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: http://mendel.imp.ac.at/sat/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, production service resource, data analysis service, service resource

Defining Citation: PMID:10497036, PMID:10871885

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

Funding:

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: 20250426T055450+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 50 mentions in open access literature.

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

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.

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.

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).

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

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.

Shi J, et al. (2020) The Caenorhabditis elegans CUB-like-domain containing protein RBT-1 functions as a receptor for Bacillus thuringiensis Cry6Aa toxin. PLoS pathogens, 16(5), e1008501.

Mo ZQ, et al. (2019) Characterization and immune regulation role of an immobilization antigen from Cryptocaryon irritans on groupers. Scientific reports, 9(1), 1029.

Zhou K, et al. (2019) Glycosylphosphatidylinositol-Anchored Proteins in Arabidopsis and One of Their Common Roles in Signaling Transduction. Frontiers in plant science, 10, 1022.

Oh SH, et al. (2019) Agglutinin-Like Sequence (ALS) Genes in the Candida parapsilosis Species Complex: Blurring the Boundaries Between Gene Families That Encode Cell-Wall Proteins. Frontiers in microbiology, 10, 781.

Wang Q, et al. (2019) Hepatocellular carcinoma-associated antigen 59 of Haemonchus contortus modulates the functions of PBMCs and the differentiation and maturation of monocyte-derived dendritic cells of goats in vitro. Parasites & vectors, 12(1), 105.

Ehsan M, et al. (2018) The Serine/Threonine-Protein Phosphatase 1 From Haemonchus contortus Is Actively Involved in Suppressive Regulatory Roles on Immune Functions of Goat Peripheral Blood Mononuclear Cells. Frontiers in immunology, 9, 1627.

Guo J, et al. (2018) A novel Babesia orientalis 135-kilodalton spherical body protein like: identification of its secretion into cytoplasm of infected erythrocytes. Parasites & vectors, 11(1), 205.

Zheng Y, et al. (2018) Canine Influenza Virus is Mildly Restricted by Canine Tetherin Protein. Viruses, 10(10).

Guo J, et al. (2018) Characterization of a novel secretory spherical body protein in Babesia orientalis and Babesia orientalis-infected erythrocytes. Parasites & vectors, 11(1), 433.