvG.coilseq.lupas_14	15-Feb-2016 15:14	5.1K
jp_ZVwqlvG.coilseq.lupas_21	15-Feb-2016 15:14	5.1K
jp_ZVwqlvG.coilseq.lupas_28	15-Feb-2016 15:14	5.1K
jp_ZVwqlvG.concise	15-Feb-2016 15:14	112K
jp_ZVwqlvG.concise.blc	15-Feb-2016 15:14	57K
jp_ZVwqlvG.concise.fasta	15-Feb-2016 15:14	57K
jp_ZVwqlvG.concise.pdf	15-Feb-2016 15:14	315K
jp_ZVwqlvG.e4778868	15-Feb-2016 15:14	0
jp_ZVwqlvG.e9835073	15-Feb-2016 15:14	0
jp_ZVwqlvG.fasta	15-Feb-2016 15:14	136
jp_ZVwqlvG.full_MSA.fasta	15-Feb-2016 15:14	338K
jp_ZVwqlvG.full_MSA.o.fasta	15-Feb-2016 15:14	150K
jp_ZVwqlvG.hmm	15-Feb-2016 15:14	23K
jp_ZVwqlvG.html	15-Feb-2016 15:14	145K
jp_ZVwqlvG.input	15-Feb-2016 15:14	129
jp_ZVwqlvG.jalview	15-Feb-2016 15:14	3.2K
jp_ZVwqlvG.jnet	15-Feb-2016 15:14	4.5K
jp_ZVwqlvG.o4778868	15-Feb-2016 15:14	0
jp_ZVwqlvG.o9835073	15-Feb-2016 15:14	0
jp_ZVwqlvG.pe4778868	15-Feb-2016 15:14	0
jp_ZVwqlvG.pe9835073	15-Feb-2016 15:14	0

jp_ZVwqlvG.po4778868	15-Feb-2016 15:14	0
jp_ZVwqlvG.po9835073	15-Feb-2016 15:14	0
jp_ZVwqlvG.profile	15-Feb-2016 15:14	20K
jp_ZVwqlvG.pssm	15-Feb-2016 15:14	26K
jp_ZVwqlvG.results.html	15-Feb-2016 15:14	57K
jp_ZVwqlvG.results_jalview.html	15-Feb-2016 15:14	13K
jp_ZVwqlvG.results_jalview_app.html	15-Feb-2016 15:14	16K
jp_ZVwqlvG.seq	15-Feb-2016 15:14	136
jp_ZVwqlvG.simple.html	15-Feb-2016 15:14	1.2K
jp_ZVwqlvG.svg.html	15-Feb-2016 15:14	49K
jp_ZVwqlvG.tar.gz	15-Feb-2016 15:14	690K

You can find all the files overviewed in this tutorial and more in the results directory (linked from the results summary HTML page as well as archived and available for download in *.TAR.GZ)

The README file explains what each of the files contains.

README

README file documents results files descriptions.

Filename	Description
-----	-----
jp_ZVwqlvG.align format	PSIBLAST alignment with gaps and redundancy removed in FASTA format
jp_ZVwqlvG.als	Alscript command file. Used to generate PS/PDF
outputjp_ZVwqlvG.blast.gz	PSIBLAST output (compressed)
jp_ZVwqlvG.coils.csv	The output from coils in CSV format
jp_ZVwqlvG.coilseq.lupas_14	The output from coils using a window length of 14
jp_ZVwqlvG.coilseq.lupas_21	The output from coils using a window length of 21
jp_ZVwqlvG.coilseq.lupas_28	The output from coils using a window length of 28
jp_ZVwqlvG.concise prediction, solvent accessibility and the sequence alignment	The prediction in pseudo-CSV format, including the coiled-coil prediction
jp_ZVwqlvG.concise.blc	A BLC file of the prediction and alignment
jp_ZVwqlvG.concise.pdf	A PDF file of the prediction and alignment
jp_ZVwqlvG.fasta	Input query sequence in FASTA format
jp_ZVwqlvG.full_MSA.fasta	The full multiple sequence alignment before JPred filters.
Gaps/insertions shown. FASTA format.	
jp_ZVwqlvG.hmm	The HHMer2 profile of the alignment
jp_ZVwqlvG.html	A HTML file of the prediction and alignment
jp_ZVwqlvG.input	Your raw input
jp_ZVwqlvG.jalview	A Jalview annotation file to be read in with the .align file
to view the predictions in Jalview	
jp_ZVwqlvG.jnet	The output from Jnet
jp_ZVwqlvG.profile	PSIBLAST profile
jp_ZVwqlvG.pssm	PSIBLAST PSSM in a format for Jnet
jp_ZVwqlvG.seq	Your sequence
jp_ZVwqlvG.simple.html	The brief HTML output of the query sequence and prediction
only	
jp_ZVwqlvG.svg.html	A Jalview generated SVG file with summary of the results.

