

Resource Summary Report

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big-PI Predictor

RRID:SCR_001599

Type: Tool

Proper Citation

big-PI Predictor (RRID:SCR_001599)

Resource Information

URL: https://mendel.imp.ac.at/gpi/gpi_server.html

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Description: Prediction tool locating potential GPI-modification sites in precursor sequences applied for large-scale protein sequence database searches. The composite prediction function (with separate parametrization for metazoan and protozoan proteins) consists of terms evaluating both amino acid type preferences at sequence positions near a supposed omega-site as well as the concordance with general physical properties encoded in multi-residue correlation within the motif sequence. The latter terms are especially successful in rejecting non-appropriate sequences from consideration. The algorithm has been validated with a self-consistency and two jack-knife tests for the learning set of fully annotated sequences from the SWISS-PROT database as well as with a newly created database big-Pi (more than 300 GPI-motif mutations extracted from original literature sources). The accuracy of predicting the effect of mutations in the GPI sequence motif was above 83 %.

Abbreviations: big-PI Predictor

Synonyms: big-PI Predictor: GPI Modification Site Prediction

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

Defining Citation: [PMID:10497036](#), [PMID:10871885](#)

Keywords: prediction, glycoprotein, protein, glycosylphosphatidylinositol, genome annotation, target selection, FASEB list

Availability: Free, Freely available

Resource Name: big-PI Predictor

Resource ID: SCR_001599

Alternate IDs: nlx_153855

Old URLs: http://www.embl.de/beisenha/gpi/gpi_p%20rediction.html

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260919T195630+0000

Ratings and Alerts

No rating or validation information has been found for big-PI Predictor.

No alerts have been found for big-PI Predictor.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 59 mentions in open access literature.

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

Yang X, et al. (2026) Knockout of aminopeptidase N3 confers resistance to low concentrations of Bacillus thuringiensis Cry4Ba protoxin in Aedes aegypti. Parasites & vectors, 19(1).

Seifi N, et al. (2026) Design and in silico evaluation of an mRNA vaccine against HTLV-1 using AI-driven reverse vaccinology approaches. PloS one, 21(5), e0340201.

Islam S, et al. (2026) Bioinformatics-Guided structural characterization and immunogenicity assessment of multi-epitope vaccine candidates against Zika virus. Journal, genetic engineering & biotechnology, 24(1), 100641.

Teimoori P, et al. (2026) Computational Design of an mRNA Vaccine Targeting LRP6 for Triple-Negative Breast Cancer Therapy. Cancer reports (Hoboken, N.J.), 9(5), e70567.

Zhang Y, et al. (2023) Genome-Wide Comparative Analysis of the Fasciclin-like Arabinogalactan Proteins (FLAs) in Salicacea and Identification of Secondary Tissue Development-Related Genes. International journal of molecular sciences, 24(2).

Li K, et al. (2023) Belly roll, a GPI-anchored Ly6 protein, regulates Drosophila melanogaster escape behaviors by modulating the excitability of nociceptive peptidergic interneurons. eLife, 12.

Lauriello A, et al. (2022) GluR2Q and GluR2R AMPA Subunits are not Targets of lypd2 Interaction. PloS one, 17(11), e0278278.

Koizumi A, et al. (2022) Cleavage of α -1,4-glycosidic linkages by the glycosylphosphatidylinositol-anchored α -amylase AgtA decreases the molecular weight of cell wall α -1,3-glucan in *Aspergillus oryzae*. *Frontiers in fungal biology*, 3, 1061841.

Tinti M, et al. (2022) Visualisation of experimentally determined and predicted protein N-glycosylation and predicted glycosylphosphatidylinositol anchor addition in *Trypanosoma brucei*. *Wellcome open research*, 7, 33.

Bernardes WPOS, et al. (2022) SmTAL-9, a Member of the *Schistosoma mansoni* Tegument Allergen-Like Family, Is Important for Parasite Survival and a Putative Target for Drug/Vaccine Development. *Frontiers in immunology*, 13, 889645.

Amos B, et al. (2022) VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. *Nucleic acids research*, 50(D1), D898.

Han Z, et al. (2021) Identification of a novel variant erythrocyte surface antigen-1 (VESA1) in *Babesia orientalis*. *Parasitology research*, 120(8), 2863.

Ehsan M, et al. (2021) *Fasciola gigantica* tegumental calcium-binding EF-hand protein 4 exerts immunomodulatory effects on goat monocytes. *Parasites & vectors*, 14(1), 276.

Oliveira ACS, et al. (2021) Biological and Molecular Effects of *Trypanosoma cruzi* Residence in a LAMP-Deficient Intracellular Environment. *Frontiers in cellular and infection microbiology*, 11, 788482.

Zimmermann W, et al. (2021) The immune-modulating pregnancy-specific glycoproteins evolve rapidly and their presence correlates with hemochorial placentation in primates. *BMC genomics*, 22(1), 128.

Yousafi Q, et al. (2021) In silico annotation of unreviewed acetylcholinesterase (AChE) in some lepidopteran insect pest species reveals the causes of insecticide resistance. *Saudi journal of biological sciences*, 28(4), 2197.

Guo Z, et al. (2020) MAPK-dependent hormonal signaling plasticity contributes to overcoming *Bacillus thuringiensis* toxin action in an insect host. *Nature communications*, 11(1), 3003.

Zhang Z, et al. (2020) Identification of *Toxoplasma Gondii* Tyrosine Hydroxylase (TH) Activity and Molecular Immunoprotection against Toxoplasmosis. *Vaccines*, 8(2).

Kuo CC, et al. (2020) CaNRT2.1 Is Required for Nitrate but Not Nitrite Uptake in Chili Pepper Pathogen *Colletotrichum acutatum*. *Frontiers in microbiology*, 11, 613674.

Zhang Z, et al. (2020) The Molecular Characterization and Immunity Identification of *Trichomonas vaginalis* Adhesion Protein 33 (AP33). *Frontiers in microbiology*, 11, 1433.