

Resource Summary Report

Generated by [SPARC SAWG](#) on Jul 28, 2026

DynaMine

RRID:SCR_014559

Type: Tool

Proper Citation

DynaMine (RRID:SCR_014559)

Resource Information

URL: <http://dynamine.ibsquare.be/submission/>

Proper Citation: DynaMine (RRID:SCR_014559)

Description: An NMR based method for protein folding prediction. Users can enter a UniProt identifier, FASTA sequences, or upload a file containing FASTA sequences and results are returned., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: web application, software resource

Defining Citation: [PMID:24225580](#)

Keywords: nmr, protein folding, prediction, fasta, sequence, dynamics

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: DynaMine

Resource ID: SCR_014559

Alternate URLs: <http://dynamine.ibsquare.be>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260728T043440+0000

Ratings and Alerts

No rating or validation information has been found for DynaMine.

No alerts have been found for DynaMine.

Data and Source Information

Usage and Citation Metrics

We found 39 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Lin S, et al. (2025) Dr.??Kinase: predicting the drug-resistance hotspots of protein kinases. *Nucleic acids research*, 53(W1), W258.

Ghosh S, et al. (2025) Exploring the potential role of GyrA inhibiting quinoline analog: an in silico study. *Scientific reports*, 15(1), 23136.

Basu S, et al. (2024) Cefiderocol susceptibility endows hope in treating carbapenem-resistant *Pseudomonas aeruginosa*: insights from in vitro and in silico evidence. *RSC advances*, 14(30), 21328.

Zheng M, et al. (2024) MetaDegron: multimodal feature-integrated protein language model for predicting E3 ligase targeted degrons. *Briefings in bioinformatics*, 25(6).

Debroy R, et al. (2023) Translational protein RpsE as an alternative target for novel nucleoside analogues to treat MDR *Enterobacter cloacae* ATCC 13047: network analysis and molecular dynamics study. *World journal of microbiology & biotechnology*, 39(7), 187.

Cogez V, et al. (2023) N-Glycan on the Non-Consensus N-X-C Glycosylation Site Impacts Activity, Stability, and Localization of the Sda Synthase B4GALNT2. *International journal of molecular sciences*, 24(4).

Orlando G, et al. (2022) Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. *Journal of molecular biology*, 434(12), 167579.

Mendes LFS, et al. (2022) Resurrecting Golgi proteins to grasp Golgi ribbon formation and self-association under stress. *International journal of biological macromolecules*, 194, 264.

Sutinen A, et al. (2022) Structural insights into Charcot-Marie-Tooth disease-linked mutations in human GDAP1. *FEBS open bio*, 12(7), 1306.

Adebayo JO, et al. (2022) Iloneoside, an antimalarial pregnane glycoside isolated from *Gongronema latifolium* leaf, potentiates the activity of chloroquine against multidrug resistant *Plasmodium falciparum*. *Molecular and biochemical parasitology*, 249, 111474.

Kind L, et al. (2022) Structural and biophysical characterization of transcription factor HNF-1A as a tool to study MODY3 diabetes variants. *The Journal of biological chemistry*, 298(4), 101803.

Borisenko I, et al. (2022) Novel protein from larval sponge cells, ilborin, is related to energy turnover and calcium binding and is conserved among marine invertebrates. *Open biology*, 12(2), 210336.

Sneha S, et al. (2022) In silico structural and functional characterization of *Antheraea mylitta* cocoonase. *Journal, genetic engineering & biotechnology*, 20(1), 102.

Lambrughi M, et al. (2021) Ubiquitin Interacting Motifs: Duality Between Structured and Disordered Motifs. *Frontiers in molecular biosciences*, 8, 676235.

Kagami LP, et al. (2021) b2bTools: online predictions for protein biophysical features and their conservation. *Nucleic acids research*, 49(W1), W52.

Mauri T, et al. (2021) O-GlcNAcylation Prediction: An Unattained Objective. *Advances and applications in bioinformatics and chemistry : AABC*, 14, 87.

Grau I, et al. (2021) Interpreting a black box predictor to gain insights into early folding mechanisms. *Computational and structural biotechnology journal*, 19, 4919.

Jacob JJ, et al. (2021) Evolutionary Tracking of SARS-CoV-2 Genetic Variants Highlights an Intricate Balance of Stabilizing and Destabilizing Mutations. *mBio*, 12(4), e0118821.

Shankar C, et al. (2021) Aerobactin Seems To Be a Promising Marker Compared With Unstable RmpA2 for the Identification of Hypervirulent Carbapenem-Resistant *Klebsiella pneumoniae*: In Silico and In Vitro Evidence. *Frontiers in cellular and infection microbiology*, 11, 709681.

Telek E, et al. (2021) The C-terminal tail extension of myosin 16 acts as a molten globule, including intrinsically disordered regions, and interacts with the N-terminal ankyrin. *The Journal of biological chemistry*, 297(1), 100716.