Resource Summary Report

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PRED-TMBB

RRID:SCR_006190
Type: Tool

Proper Citation

PRED-TMBB (RRID:SCR_006190)

Resource Information

URL: http://bioinformatics.biol.uoa.gr/PRED-TMBB/

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Description: A web tool, based on a Hidden Markov Model, capable of predicting the transmembrane beta-strands of the gram-negative bacteria outer membrane proteins, and of discriminating such proteins from water-soluble ones when screening large datasets. The model is trained in a discriminative manner, aiming at maximizing the probability of the correct prediction rather than the likelihood of the sequences. The training is performed on a non-redundant database consisting of 16 outer membrane proteins (OMP''s) with their structures known at atomic resolution. We show that we can achieve predictions at least as good comparing with other existing methods, using as input only the amino-acid sequence, without the need of evolutionary information included in multiple alignments. The method is also powerful when used for discrimination purposes, as it can discriminate with a high accuracy the outer membrane proteins from water soluble in large datasets, making it a quite reliable solution for screening entire genomes. This web-server can help you run a discriminating process on any amino-acid sequence and thereafter localize the transmembrane strands and find the topology of the loops.

Abbreviations: PRED-TMBB

Synonyms: PRED-TMBB: A Hidden Markov Model method capable of predicting and discriminating beta-barrel outer membrane proteins

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

Defining Citation: PMID:15215419, PMID:15070403

Keywords: protein, hidden markov model, prediction, membrane protein, beta-barrel outer membrane protein, gram-negative bacteria, topology, outer membrane protein, beta-barrel protein, probability, transmembrane strand, bio.tools, FASEB list

Funding: Greek Ministry of National Education and Religious Affairs

Availability: Acknowledgement requested

Resource Name: PRED-TMBB

Resource ID: SCR_006190

Alternate IDs: biotools:pred-tmbb, nlx_151734

Alternate URLs: https://bio.tools/pred-tmbb

Record Creation Time: 20220129T080234+0000

Record Last Update: 20250429T055036+0000

Ratings and Alerts

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

No alerts have been found for PRED-TMBB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 53 mentions in open access literature.

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

Kamaruzaman INA, et al. (2024) Characterisation of Putative Outer Membrane Proteins from Leptospira borgpetersenii Serovar Hardjo-Bovis Identifies Novel Adhesins and Diversity in Adhesion across Genomospecies Orthologs. Microorganisms, 12(2).

Fatehi Z, et al. (2023) Oral vaccination with novel Lactococcus lactis mucosal live vector-secreting Brucella lumazine synthase (BLS) protein induces humoral and cellular immune protection against Brucella abortus. Archives of microbiology, 205(4), 122.

Murali R, et al. (2023) Physiological potential and evolutionary trajectories of syntrophic sulfate-reducing bacterial partners of anaerobic methanotrophic archaea. PLoS biology,

21(9), e3002292.

Tabibpour NS, et al. (2023) Putative novel outer membrane antigens multi-epitope DNA vaccine candidates identified by Immunoinformatic approaches to control Acinetobacter baumannii. BMC immunology, 24(1), 46.

Bu L, et al. (2023) A genome sequence for Biomphalaria pfeifferi, the major vector snail for the human-infecting parasite Schistosoma mansoni. PLoS neglected tropical diseases, 17(3), e0011208.

Cavenague MF, et al. (2023) LIC12254 Is a Leptospiral Protein That Interacts with Integrins via the RGD Motif. Tropical medicine and infectious disease, 8(5).

Jiang C, et al. (2022) TurboID Screening of the OmpP2 Protein Reveals Host Proteins Involved in Recognition and Phagocytosis of Glaesserella parasuis by iPAM Cells. Microbiology spectrum, 10(5), e0230722.

Lingappa UF, et al. (2021) An ecophysiological explanation for manganese enrichment in rock varnish. Proceedings of the National Academy of Sciences of the United States of America, 118(25).

Haynes AM, et al. (2021) Transcriptional and immunological analysis of the putative outer membrane protein and vaccine candidate TprL of Treponema pallidum. PLoS neglected tropical diseases, 15(1), e0008812.

Elhosseiny NM, et al. (2021) Development of an Immunochromatographic Strip Using Conjugated Gold Nanoparticles for the Rapid Detection of Klebsiella pneumoniae Causing Neonatal Sepsis. Pharmaceutics, 13(8).

Staton GJ, et al. (2021) Dissecting the molecular diversity and commonality of bovine and human treponemes identifies key survival and adhesion mechanisms. PLoS pathogens, 17(3), e1009464.

Hui X, et al. (2021) Computational prediction of secreted proteins in gram-negative bacteria. Computational and structural biotechnology journal, 19, 1806.

Pinaud S, et al. (2021) New Insights Into Biomphalysin Gene Family Diversification in the Vector Snail Biomphalaria glabrata. Frontiers in immunology, 12, 635131.

Clawson ML, et al. (2020) Differences between predicted outer membrane proteins of genotype 1 and 2?Mannheimia haemolytica. BMC microbiology, 20(1), 250.

Arbour TJ, et al. (2020) Diverse Microorganisms in Sediment and Groundwater Are Implicated in Extracellular Redox Processes Based on Genomic Analysis of Bioanode Communities. Frontiers in microbiology, 11, 1694.

Staton GJ, et al. (2020) Putative ?-Barrel Outer Membrane Proteins of the Bovine Digital Dermatitis-Associated Treponemes: Identification, Functional Characterization, and Immunogenicity. Infection and immunity, 88(5).

Maiti B, et al. (2020) Application of Outer Membrane Protein-Based Vaccines Against Major Bacterial Fish Pathogens in India. Frontiers in immunology, 11, 1362.

Fereshteh S, et al. (2020) New putative vaccine candidates against Acinetobacter baumannii using the reverse vaccinology method. Microbial pathogenesis, 143, 104114.

Han MJ, et al. (2020) Novel Bacterial Surface Display System Based on the Escherichia coli Protein MipA. Journal of microbiology and biotechnology, 30(7), 1097.

Zhou Y, et al. (2019) Surface-exposed loops L7 and L8 of Haemophilus (Glaesserella) parasuis OmpP2 contribute to the expression of proinflammatory cytokines in porcine alveolar macrophages. Veterinary research, 50(1), 105.