## Predictions for Entire Proteomes

**RRID:** SCR_002803  
**Type:** Tool

### Proper Citation

Predictions for Entire Proteomes (RRID:SCR_002803)

### Resource Information

**URL:** [http://www.predictprotein.org/](http://www.predictprotein.org/)

**Description:** Web application for sequence analysis and the prediction of protein structure and function. The user interface intakes protein sequences or alignments and returned multiple sequence alignments, motifs, and nuclear localization signals.

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**Resource Type:** Resource, data analysis software, data processing software, software application, sequence analysis software, web application, software resource

**Keywords:** sequence analysis database, protein structure prediction, protein structure, protein function

**Resource ID:** SCR_002803

**Parent Organization:** Columbia University; New York; USA

**Funding Agency:** BMBF

**References:** PMID:24799431

**Availability:** Open for academic use, Acknowledgement requested

**Website Status:** Last checked up

**Alternate IDs:** nif-0000-00136
Old URLs: http://cubic.bioc.columbia.edu/pep/

Mentions Count: 229

Ratings and Alerts

No rating or validation information has been found for Predictions for Entire Proteomes.

No alerts have been found for Predictions for Entire Proteomes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 229 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch Infrastructure.


