

Resource Summary Report

Generated by [NIF](#) on Sep 3, 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: software resource, web application

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: 20260829T182822+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 44 mentions in open access literature.

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

So?tys K, et al. (2025) The intrinsically disordered AB region: a key modulator of the molecular properties of human RXR?. Cell communication and signaling : CCS, 23(1), 243.

Soza?ska N, et al. (2025) The molecular properties of the bHLH TCF4 protein as an intrinsically disordered hub transcription factor. Cell communication and signaling : CCS, 23(1), 154.

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.

Lenda R, et al. (2024) Deciphering the dual nature of nesfatin-1: a tale of zinc ion's Janus-faced influence. Cell communication and signaling : CCS, 22(1), 298.

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.

So?tys K, et al. (2023) Phase separation propensity of the intrinsically disordered AB region of human RXR?. Cell communication and signaling : CCS, 21(1), 92.

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).

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

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.

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.

Lenda R, et al. (2022) Does one plus one always equal two? Structural differences between nesfatin-1, -2, and nesfatin-1/2. *Cell communication and signaling : CCS*, 20(1), 163.

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.

Lambrugh 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.