

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 2, 2026

IDDT

RRID:SCR_024524

Type: Tool

Proper Citation

IDDT (RRID:SCR_024524)

Resource Information

URL: <https://swissmodel.expasy.org/lddt>

Proper Citation: IDDT (RRID:SCR_024524)

Description: Web server for local superposition free score for comparing protein structures and models using distance difference tests. Superposition free score that evaluates local distance differences of all atoms in model, including validation of stereochemical plausibility.

Synonyms: Local Distance Difference Test

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

Defining Citation: [PMID:23986568](#)

Keywords: local superposition free score, comparing protein structures and models, distance difference tests,

Availability: Free, Freely available

Resource Name: IDDT

Resource ID: SCR_024524

Record Creation Time: 20231002T161337+0000

Record Last Update: 20260801T190828+0000

Ratings and Alerts

No rating or validation information has been found for IDDT.

No alerts have been found for IDDT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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.