

Resource Summary Report

Generated by [dkNET](#) on May 1, 2025

PRED-TMR

RRID:SCR_006203

Type: Tool

Proper Citation

PRED-TMR (RRID:SCR_006203)

Resource Information

URL: <http://athina.biol.uoa.gr/PRED-TMR/>

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Description: A web server that predicts transmembrane domains in proteins using solely information contained in the sequence itself. The algorithm refines a standard hydrophobicity analysis with a detection of potential termini (edges, starts and ends) of transmembrane regions. This allows both to discard highly hydrophobic regions not delimited by clear start and end configurations and to confirm putative transmembrane segments not distinguishable by their hydrophobic composition. The accuracy obtained on a test set of 101 non homologous transmembranes proteins with reliable topologies compares well with that of other popular existing methods. Only a slight decrease in prediction accuracy was observed when the algorithm was applied to all transmembrane proteins of the SwissProt database (release 35).

Abbreviations: PRED-TMR

Synonyms: PRED-TMR: A novel method for predicting transmembrane segment in proteins based on a statistical analysis of the SwissProt database

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

Defining Citation: [PMID:10360978](#)

Keywords: predict, transmembrane segment, protein, algorithm, sequence, membrane protein, protein structure, transmembrane region, hydrophobicity analysis

Funding: European Union ERBFMRXCT960019

Resource Name: PRED-TMR

Resource ID: SCR_006203

Alternate IDs: nlx_151765

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250430T055424+0000

Ratings and Alerts

No rating or validation information has been found for PRED-TMR.

No alerts have been found for PRED-TMR.

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 [dkNET](#).

Szutkowski K, et al. (2019) Structural Analysis and Dynamic Processes of the Transmembrane Segment Inside Different Micellar Environments-Implications for the TM4 Fragment of the Bilitranslocase Protein. International journal of molecular sciences, 20(17).

Marschall R, et al. (2016) Update on Nox function, site of action and regulation in Botrytis cinerea. Fungal biology and biotechnology, 3, 8.

Taylor-Wells J, et al. (2014) The Signature Sequence Region of the Human Drug Transporter Organic Anion Transporting Polypeptide 1B1 Is Important for Protein Surface Expression. Journal of drug delivery, 2014, 129849.

Kupferschmied P, et al. (2014) Domain shuffling in a sensor protein contributed to the evolution of insect pathogenicity in plant-beneficial Pseudomonas protegens. PLoS pathogens, 10(2), e1003964.

Henrichs S, et al. (2012) Regulation of ABCB1/PGP1-catalysed auxin transport by linker phosphorylation. The EMBO journal, 31(13), 2965.

Madan LL, et al. (2008) Addition of a polypeptide stretch at the N-terminus improves the expression, stability and solubility of recombinant protein tyrosine phosphatases from

Drosophila melanogaster. Protein expression and purification, 57(2), 234.

de Brevern AG, et al. (2005) A structural model of a seven-transmembrane helix receptor: the Duffy antigen/receptor for chemokine (DARC). *Biochimica et biophysica acta*, 1724(3), 288.