

Resource Summary Report

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

TMDet

RRID:SCR_011964

Type: Tool

Proper Citation

TMDet (RRID:SCR_011964)

Resource Information

URL: <http://tmdet.enzim.hu/>

Proper Citation: TMDet (RRID:SCR_011964)

Description: Web server for the detection of the transmembrane regions of membrane proteins using their 3D structure only.

Abbreviations: TMDet

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:15539454](#), [PMID:15180935](#)

Resource Name: TMDet

Resource ID: SCR_011964

Alternate IDs: OMICS_01615

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260905T133201+0000

Ratings and Alerts

No rating or validation information has been found for TMDet.

No alerts have been found for TMDet.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Tusnady GE, et al. (2025) TmDet 4.0: determining membrane orientation of transmembrane proteins from 3D structure. Nucleic acids research, 53(W1), W542.

Sun J, et al. (2023) TMKit: a Python interface for computational analysis of transmembrane proteins. Briefings in bioinformatics, 24(5).

Zribi I, et al. (2023) Genome-Wide Identification and Expression Profiling of Pathogenesis-Related Protein 1 (PR-1) Genes in Durum Wheat (*Triticum durum* Desf.). Plants (Basel, Switzerland), 12(10).

Ozvardik K, et al. (2021) Assembly of Biomolecular Gigastructures and Visualization with the Vulkan Graphics API. Journal of chemical information and modeling, 61(10), 5293.

Younis S, et al. (2017) Alpha conotoxin-BuIA globular isomer is a competitive antagonist for oleoyl-L-alpha-lysophosphatidic acid binding to LPAR6; A molecular dynamics study. PloS one, 12(12), e0189154.

Alford RF, et al. (2015) An Integrated Framework Advancing Membrane Protein Modeling and Design. PLoS computational biology, 11(9), e1004398.

Bogdanov M, et al. (2005) Transmembrane protein topology mapping by the substituted cysteine accessibility method (SCAM(TM)): application to lipid-specific membrane protein topogenesis. Methods (San Diego, Calif.), 36(2), 148.