

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

IntFOLD

RRID:SCR_024523

Type: Tool

Proper Citation

IntFOLD (RRID:SCR_024523)

Resource Information

URL: <https://www.reading.ac.uk/bioinf/IntFOLD/>

Proper Citation: IntFOLD (RRID:SCR_024523)

Description: Web integrated protein structure and function prediction server. Integrated server for modelling protein structures and functions from amino acid sequences.

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:25820431](#)

Keywords: protein structure prediction, protein function prediction, modelling protein structures and functions from amino acid sequences,

Availability: Free, Freely available

Resource Name: IntFOLD

Resource ID: SCR_024523

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260905T133032+0000

Ratings and Alerts

No rating or validation information has been found for IntFOLD.

No alerts have been found for IntFOLD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Savelieva EM, et al. (2026) An Unusual Component of the Multistep Phosphorelay from Tea Plant (*Camellia sinensis* L.). *International journal of molecular sciences*, 27(10).

Al-Asadi SA, et al. (2024) Unraveling antibiotic resistance in *Achromobacter mucicolens* IA strain: genomic insights, structural analysis, and prospects for targeted therapeutics. *Microbiology spectrum*, 12(12), e0392623.

Bibi M, et al. (2023) In Silico Characterisation of the *Aedes aegypti* Gustatory Receptors. *International journal of molecular sciences*, 24(15).

Lomin SN, et al. (2023) Canonical and Alternative Auxin Signaling Systems in Mono-, Di-, and Tetraploid Potatoes. *International journal of molecular sciences*, 24(14).

La Paglia L, et al. (2023) Bioactive Molecules from the Innate Immunity of Ascidians and Innovative Methods of Drug Discovery: A Computational Approach Based on Artificial Intelligence. *Marine drugs*, 22(1).

Muñoz-Muñoz PLA, et al. (2023) Structural Insights into the *Giardia lamblia* Target of Rapamycin Homolog: A Bioinformatics Approach. *International journal of molecular sciences*, 24(15).

Kim KH, et al. (2022) Novel Polymorphisms and Genetic Characteristics of the Prion Protein Gene in Pheasants. *Frontiers in veterinary science*, 9, 935476.

Toth JM, et al. (2021) ResiRole: residue-level functional site predictions to gauge the accuracies of protein structure prediction techniques. *Bioinformatics (Oxford, England)*, 37(3), 351.