

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

ModFOLD

RRID:SCR_024518

Type: Tool

Proper Citation

ModFOLD (RRID:SCR_024518)

Resource Information

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

Proper Citation: ModFOLD (RRID:SCR_024518)

Description: Web server for the global and local quality estimation of 3D protein models

Synonyms: ModFOLD6, ModFOLD8

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

Defining Citation: [PMID:28460136](#)

Keywords: quality estimation, 3D protein models,

Availability: Restricted

Resource Name: ModFOLD

Resource ID: SCR_024518

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260728T043709+0000

Ratings and Alerts

No rating or validation information has been found for ModFOLD.

No alerts have been found for ModFOLD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Edmunds NS, et al. (2024) Benchmarking of AlphaFold2 accuracy self-estimates as indicators of empirical model quality and ranking: a comparison with independent model quality assessment programmes. *Bioinformatics* (Oxford, England), 40(8).

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.