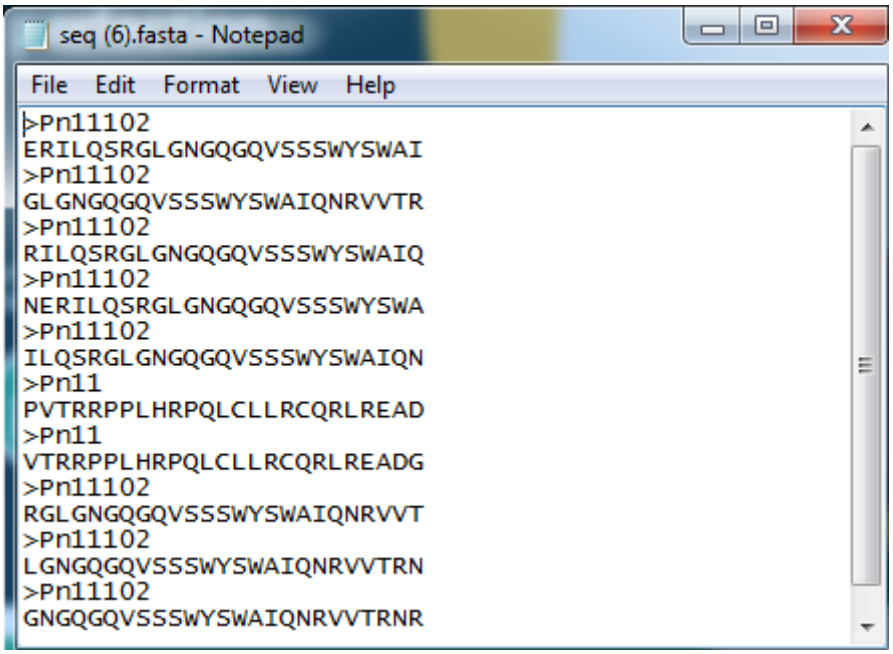
MANUAL

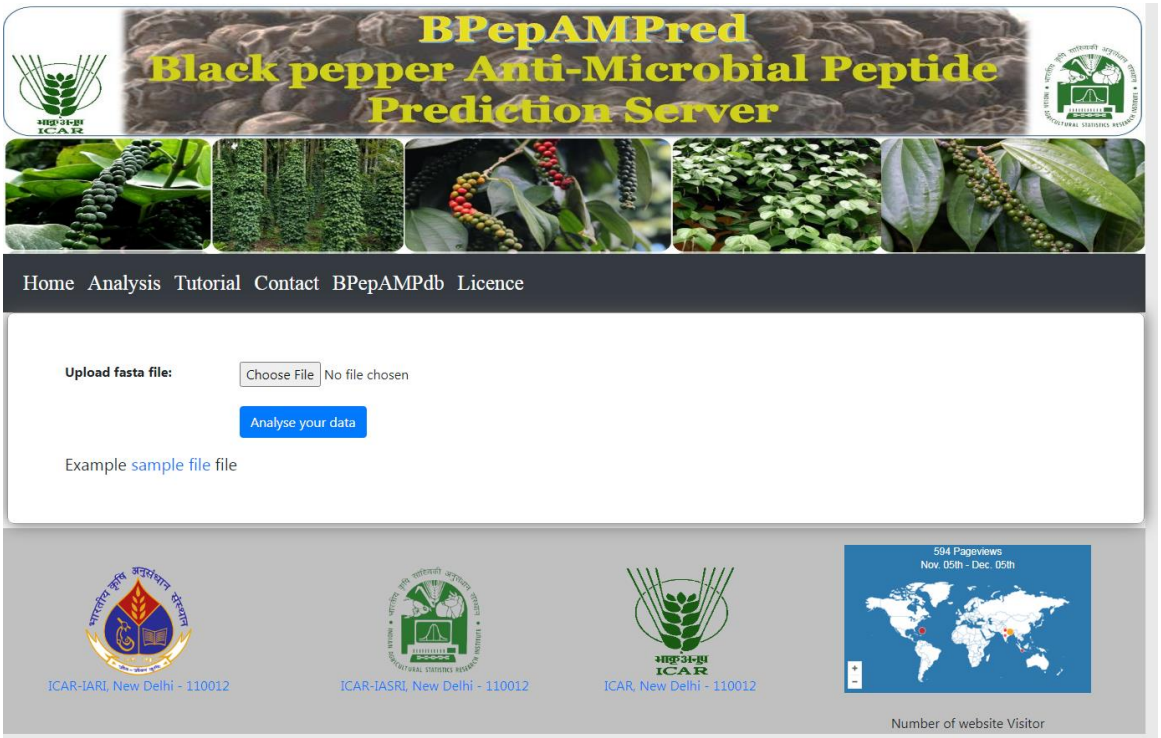
Step by step procedure for analysis of Black Pepper AMP Prediction

1. **Take the protein sequence in fasta format (can also use multiple fasta), shown below the image**



2. **Click on the Analysis for analyzing the protein sequences in fasta file, shown below**

