

User manual for *iAMPpred*

The *iAMPpred* can be used to predict the propensity of a candidate peptide as antibacterial, antiviral or antifungal with certain probability. The performance of this server is comparable with the existing tools (AntiBP¹, CAMP², AntiBP2³, AVPpred⁴, *iAMP-2L*⁵, ClassAMP⁶ and EFC-FCBF⁷) meant for prediction of AMPs. The antimicrobial peptides predicted by this server will help enable the designing of peptide based antibiotics. A detailed description about the types of features (compositional, physic-chemical and structural) and the machine learning classifier (support vector machine) used in this server are provided in the menu “About *iAMPpred*”.



Figure 1. Home page of *iAMPpred*

Using *iAMPpred*

To predict the Antimicrobial peptides from a user input click on “Run *iAMPpred*” link from the main menu. This link will be redirected to the following page *iAMPpred* server page. To predict AMPs, the peptide sequences in FASTA format may be pasted as given below:

```
>AP00001
GLWSKIKEVGKEAAKAAAKAAGKAALGAVSEAV
>AP00004
NLCERASLTWTGNCGNTGHCDTQCRNWESAKHGACHKRGNGWKCFYFDC
>AP00006
GNNRPVYIPQPRPPHPRI
```

For a better understanding user may run the server with example peptide dataset by clicking on “Load Example Data” link.



Figure 2. Server page of iAMPpred

User can remove the existing entries in the text-box by using the “Clear Text area” button. After clicking on the load example data, the example dataset will be loaded in the text area as shown in Figure 3.

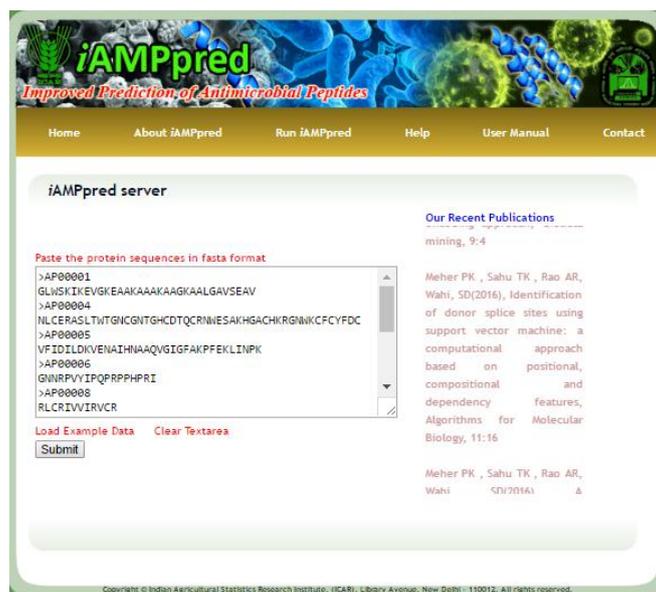


Figure 3. Server page showing the text area loaded with the example data

Then, “Submit” button has to be clicked which will display the result in the redirected page. The result page obtained after submitting the example dataset is shown in Figure 4.

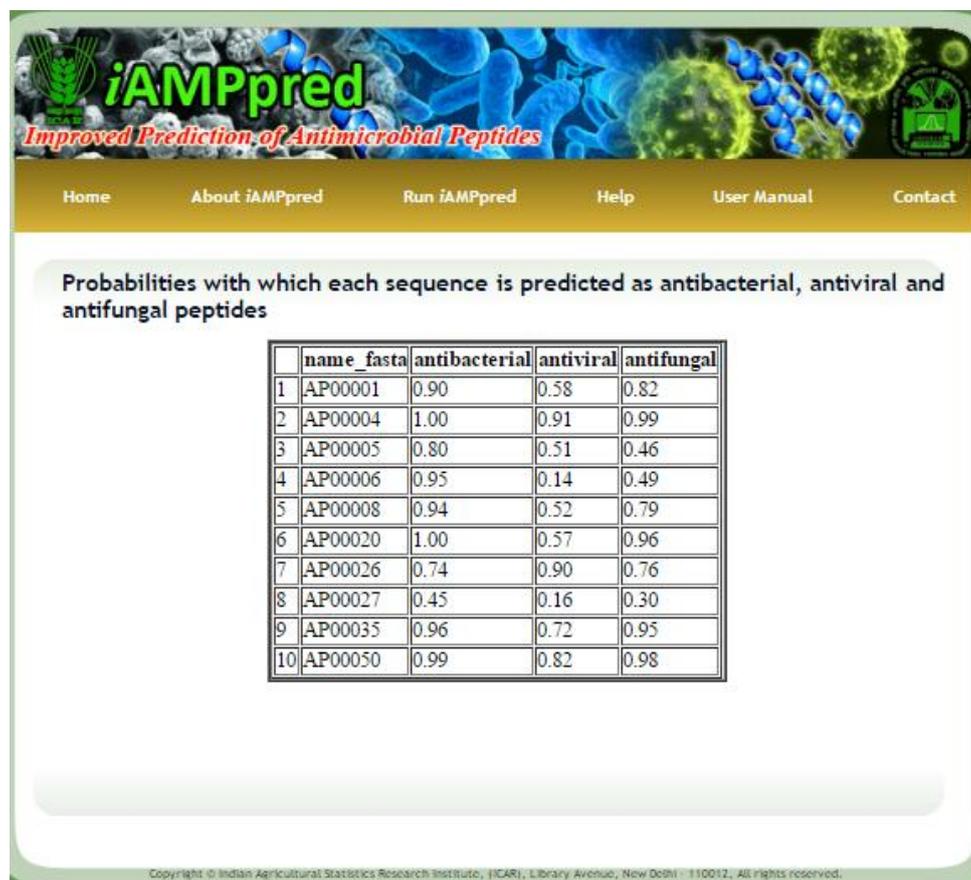


Figure 4. Result page after execution of an example dataset

Results of the prediction are shown in a tabular format as shown in Figure 4. In first two columns sequence no, sequence name are given. Third, fourth and fifth columns of the table show the probabilities with which the peptide sequences are predicted as antibacterial, antiviral and antifungal.

Interpretation of result

Since, the value of probability lies between 0 and 1, the probability with which a sequence is predicted as antibacterial or antiviral or antifungal lie between 0 and 1. Therefore, if the probabilities are >0.5 in each case the sequence is said to be predicted as antibacterial, antiviral and antifungal otherwise non-antibacterial, non-antiviral and non-antifungal. For example, from the above result it can be inferred that the 3rd peptide sequence can have high antibacterial but little antiviral properties whereas, the 4th peptide sequence can have only high antibacterial property.

References

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