

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 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: software resource, data access protocol, 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: 20260801T190817+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 3 mentions in open access literature.

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

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.

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).

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.