Resource Summary Report

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TMRPres2D

RRID:SCR_007382
Type: Tool

Proper Citation

TMRPres2D (RRID:SCR_007382)

Resource Information

URL: http://bioinformatics.biol.uoa.gr/TMRPres2D/

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Description: Software that automates the creation of uniform, two-dimensional, high analysis graphical images/models of alpha-helical or beta-barrel transmembrane proteins. Protein sequence data and structural information may be acquired from public protein knowledge bases, emanate from prediction algorithms, or even be defined by the user. Several important biological and physical sequence attributes can be embedded in the graphical representation. The application has been written using the platform independent Java language by Sun Microsystems. The implementation is likely to encapsulate the Applet and JavaBean technology. Consequently, the tool, apart from standalone application, may be used as an applet or even embedded in a web-server. Thus, it can serve to exhibit transmembrane protein schematic models in web pages. Requirements for the stand-alone application: Java Runtime Environment 1.4.x The source code is available to any interested party, upon request from the authors.

Abbreviations: TMRPress2D

Synonyms: TransMembrane protein Re-Presentation in 2 Dimensions tool, TMRPres2D: High quality visual representation of transmembrane protein models

Resource Type: source code, software resource

Defining Citation: PMID:15201184

Keywords: two-dimensional, graphic, image, model, alpha-helical, beta-barrel, transmembrane protein, protein sequence, graphical representation, visualization software, data visualization software

Availability: Please cite.

Resource Name: TMRPres2D

Resource ID: SCR_007382

Alternate IDs: nif-0000-00382

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260801T191133+0000

Ratings and Alerts

No rating or validation information has been found for TMRPres2D.

No alerts have been found for TMRPres2D.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Bertuccini L, et al. (2024) Unveiling Cryptosporidium parvum sporozoite-derived extracellular vesicles: profiling, origin, and protein composition. Frontiers in cellular and infection microbiology, 14, 1367359.

Nunes A, et al. (2023) Recurrent Campylobacter jejuni Infections with In Vivo Selection of Resistance to Macrolides and Carbapenems: Molecular Characterization of Resistance Determinants. Microbiology spectrum, 11(4), e0107023.

Lopes CE, et al. (2022) Genetic and molecular Omp25 analyses from worldwide Brucella canis strains: Possible mutational influences in protein function. Gene, 817, 146175.

Martínez Velázquez M, et al. (2021) Immunoprotection evaluation of the recombinant N-terminal domain of Cys-loop receptors against Rhipicephalus (Boophilus) microplus tick infestation. Parasite (Paris, France), 28, 65.

Bibi N, et al. (2020) Identification and Computational Analysis of Novel TYR and SLC45A2 Gene Mutations in Pakistani Families With Identical Non-syndromic Oculocutaneous Albinism. Frontiers in genetics, 11, 749.

Begam RA, et al. (2020) The Arabidopsis L-Type Amino Acid Transporter 5 (LAT5/PUT5) Is Expressed in the Phloem and Alters Seed Nitrogen Content When Knocked Out. Plants (Basel, Switzerland), 9(11).

Sanchez VB, et al. (2019) Transmembrane 163 (TMEM163) protein effluxes zinc. Archives of biochemistry and biophysics, 677, 108166.

Puentes-Cala E, et al. (2019) An RND transporter in the monoterpene metabolism of Castellaniella defragrans. Biodegradation, 30(1), 1.

Abdali N, et al. (2018) Identification and characterization of smallest pore-forming protein in the cell wall of pathogenic Corynebacterium urealyticum DSM 7109. BMC biochemistry, 19(1), 3.

Castilho A, et al. (2018) An oligosaccharyltransferase from Leishmania major increases the N-glycan occupancy on recombinant glycoproteins produced in Nicotiana benthamiana. Plant biotechnology journal, 16(10), 1700.

Dean P, et al. (2018) Transporter gene acquisition and innovation in the evolution of Microsporidia intracellular parasites. Nature communications, 9(1), 1709.

Jeiranikhameneh M, et al. (2017) Designing novel construction for cell surface display of protein E on Escherichia coli using non-classical pathway based on Lpp-OmpA. AMB Express, 7(1), 53.

Panzer AA, et al. (2017) Nkx2-5 and Sarcospan genetically interact in the development of the muscular ventricular septum of the heart. Scientific reports, 7, 46438.

Con P, et al. (2017) Salinity-Dependent Shift in the Localization of Three Peptide Transporters along the Intestine of the Mozambique Tilapia (Oreochromis mossambicus). Frontiers in physiology, 8, 8.

Tal I, et al. (2016) The Arabidopsis NPF3 protein is a GA transporter. Nature communications, 7, 11486.

Zhang L, et al. (2016) SepG coordinates sporulation-specific cell division and nucleoid organization in Streptomyces coelicolor. Open biology, 6(4), 150164.

Wu X, et al. (2016) FmvB: A Francisella tularensis Magnesium-Responsive Outer Membrane Protein that Plays a Role in Virulence. PloS one, 11(8), e0160977.

Guo H, et al. (2015) Identification and application of keto acids transporters in Yarrowia lipolytica. Scientific reports, 5, 8138.

Novick PA, et al. (2015) Evolutionary dynamics of rhomboid proteases in Streptomycetes. BMC research notes, 8, 234.

Flores-Fernández JM, et al. (2014) Molecular cloning and characterization of a glycine-like receptor gene from the cattle tick Rhipicephalus (Boophilus) microplus (Acari: Ixodidae). Parasite (Paris, France), 21, 43.