The Usage of EPMeta Offline Tool

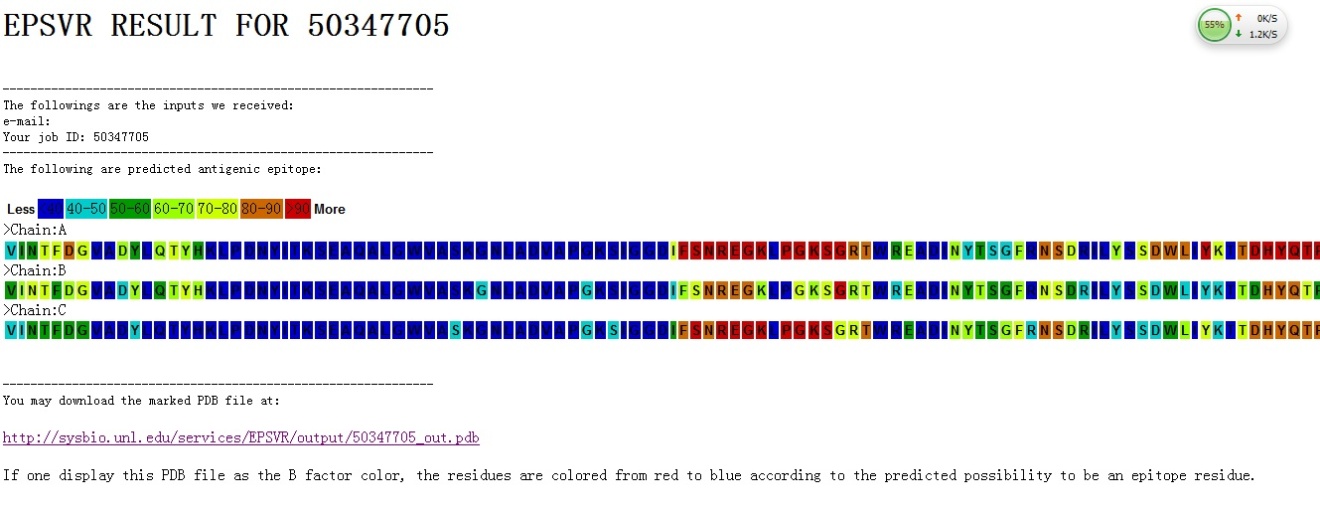
Date: 07/29/2013

EPMeta server is a meta server to combine the results of EPSVR, EPCES, DiscoTope, Seppa, BEpro, and Epitopia servers to get a consensus prediction. Our test shows that the consensus prediction by EPMeta may obtain a higher accuracy than any single member used in EPMeta.

1. **How to download EPMeta offline tool**
2. Go to <http://sysbio.unl.edu/>, download its installation package “EPMeta Installation Package.tar”
3. Unzip “EPMeta Installation Package.tar”
4. Confirm that the files EPMeta\_Server.sh, meta.out, pdb\_fasta.pl are contained in the unzipped filefold
5. **The preparation before use EPMeta offline tool**

