

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 3, 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:** data access protocol, web service, 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:** 20260803T040915+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 [PRECISE-TBI](#) .

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.