

# Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

## SVM-fold: Protein Fold Prediction

RRID:SCR\_006834

Type: Tool

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### Proper Citation

SVM-fold: Protein Fold Prediction (RRID:SCR\_006834)

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### 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:** 20260919T195119+0000

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### 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.