

Resource Summary Report

Generated by T1D on Aug 24, 2026

SPROUTS- Structural Prediction for Protein Folding Utility System

RRID:SCR_005118

Type: Tool

Proper Citation

SPROUTS- Structural Prediction for Protein Folding Utility System (RRID:SCR_005118)

Resource Information

URL: <http://bioinformatics.engineering.asu.edu/springs/Sprouts/index.html>

Proper Citation: SPROUTS- Structural Prediction for Protein Folding Utility System (RRID:SCR_005118)

Description: SPROUTS is a database of predicted protein folding related data. It was designed to gather all the results from a study concerning the comparison between tools devoted to the prediction of stability changes upon point mutations. The second aim of this database is to offer simple and user-friendly tools to better visualize and analyze the results obtained. We are now able to propose three ways of visualization and analysis: the first one consists in getting raw Delta Delta G values in a table. The second one is a 2D graph representation of a computed stability score for each residue of a given sequence and for each tool. The last one is based on a Jmol applet (Jmol) with the possibility to represent the 3D structure of a given protein with symbols representing the information stored in the database. We assume that each visualization mode offers a different look on the data stored in the database and will suit to every scientists willing to query the database whether they are more used to handle 3D protein structure or 1D/2D sequence problems. Finally, the ultimate objective is to integrate these data and their analysis with other structural bioinformatic concepts in order to improve other methods that may be related to this concept. We are currently working at adding the information extracted from our other projects related to the prediction of protein folding nucleus in order to obtain a meta server devoted to the characterization of the folding core of proteins. As of today, this database has grown up and consists in more than 100 structures which have been computed for a total of around 16500 amino acids.

Abbreviations: SPROUTS

Synonyms: Structural Prediction for Protein Folding Utility System

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Keywords: protein conformation, protein folding, protein structure

Funding: NSF IIS-0223042;
NSF 0738403;
NSF IIS-0431174;
NSF 0551444

Resource Name: SPROUTS- Structural Prediction for Protein Folding Utility System

Resource ID: SCR_005118

Alternate IDs: nif-0000-03491

Old URLs: <http://bioinformatics.eas.asu.edu/springs/Sprouts/projectsSprouts.html>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260821T193731+0000

Ratings and Alerts

No rating or validation information has been found for SPROUTS- Structural Prediction for Protein Folding Utility System.

No alerts have been found for SPROUTS- Structural Prediction for Protein Folding Utility System.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.