

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

SVM based method for predicting beta hairpin structures in proteins

RRID:SCR_008349

Type: Tool

Proper Citation

SVM based method for predicting beta hairpin structures in proteins (RRID:SCR_008349)

Resource Information

URL: <http://www.imtech.res.in/raghava/bhairpred/>

Proper Citation: SVM based method for predicting beta hairpin structures in proteins (RRID:SCR_008349)

Description: Bhairpred server is based on machine learning technique SVM using single sequence information, evolutionary profile, predicted and observed secondary structure (as obtained using Psipred and DSSP), predicted and observed accessibility values (as obtained from Netasa and DSSP). The methods were trained and tested on dataset of 2880 proteins and their performance was evaluated on dataset of 534 proteins used by Thornton (PNAS, 2002). Best prediction results were obtained with hybrid approach that combined prediction results from evolutionary profile, predicted secondary structure and accessibility.

Synonyms: BhairPred

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Keywords: evolutionary, information, protein, protein structure prediction, secondary, sequence, single, svm, technique, bio.tools

Funding: Institute of Microbial Technology

Resource Name: SVM based method for predicting beta hairpin structures in proteins

Resource ID: SCR_008349

Alternate IDs: nif-0000-25213, biotools:bhairpred

Alternate URLs: <https://bio.tools/bhairpred>

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260919T195717+0000

Ratings and Alerts

No rating or validation information has been found for SVM based method for predicting beta hairpin structures in proteins.

No alerts have been found for SVM based method for predicting beta hairpin structures in proteins.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Bussaglia E, et al. (2019) TET2 missense variants in human neoplasia. A proposal of structural and functional classification. Molecular genetics & genomic medicine, 7(7), e00772.

Fox JA, et al. (2005) The Bioinformatics Links Directory: a compilation of molecular biology web servers. Nucleic acids research, 33(Web Server issue), W3.