

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SVM-fold: Protein Fold Prediction

RRID:SCR_006834

Type: Tool

Proper Citation

SVM-fold: Protein Fold Prediction (RRID:SCR_006834)

Resource Information

URL: <http://rankprop.gs.washington.edu/svm-fold/>

Proper Citation: SVM-fold: Protein Fold Prediction (RRID:SCR_006834)

Description: This web server makes predictions of family, superfamily and fold level classifications of proteins based on the Structural Classification of Proteins (SCOP) hierarchy using the Support Vector Machine (SVM) learning algorithm. SVM-FOLD detects subtle protein sequence similarities by learning from all available annotated proteins, as well as utilizing potential hits as identified by PSI-BLAST. Predictions of classes of proteins that do not have any known example with a significant pairwise PSI-BLAST E-value can still be found using SVMs.

Abbreviations: SVM-fold

Synonyms: SVM-fold, Support Vector Machine fold

Resource Type: service resource

Funding: NIGMS GM74257-01;
NSF EIA-0312706

Resource Name: SVM-fold: Protein Fold Prediction

Resource ID: SCR_006834

Alternate IDs: nlx_17631

Old URLs: <http://svm-fold.c2b2.columbia.edu/>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260905T132602+0000

Ratings and Alerts

No rating or validation information has been found for SVM-fold: Protein Fold Prediction.

No alerts have been found for SVM-fold: Protein Fold Prediction.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.