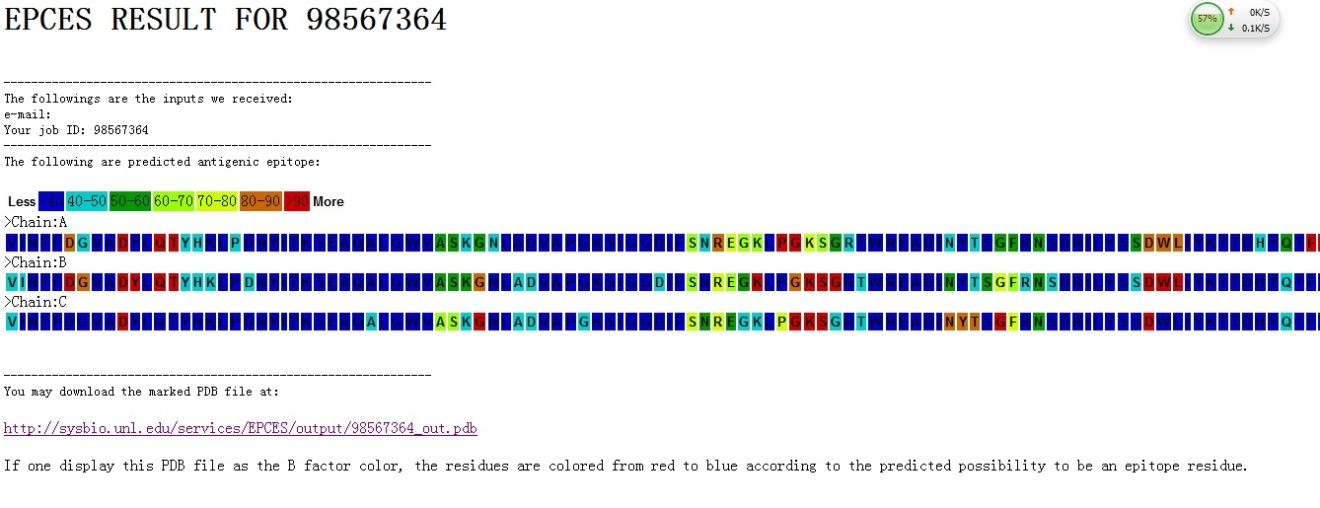
EPMeta offline tool require six or less prediction results from EPSVR, EPCES, DiscoTope, SEPPA, BEpro, and Epitopia. Hence, before using EPMeta offline, we must obtain the six predictions from the relevant online servers respectively.

1. Get the prediction from EPSVR, go to <http://sysbio.unl.edu/EPSVR/> (using 1A2P protein structure as example)



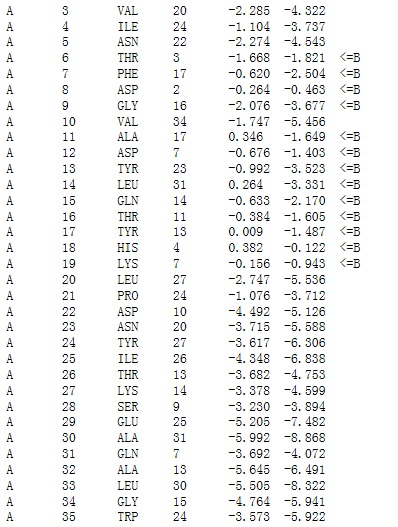
On the result webpage, click the marked pdb file and download it. Rename this file as ‘EPSVR.pdb’.

1. Get the prediction from EPCES, go to <http://sysbio.unl.edu/EPCES/>



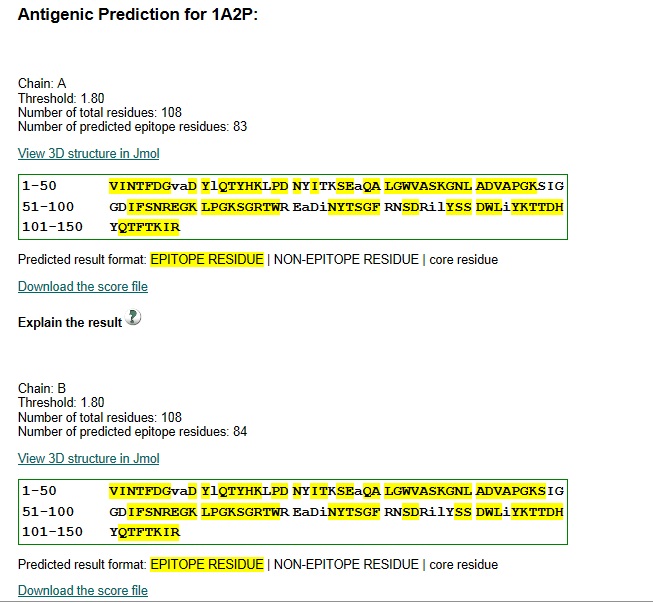
On the result webpage, click the marked pdb file and download it. Rename this file as ‘EPCES.pdb’.

