

Resource Summary Report

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CW-PRED

RRID:SCR_006188

Type: Tool

Proper Citation

CW-PRED (RRID:SCR_006188)

Resource Information

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

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Description: A web tool for the prediction of Cell Wall-Anchored Proteins in Gram+ Bacteria. Gram-positive bacteria have surface proteins that are often implicated in virulence. A group of extracellular proteins attached to the cell wall contains an LPXTG-like motif that is target for cleavage and covalent coupling to peptidoglycan by sortase enzymes. A new Hidden Markov Model (HMM), an extension to the HMM model from Litou et al., <http://www.ncbi.nlm.nih.gov/pubmed/18464329>, was developed for predicting the LPXTG and LPXTG-like cell-wall proteins of Gram-positive bacteria. An analysis of 177 completely sequenced genomes has been performed as well. We identified in total 1456 cell-wall proteins, from which 1283 have the LPXTG motif, 39 the NPXTG motif, 53 have the LPXTA and 81 the LAXTG motif.

Abbreviations: CW-PRED

Synonyms: CW-PRED: A HMM-based method for the classification of cell wall-anchored proteins of Gram-positive bacteria

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

Keywords: hidden markov model, gram-positive bacteria, protein, classification, cell-wall protein

Availability: Free for academic use, Acknowledgement requested

Resource Name: CW-PRED

Resource ID: SCR_006188

Alternate IDs: nlx_151733

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260807T042633+0000

Ratings and Alerts

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

No alerts have been found for CW-PRED.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Wu H, et al. (2021) Fucosidases from the human gut symbiont *Ruminococcus gnavus*. Cellular and molecular life sciences : CMLS, 78(2), 675.

Viana MVC, et al. (2020) Taxonomic classification of strain PO100/5 shows a broader geographic distribution and genetic markers of the recently described *Corynebacterium silvaticum*. PloS one, 15(12), e0244210.

Douillard FP, et al. (2018) Comparative genomic analysis of the multispecies probiotic-marketed product VSL#3. PloS one, 13(2), e0192452.

Subedi R, et al. (2018) Genomic analyses reveal two distinct lineages of *Corynebacterium ulcerans* strains. New microbes and new infections, 25, 7.

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.

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.

Chuzeville S, et al. (2017) Serotype-specific role of antigen I/II in the initial steps of the pathogenesis of the infection caused by *Streptococcus suis*. Veterinary research, 48(1), 39.

Popowska M, et al. (2017) InlL from *Listeria monocytogenes* Is Involved in Biofilm Formation and Adhesion to Mucin. Frontiers in microbiology, 8, 660.

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

Andreevskaya M, et al. (2016) *Lactobacillus oligofermentans* glucose, ribose and xylose transcriptomes show higher similarity between glucose and xylose catabolism-induced responses in the early exponential growth phase. *BMC genomics*, 17, 539.

Miljkovic M, et al. (2015) AggLb Is the Largest Cell-Aggregation Factor from *Lactobacillus paracasei* Subsp. *paracasei* BGNJ1-64, Functions in Collagen Adhesion, and Pathogen Exclusion In Vitro. *PloS one*, 10(5), e0126387.

Chuzeville S, et al. (2015) Antigen I/II encoded by integrative and conjugative elements of *Streptococcus agalactiae* and role in biofilm formation. *Microbial pathogenesis*, 88, 1.

Crost EH, et al. (2013) Utilisation of mucin glycans by the human gut symbiont *Ruminococcus gnavus* is strain-dependent. *PloS one*, 8(10), e76341.

Douillard FP, et al. (2013) Comparative genome analysis of *Lactobacillus casei* strains isolated from Actimel and Yakult products reveals marked similarities and points to a common origin. *Microbial biotechnology*, 6(5), 576.

Renier S, et al. (2012) Subcellular localization of extracytoplasmic proteins in monoderm bacteria: rational secretomics-based strategy for genomic and proteomic analyses. *PloS one*, 7(8), e42982.