Jalview Desktop Application

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Options to view results in Jalview (www.jalview.org)

Three types of results are available to work with in Jalview:

Choose option 1 if you are mainly interested in the prediction for your sequence, but also want to see the patterns of residue conservation in the alignment that was used. This view deletes any residues not in the Query sequence that would lead to a gap in the query sequence. (The PSI-BLAST Multiple Sequence Alignment (MSA) as used by JNet for the prediction.)

Choose option 2 if you want to see the full-length sequences shown in option 1. This is useful if you want to use the alignment for further analysis, or make changes to it. The alignment includes gaps and insertions but is filtered for redundancy and reduced to a maximum of 1000 entries.

Choose option 3 if you want to see the full results of the PSI-BLAST search. Useful as a way to explore the sequences related to the one you are interested in. This option can give very large alignments that may not load on smaller memory computers.

Clicking the Jalview logo will download and start a local copy of the Jalview application to your computer.

IMPORTANT NOTE: The default setting is to use 7GB of memory for Option 3 and 1 GB for Options 1 and 2. This should allow you to work with most MSAs produced by JPred. However, if your PC has less or more memory, you can choose a different value. We recommend selecting a value that is slightly less than half the memory (RAM) on your computer.

1GB Memory to be used: 7GB

Option	Open full Jalview Desktop application
1. With filtered multiple alignment (MSA: no gaps in the query sequence) - most compact and fastest	
2. With filtered MSA but including all gaps as hidden columns	
3. With full MSA returned by PSI-BLAST (Warning, this can be very large!)	

1. Clicking on “View results in Jalview” will take you to a separate page, which runs the Jalview Java Desktop (you will need a browser that supports Java 1.6, this includes most modern browsers, and Java installed on your computer)

Jalview Java Applet

Options to view results in Jalview (www.jalview.org)

Three types of results are available to work with in Jalview:

Choose option 1 if you are mainly interested in the prediction for your sequence, but also want to see the patterns of residue conservation in the alignment that was used. This view deletes any residues not in the Query sequence that would lead to a gap in the query sequence. (The PSI-BLAST Multiple Sequence Alignment (MSA) as used by JNet for the prediction.)

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Choose option 3 if you want to see the full results of the PSI-BLAST search. Useful as a way to explore the sequences related to the one you are interested in. This option can give very large alignments that may not load on smaller memory computers.

Clicking the “Start Jalview” button will launch the JalviewLite applet that runs in your web browser.

IMPORTANT NOTE: The default setting is to use 7GB of memory for Option 3 and 1 GB for Options 1 and 2. This should allow you to work with most MSAs produced by JPred. However, if your PC has less or more memory, you can choose a different value. We recommend selecting a value that is slightly less than half the memory (RAM) on your computer.

1GB Memory to be used: 7GB

Option	Open Jalview applet in web page
1. With filtered multiple alignment (MSA: no gaps in the query sequence) - most compact and fastest	<input type="button" value="Start Jalview"/>
2. With filtered MSA but including all gaps as hidden columns	<input type="button" value="Start Jalview"/>
3. With full MSA returned by PSI-BLAST (Warning, this can be very large!)	<input type="button" value="Start Jalview"/>

1. Similarly, clicking on “View results using in-browser Jalview Java applet” will take you to a separate page, which runs the Jalview Java Applet (you will need a browser that supports Java 1.6, this includes most modern browsers, and Java installed on your computer)

2. Allow Java applet to run and push “Start Jalview”.

Jalview Java Applet

Jpred 4 Incorporating Jnet

http://www.compbio.dundee.ac.uk/jpred4/results/jp_ZVwqlvG/jp_ZVwqlvG.full_MSA.o.fasta

