Calculate | Web Service

MAFFT Alignm

Alignment ▶
Secondary Structure Prediction ▶ | JPred Secondary Structure Prediction
Protein Disorder ▶
Analysis ▶ | http://www.compbio.dundee.ac.uk/jabaws
Conservation ▶ | RNAAliFold Prediction
Fetch DB References ▶ | Change RNAAliFold settings...

90
VGIDLPYSC
VGIELPYSC
AGIDLPYSC
EGIDLPYSC
AGIDLPYSC
AGIDLPYSCRAGSCSSCAGKVV
AGIDLPYSCRAGSCSSCAGKVV
AGLDLPYSCRAGSCSSCAGKVV

JPred Secondary Structure Prediction

JPred Secondary Structure Prediction - finished | New Window

Drozdetskiy A, Cole C, Procter J & Barton GJ. (2015)
JPred4: a protein secondary structure prediction server
Nucleic Acids Research, Web Server issue (first published 15th April 2015)
doi://10.1093/nar/gkv332

Job details for visible MSA based prediction (MAFFT Multiple Sequence Alignment of Retrieved from Uniprot) on sequence :
>FER_CAPAA
ASYKVKLITPDGPIEFDCPDDVYILDQAEEAGHDLPYSCRAGSCSSCAGKIAGGAVDQTDGNFLDDDQLE
EGWVLTCVAYPQSDVTIETHKEAELVG
Job Complete.
** Vamsas@Dundee University Life Sciences Bioinformatics Cluster Job **
** Public Job Limits are 1 hour of CPU time and 1G of memory.
**
** If you experience any problems, please email jalview-discuss@jalview.org
** as soon as possible!
**
Running Jpred Server version 4.0.0

--/homes/www-jpred/live4/bin/webrun -ipline 10.0.115.189 -log
/homes/www-jpred/live4/public_html/results/jp_Xv9jUrW/LOG -sequence
/homes/www-jpred/live4/public_html/results/jp_Xv9jUrW/jp_Xv9jUrW.seq -format msf -id
jp_Xv9jUrW
--TIMEOUT set at 10800 seconds
--Started work on jp_Xv9jUrW at Wed Feb 15 16:52:01 2017
--On machine fc-022
--format = msf
>>10% complete