

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

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Availability: Acknowledgement requested

Resource Name: PRED-TMBB

Resource ID: SCR_006190

Alternate IDs: biotools:pred-tmabb, nlx_151734

Alternate URLs: <https://bio.tools/pred-tmabb>

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260811T043247+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 58 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

Ma Y, et al. (2026) The hidden Markov model and its applications in bioinformatics analysis. *Genes & diseases*, 13(1), 101729.

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against *Brucella melitensis* in mice. *Scientific reports*, 15(1), 27210.

Liu R, et al. (2025) Small molecule inhibitor targets OmpV to treat pandemic *Vibrio cholerae* infection. *Nature communications*, 17(1), 826.

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 Genomespecies Orthologs. *Microorganisms*, 12(2).

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.

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.

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.

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.

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).

Rahbar MR, et al. (2022) A unique antigen against SARS-CoV-2, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*. Scientific reports, 12(1), 10852.

Chantes-Guerra A, et al. (2022) A putative siderophore receptor of *Gallibacterium anatis* 12656-12 under Fur control also binds hemoglobin. Frontiers in microbiology, 13, 951173.

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.

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.

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).

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.

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).

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

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

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.

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