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MQVWP I E G I K K F E T L S Y L P P L T V E D L L K Q I E Y L L R S K W V P C L E F S K V G F V Y R E N H
 UniRef90_Q40250 MKVWP P I G L K K Y E T L S Y L P P L S D E A L S K E I D Y L I R N K W I P C L E F E E H G F V Y R E H H
 UniRef90_A7YVW5 MQVWP P L G K R K F E T L S Y L P P L P V D A L L K Q I D Y L I R S G W I P C I E F T V E G F V Y R E H H
 UniRef90_P04714 MQVWP P Y G K K K Y E T L S Y L P D L T D E Q L L K E I E Y L L N K G W V P C L E F T E H G F V Y R E Y H
 UniRef90_W9RUVU9 MQVWP P R G K L K F E T L S Y L P D L T D E Q L L K E I D Y L L R S N W I P C L E F E V K A H I Y R E N N
 UniRef90_K3ZA66 MQVW - P I G G K K F E T L S Y L P P L S T D D L L K Q I D Y L I R K N W I P C L E F S K V G F V Y R E N N
 UniRef90_V4UW80 MKVWP P T G L K K F E T L S Y L P P L S D E A L L K E I S Y L I R S G W I P C L E F E E K G W V Y R E H H
 UniRef90_A9PF56 MQVWP P T G L K K F E T L S Y L P D L T E E L A K E I D Y L L R S K W V P C L E F E E K G W V Y R E H H
 UniRef90_Q9ZP07 MQVWP P I G K K K F E T L S Y L P P L T E E Q L L K E Y L L R K G W V P C L E F E E K G F V Y R E H N
 UniRef90_Q96542 MQVWP P L G L K K F E T L S Y L P P L S S E Q L A K E M D Y L L R K N L I P C L E F E E H G F V Y R E H N
 UniRef90_P08474 MKVWP P L G L R K F E T L S Y L P D M S N E Q L S K E C D Y L L R N G W V P C V E F D I S G F V Y R E N H
 UniRef90_Q48550 MQVWP P E G K K K F E T L S Y L P P L T R E Q L G Q E M D Y L I R N G W I P C I E F C K V G F V Y R E Y H
 UniRef90_P05348 MQVWP A Y G N K K F E T L S Y L P P L S T D D L L K Q V D Y L L R N G W I P C L E F S K V G F V Y R E N S
 UniRef90_Q9T4H0 MQVWP T R G K K K F E T L S Y L P P L S R E Q L A S E I D Y L L R S G W I P C L E F E E H G F V Y R A H G
 UniRef90_Q8VX71 MQVWP P E G K I K F E T L S Y L P P L S E A D L L A Q I N Y L L I N G W V P C L E F D M P G A V Y R E H H
 UniRef90_Q43032 MKVWP T Q N M K R Y E T L S Y L P P L T D Q L A R Q V D Y L L N N K W V P C L E F T D H G F V Y R E H H
 UniRef90_E7E1K9 MQVWP P V G K K F E T L S Y L P P L S E E E L L K E M N Y L L R M G W I P C L E F P Q M E P F P Y R E N C
 UniRef90_UPI0002C2FBF1 MQVWP P V G L K K F E T L S Y L P P L S V E S L A K E M Y L L R N K W V P C L E F E E H G F V Y R E H G
 UniRef90_Q9XQ85 MQVWP T I G K K K F E T L S Y L P D L T E E Q L G K E M D Y L L R S G W I P C L E F E K D A F P H R E N N
 UniRef90_P31333 MQVWP P L G K K K F E T L S Y L P D L T P V Q L A K E M D Y L L R S K W I P C L E F E E G F V H R K Y S
 UniRef90_Q24634 MKVWP I V G L R K F E T L S Y L P T L S V E S L L K Q I E Y L I R N G W V P C L E F S L E G F V S R D M N
 UniRef90_UPI00042AFD44 MQVWP P L G K K K F E T L S Y L P D L T R E R L F K E M Y L L R N K W V P C L E F S S H G F V Y R E N L
 UniRef90_S8C9X5 MQVWP T V G V K K F E T L S Y L P E L T R E Q L A K E I D Y L I R S K W I P C L E F E L G P F V Y R E N S
 UniRef90_Q22077 MKVWP P L G L Q K F E T L S Y L P P L S I E S L A K Q I E Y L I L K G W I P C L E F E E H P F V Y R E N N

Lupas_21
 Lupas_14
 Lupas_28
 jnetpred
 JNETCONF

Sequence 1 ID: QUERY Residue: GLU (7)

For more information and tutorials on Jalview please visit <http://www.jalview.org/>

Options 1 and 2. This should allow you to work with most MSAs produced by JPred. However, if your PC has less or more memory, you can choose a different value. We recommend selecting a value that is slightly less than half the memory (RAM) on your computer.

JPred help

- For help on JPred please email:

- www-jpred@compbio.dundee.ac.uk