3. **After clicking on the Analysis tab, upload fasta file and then click on analysis your data, shown in below image**



4. **Finally,** the result will be displayed on the screen, shown in the image below

Sl.No.	Sequence ID	Fragment	Model Prediction
1	Pn11102	ERILQSRGLGNGQGQVSSSWYSWAI	Absent
2	Pn11102	GLGNGQGQVSSSWYSWAIQNRVVTR	Absent
3	Pn11102	RILQSRGLGNGQGQVSSSWYSWAIQ	Absent
4	Pn11102	NERILQSRGLGNGQGQVSSSWYSWA	Absent
5	Pn11102	ILQSRGLGNGQGQVSSSWYSWAIQN	Absent
6	Pn11	PVTRRPPLHRPQLCLLRCQRLREAD	Absent
7	Pn11	VTRRPPLHRPQLCLLRCQRLREADG	Absent
8	Pn11102	RGLGNGQGQVSSSWYSWAIQNRVVT	Absent
9	Pn11102	LGNGQGQVSSSWYSWAIQNRVVTRN	Absent
10	Pn11102	GNGQGQVSSSWYSWAIQNRVVTRNR	Absent

5. Blackpepper AMP Database:

(Click on BPepAMPdb)

Welcome to BPepAMPred

Antimicrobial peptides (AMPs),known as 'nature's antibiotics',involved in host defence mechanism of several species and are part of innate immunity in response to several pathogenic micro-organisms. These peptides are often the first line of defense against invading pathogens which can inhibit bacterial growth by interacting with microbial membranes or intracellular targets.The increase in the AMP resistance in plants and animals has gained huge attention due to its effectiveness against chemical antibiotics resistant microbial pathogens. Optimization and engineering of peptides can take care of toxicity and stability issues but higher production cost makes screening of large numbers of peptides very expensive. Computational approaches for AMP prediction may be one of the ways to overcome the cost constraint.

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We perform the computation on a Linux based HPC cluster environment using 100 cluster cores of Intel Xeon Gold 6148 CPU with 2.40 GHz clock speed for each training instance. For implementation, Keras (Chollet Francois, 2015) a high-level API for deep learning based on TensorFlow (Abadi *et al.*, 2016) was used.

BlackPepAMP is a user-friendly AMP prediction server where the user inputs the sequence in fasta format. The multiple sequences can be uploaded but not exceeding 500. The prediction accuracy of the server is 99.34%, MCC 0.9868 and F-score 99.30 was achieved for the combined dataset which was implemented in the server.

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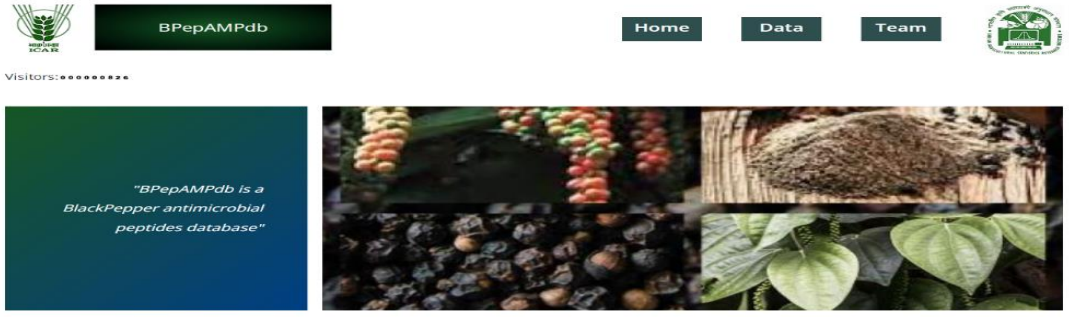
Number of website Visitor

6. Blackpepper AMP Database



Data

Team

About BPepAMPdb

Antimicrobial peptides (AMPs; also called Nature's antibioitics, 5–100 amino acid residues) are produced by most organisms as an innate immune response against microbes (World Health Organization, 2014). From time immemorial, black pepper has traditionally been used for the treatment of various diseases due to its antimicrobial, anti-inflammatory, antioxidant and anti-cancerous properties along with its wider applications and significance in dietary, nutrition, medicine, preservative, perfumery, insecticide and agricultural field (Hu et al., 2015; Gulcin, 2005; Raja and Sethuraman, 2008; Vijayan and Thampuran, 2000) making it a potent source for antimicrobial peptides that can combat against disease-causing pathogens. It is found to exhibit excellent antimicrobial activity with inhibitory effects against Gram-positive and Gram-negative bacteria (Zou et al. 2015). Their potent activity has led to strong interest in these molecules as targets for pharmaceutical research. This database provides comprehensive functional analyses for AMPs based on the large-scale black pepper proteome data and a downloadable package to discover known and novel AMPs on chromosome level. A total of 43,759 AMP sequence segments have been predicted from black pepper peptides and were found functionally associated with 10,935 unique genes retrieved from their respective gene ids obtained from the gtf file available online. The chromosome number, genomic location of AMPs, their associated gene ids and functional properties were cataloged in the database.

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