

Resource Summary Report

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PRED-LIPO

RRID:SCR_006187

Type: Tool

Proper Citation

PRED-LIPO (RRID:SCR_006187)

Resource Information

URL: <http://bioinformatics.biol.uoa.gr/PRED-LIPO/>

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Description: A web tool using the Hidden Markov Model method for the prediction of lipoprotein signal peptides of Gram-positive bacteria, trained on a set of 67 experimentally verified lipoproteins. The method outperforms LipoP and the methods based on regular expression patterns, in various data sets containing experimentally characterized lipoproteins, secretory proteins, proteins with an N-terminal TM segment and cytoplasmic proteins. The method is also very sensitive and specific in the detection of secretory signal peptides and in terms of overall accuracy outperforms even SignalP, which is the top-scoring method for the prediction of signal peptides.

Abbreviations: PRED-LIPO

Synonyms: PRED-LIPO: Prediction of Lipoprotein and Secretory Signal Peptides in Gram-positive Bacteria with Hidden Markov Models

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

Defining Citation: [PMID:19367716](#)

Keywords: hidden markov model, lipoprotein signal peptide, gram-positive bacteria, lipoprotein, prediction, peptide, protein, signal peptide, bio.tools

Funding: National Scholarships Foundation of Greece

Availability: Free

Resource Name: PRED-LIPO

Resource ID: SCR_006187

Alternate IDs: nlx_151732, biotools:pred-lipo

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

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260821T193759+0000

Ratings and Alerts

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

No alerts have been found for PRED-LIPO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Malakar B, et al. (2023) Phosphorylation of CFP10 modulates Mycobacterium tuberculosis virulence. mBio, 14(5), e0123223.

Rasheed MA, et al. (2021) Identification of Lead Compounds against Scm (fms10) in Enterococcus faecium Using Computer Aided Drug Designing. Life (Basel, Switzerland), 11(2).

Pal S, et al. (2021) Complete genome sequence and identification of polyunsaturated fatty acid biosynthesis genes of the myxobacterium Minicystis rosea DSM 24000T. BMC genomics, 22(1), 655.

Keffeler EC, et al. (2021) Influence of the Alternative Sigma Factor RpoN on Global Gene Expression and Carbon Catabolism in Enterococcus faecalis V583. mBio, 12(3).

Garcion C, et al. (2021) Comparison of Current Methods for Signal Peptide Prediction in Phytoplasmas. Frontiers in microbiology, 12, 661524.

Karched M, et al. (2019) Proteomic Analysis and Virulence Assessment of Granulicatella adiacens Secretome. Frontiers in cellular and infection microbiology, 9, 104.

Solanki V, et al. (2019) Prioritization of potential vaccine targets using comparative proteomics and designing of the chimeric multi-epitope vaccine against Pseudomonas aeruginosa. Scientific reports, 9(1), 5240.

Otarigho B, et al. (2018) Analysis of antibiotics resistant genes in different strains of Staphylococcus aureus. Bioinformation, 14(3), 113.

Paes JA, et al. (2018) Comparative proteomics of two *Mycoplasma hyopneumoniae* strains and *Mycoplasma flocculare* identified potential porcine enzootic pneumonia determinants. *Virulence*, 9(1), 1230.

Rasheed MA, et al. (2017) Comparative Genomics of *Mycoplasma bovis* Strains Reveals That Decreased Virulence with Increasing Passages Might Correlate with Potential Virulence-Related Factors. *Frontiers in cellular and infection microbiology*, 7, 177.

Kant R, et al. (2017) An in silico pan-genomic probe for the molecular traits behind *Lactobacillus ruminis* gut autochthony. *PloS one*, 12(4), e0175541.

Gonzalez-Perez MN, et al. (2016) Deciphering the virulence factors of the opportunistic pathogen *Mycobacterium colombiense*. *New microbes and new infections*, 14, 98.

Weldearegay YB, et al. (2016) Proteomic characterization of pleural effusion, a specific host niche of *Mycoplasma mycoides* subsp. *mycoides* from cattle with contagious bovine pleuropneumonia (CBPP). *Journal of proteomics*, 131, 93.

Khan FA, et al. (2016) Immunoproteomic identification of MbovP579, a promising diagnostic biomarker for serological detection of *Mycoplasma bovis* infection. *Oncotarget*, 7(26), 39376.

Shahmirzadi SV, et al. (2016) Evaluation of *Staphylococcus aureus* Lipoproteins: Role in Nutritional Acquisition and Pathogenicity. *Frontiers in microbiology*, 7, 1404.

Wegmann U, et al. (2015) The pan-genome of *Lactobacillus reuteri* strains originating from the pig gastrointestinal tract. *BMC genomics*, 16, 1023.

Ciric M, et al. (2014) Metasecretome-selective phage display approach for mining the functional potential of a rumen microbial community. *BMC genomics*, 15(1), 356.