1. Get the prediction from DiscoTope, go to <http://www.cbs.dtu.dk/services/DiscoTope/>.



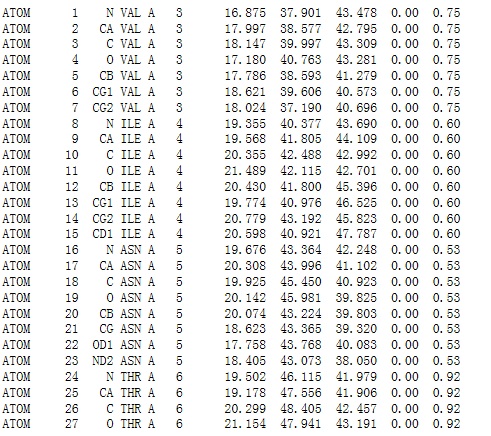
On the result page, select all the data by ‘ctrl + a’, and then copy all the data into a file named by ‘DISTOCOPE.pdb’.

1. Get the prediction from SEPPA, go to <http://lifecenter.sgst.cn/seppa/>



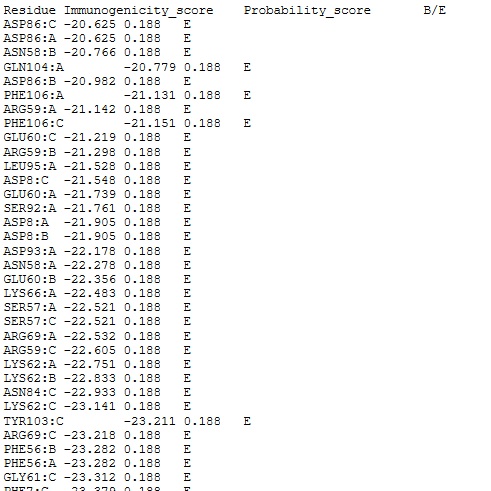
On the result page, click the links ‘Download the score file’ to download the prediction result for each chain respectively. And then combine the separate files into one file (remove the head-lines since the second separate files. That is, in the final file, only one head lines are kept. The details please refer to the example into filefold ‘SEPPA - How to combine separate chain prediction files into one file’). Name the final file as ‘SEPPA.pdb’.

1. Get the prediction from BEpro (pepito), go to <http://pepito.proteomics.ics.uci.edu/>



One the result page, select all the data by ‘ctrl + a’, and then copy all the data into a file named by ‘BEPRO.pdb’.

1. Get the prediction from Epitopia, go to http://epitopia.tau.ac.il/



One the result page, select all the data by ‘ctrl + a’, and then copy all the data into a file named by ‘EPITOPIA.pdb’.

**[Warning]:** If any prediction among the six above cannot be obtained from its relevant server, just skip it. The offline tool meta.out can ignore this server automatically if it cannot this prediction.

1. **The usage of EPMeta offline tool**

The EPMeta offline tool can only run on Linux operating system. Before use EPMeta offline tool, please confirm that Perl script can be run on your local Linux machine.

1. Change a executive permission for the file ‘EPMeta\_Server.sh’ and ‘meta.out’ by command below

chmod a+x EPMeta\_Server.sh

chmod a+x meta.out

1. Copy the prediction files (if successfully obtain) under the same filefold where ‘EPMeta\_Server.sh’, ‘meta.out’, and ‘pdb\_fasta.pl’ are located
2. Run ‘EPMeta\_Server.sh’ by

./ EPMeta\_Server.sh

If EPMeta\_Server.sh is executed successfully, two files are generated:

a) ‘EPMeta\_output.pdb’ contains the prediction of discontinuous B-cell epitope;

b) ‘EPMeta.html’ is a webpage which illustrates the prediction result.

**[Warning]:** Six prediction names must be EPSVR.pdb, EPCES.pdb, DISCOTOPE.pdb, SEPPA.pdb, BEPRO.pdb, and EPITOPIA.pdb. Our tool is case-sensitive.

**[Warning]:** Our tool also supports a meta search by any combination of the six server above. Hence if you cannot obtain all six predictions, you may do meta by less than 6 predictions.

**[Warning]:** An example is contained in the filefold ‘Example’ using protein structure 1A2P. Please refer to it.