Resource Summary Report

Generated by dkNET on Apr 22, 2025

PDBTM

RRID:SCR_011962
Type: Tool

Proper Citation

PDBTM (RRID:SCR_011962)

Resource Information

URL: http://pdbtm.enzim.hu/

Proper Citation: PDBTM (RRID:SCR_011962)

Description: Comprehensive and continuously updated transmembrane protein database of the Protein Data Bank (PDB) created by scanning all PDB entries with the TMDET algorithm. Resource for transmembrane proteins and their structures.

Abbreviations: PDBTM

Synonyms: PDBTM, Protein Data Bank of Transmembrane Proteins

Resource Type: data or information resource, database

Defining Citation: PMID:23203988

Keywords: FASEB list

Funding: Hungarian Scientific Research Fund ;
Hungarian Academy of Sciences

Availability: Free, Available for download, Freely available, Acknowledgement requested

Resource Name: PDBTM

Resource ID: SCR_011962

Alternate IDs: OMICS_01613

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250422T055637+0000

Ratings and Alerts

No rating or validation information has been found for PDBTM.

No alerts have been found for PDBTM.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 48 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Ngo K, et al. (2024) Elucidating molecular mechanisms of protoxin-II state-specific binding to the human NaV1.7 channel. The Journal of general physiology, 156(2).

Erd?s G, et al. (2024) AIUPred: combining energy estimation with deep learning for the enhanced prediction of protein disorder. Nucleic acids research, 52(W1), W176.

Gao T, et al. (2023) Secondary and Topological Structural Merge Prediction of Alpha-Helical Transmembrane Proteins Using a Hybrid Model Based on Hidden Markov and Long Short-Term Memory Neural Networks. International journal of molecular sciences, 24(6).

Pei J, et al. (2023) AFTM: a database of transmembrane regions in the human proteome predicted by AlphaFold. Database : the journal of biological databases and curation, 2023.

Ngo K, et al. (2023) Elucidating Molecular Mechanisms of Protoxin-2 State-specific Binding to the Human Na V 1.7 Channel. bioRxiv : the preprint server for biology.

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

Duart G, et al. (2022) Intra-Helical Salt Bridge Contribution to Membrane Protein Insertion. Journal of molecular biology, 434(5), 167467.

Overduin M, et al. (2022) Transmembrane Membrane Readers form a Novel Class of Proteins That Include Peripheral Phosphoinositide Recognition Domains and Viral Spikes. Membranes, 12(11).

Heged?s T, et al. (2022) Ins and outs of AlphaFold2 transmembrane protein structure predictions. Cellular and molecular life sciences : CMLS, 79(1), 73.

Seflova J, et al. (2022) Fluorescence lifetime imaging microscopy reveals sodium pump dimers in live cells. The Journal of biological chemistry, 298(5), 101865.

Kulandaisamy A, et al. (2021) MPTherm-pred: Analysis and Prediction of Thermal Stability Changes upon Mutations in Transmembrane Proteins. Journal of molecular biology, 433(11), 166646.

Sun J, et al. (2021) Improved sequence-based prediction of interaction sites in ?-helical transmembrane proteins by deep learning. Computational and structural biotechnology journal, 19, 1512.

Qu J, et al. (2021) Prediction of Metal Ion Binding Sites of Transmembrane Proteins. Computational and mathematical methods in medicine, 2021, 2327832.

Liu Z, et al. (2020) TMPSS: A Deep Learning-Based Predictor for Secondary Structure and Topology Structure Prediction of Alpha-Helical Transmembrane Proteins. Frontiers in bioengineering and biotechnology, 8, 629937.

Brielle ES, et al. (2020) Quantitative Analysis of Multiplex H-Bonds. Journal of the American Chemical Society, 142(33), 14150.

Fang C, et al. (2020) IMPContact: An Interhelical Residue Contact Prediction Method. BioMed research international, 2020, 4569037.

Xiao Y, et al. (2020) Experimental determination and data-driven prediction of homotypic transmembrane domain interfaces. Computational and structural biotechnology journal, 18, 3230.

Ding W, et al. (2020) Predicting the Real-Valued Inter-Residue Distances for Proteins. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 7(19), 2001314.

Mesdaghi S, et al. (2020) In silico prediction of structure and function for a large family of transmembrane proteins that includes human Tmem41b. F1000Research, 9, 1395.

Weinstein JY, et al. (2019) A lipophilicity-based energy function for membrane-protein modelling and design. PLoS computational biology, 15(8), e1007318.