Resource Summary Report

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Membrane Protein Explorer

RRID:SCR_014077
Type: Tool

Proper Citation

Membrane Protein Explorer (RRID:SCR_014077)

Resource Information

URL: http://blanco.biomol.uci.edu/mpex/

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Description: Software which predicts topology and other features of membrane proteins through hydropathy plots based on thermodynamic and biological principles. This version of MPEx uses two types of hydropathy scales: Experiment-based whole-residue partitioning scales and experiment-based biological partitioning scales. The whole-residue partitioning scales predict the transmembrane (TM) segments of membrane proteins of known structure. The biological scale utilizes current knowledge of the code the Sec61 translocon to identify TM segments. MPEx is a Java program (not a Java applet) deployed using Java Web Start, which is part of the Java Runtime Environment.

Abbreviations: MPEx

Synonyms: Membrane Protein Explorer (MPEx)

Resource Type: data processing software, data analysis software, software resource, software application

Defining Citation: PMID:19785006

Keywords: membrane protein, hydropathy plot, topology, software, java, bio.tools

Funding:

Availability: Available to the research community, Requires version 7 or higher of Java Runtime Environment

Resource Name: Membrane Protein Explorer

Resource ID: SCR_014077

Alternate IDs: biotools:mpex

Alternate URLs: https://bio.tools/mpex

Record Creation Time: 20220129T080318+0000

Record Last Update: 20250417T065443+0000

Ratings and Alerts

No rating or validation information has been found for Membrane Protein Explorer.

No alerts have been found for Membrane Protein Explorer.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Banday ZZ, et al. (2022) Friend or foe: Hybrid proline-rich proteins determine how plants respond to beneficial and pathogenic microbes. Plant physiology, 190(1), 860.

Pérez-Vargas J, et al. (2021) A fusion peptide in preS1 and the human protein disulfide isomerase ERp57 are involved in hepatitis B virus membrane fusion process. eLife, 10.

Wirth S, et al. (2021) What Role Might Non-Mating Receptors Play in Schizophyllum commune? Journal of fungi (Basel, Switzerland), 7(5).

Mork-Jansson AE, et al. (2019) A strategy to characterize chlorophyll protein interaction in LIL3. Plant methods, 15, 1.

Leber R, et al. (2018) Synergism of Antimicrobial Frog Peptides Couples to Membrane Intrinsic Curvature Strain. Biophysical journal, 114(8), 1945.

Krainer G, et al. (2018) A minimal helical-hairpin motif provides molecular-level insights into misfolding and pharmacological rescue of CFTR. Communications biology, 1, 154.

Sánchez-Vásquez L, et al. (2017) Near-neighbor interactions of the membrane-embedded subunits of the mitochondrial ATP synthase of a chlorophycean alga. Biochimica et biophysica acta. Bioenergetics, 1858(7), 497.

Bacalum M, et al. (2017) Modulating short tryptophan- and arginine-rich peptides activity by substitution with histidine. Biochimica et biophysica acta. General subjects, 1861(7), 1844.

Raucci R, et al. (2017) Conformational analysis of the human chemokine receptor CXCR3. Molecular immunology, 92, 76.

Kirk LM, et al. (2016) Distribution of the SynDIG4/proline-rich transmembrane protein 1 in rat brain. The Journal of comparative neurology, 524(11), 2266.

Marsh A, et al. (2016) Simvastatin Sodium Salt and Fluvastatin Interact with Human Gap Junction Gamma-3 Protein. PloS one, 11(2), e0148266.

Beveridge R, et al. (2015) Relating gas phase to solution conformations: Lessons from disordered proteins. Proteomics, 15(16), 2872.

Mork-Jansson AE, et al. (2015) Lil3 dimerization and chlorophyll binding in Arabidopsis thaliana. FEBS letters, 589(20 Pt B), 3064.

Kyrychenko A, et al. (2014) Structural plasticity in the topology of the membrane-interacting domain of HIV-1 gp41. Biophysical journal, 106(3), 610.

Siotto F, et al. (2014) Viruses infecting marine picoplancton encode functional potassium ion channels. Virology, 466-467, 103.

Badani H, et al. (2014) Peptide entry inhibitors of enveloped viruses: the importance of interfacial hydrophobicity. Biochimica et biophysica acta, 1838(9), 2180.

Walther FJ, et al. (2014) Surfactant protein C peptides with salt-bridges ("ion-locks") promote high surfactant activities by mimicking the ?-helix and membrane topography of the native protein. PeerJ, 2, e485.

Andika IB, et al. (2013) Endoplasmic reticulum export and vesicle formation of the movement protein of Chinese wheat mosaic virus are regulated by two transmembrane domains and depend on the secretory pathway. Virology, 435(2), 493.

Cui H, et al. (2013) Understanding the role of amphipathic helices in N-BAR domain driven membrane remodeling. Biophysical journal, 104(2), 404.

Moreno-Habel DA, et al. (2012) Inactivation of the budded virus of Autographa californica M nucleopolyhedrovirus by gloverin. Journal of invertebrate pathology, 110(1), 92.