

Resource Summary Report

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Phobius

RRID:SCR_015643

Type: Tool

Proper Citation

Phobius (RRID:SCR_015643)

Resource Information

URL: <http://phobius.sbc.su.se/>

Proper Citation: Phobius (RRID:SCR_015643)

Description: Web application for combined transmembrane topology and signal peptide prediction. Used for whole genome annotation of signal peptides and transmembrane regions. Predictor is based on hidden Markov model (HMM) that models different sequence regions of signal peptide and different regions of transmembrane protein in series of interconnected states.

Synonyms: PHOBIUS

Resource Type: service resource, data access protocol, software resource, production service resource, web service, analysis service resource

Defining Citation: [PMID:15111065](#), [PMID:30976793](#)

Keywords: Signal peptide prediction, whole genome annotation, transmembrane region, protein prediction, transmembrane topology, signal peptide, fasta, hidden markov model

Availability: Freely Available, Free, Available for download

Resource Name: Phobius

Resource ID: SCR_015643

Alternate IDs: SCR_018767

Alternate URLs: <http://phobius.binf.ku.dk/>, <https://www.ebi.ac.uk/Tools/pfa/phobius/>

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260729T044407+0000

Ratings and Alerts

No rating or validation information has been found for Phobius.

No alerts have been found for Phobius.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 498 mentions in open access literature.

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

Minesso S, et al. (2026) Generation, characterization, and application of caprine herpesvirus 1 secreted glycoprotein D. *Microbiology spectrum*, 14(1), e0237325.

Bai B, et al. (2025) EIAV encodes an accessory protein that antagonizes the host restriction factor equine tetherin. *Proceedings of the National Academy of Sciences of the United States of America*, 122(26), e2413703122.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. *Heliyon*, 11(1), e41714.

Stapley J, et al. (2025) Mapping genomic regions associated with temperature stress in the wheat pathogen *Zymoseptoria tritici*. *G3 (Bethesda, Md.)*, 15(6).

Thomas S, et al. (2025) The structure of the proteins of Camp Hill virus. *PloS one*, 20(10), e0331836.

Yang Y, et al. (2025) Structural elucidation and characterization of GH29A α -L-fucosidases and the effect of pH on their transglycosylation. *The FEBS journal*, 292(3), 653.

Wla?lak M, et al. (2025) Transcriptional reprogramming of *Novacetimonas hansenii* S11 during growth on glycerol. *Applied microbiology and biotechnology*, 109(1), 194.

Domínguez-Cerván H, et al. (2025) Secreted LysM proteins are required for niche competition and full virulence in *Pseudomonas savastanoi* during host plant infection. *PLoS pathogens*, 21(8), e1013121.

Liang Q, et al. (2025) Identification, characterization, and application of an NADPH-dependent carbonyl reductase in *Saccharomyces cerevisiae* AS2.346 for improving production of (13R,17S)-ethyl secol. *Synthetic and systems biotechnology*, 10(3), 983.

Yamamoto Y, et al. (2025) ADP ribosylation factor-like GTPase 6-interacting protein 5 (ARL6IP5): a prenylated Rab acceptor protein 1 (PRA1) family protein that shapes the ER membrane and regulates ER-phagy. *Autophagy reports*, 4(1), 2513466.

Ye F, et al. (2025) Evolutionary insights from the mitochondrial genomes of invasive scale insects (Hemiptera: Coccothraupidae): large-scale transfer RNA gene truncations and

tandem repeat-driven intraspecific gene rearrangements. BMC genomics, 26(1), 1003.

Ren BR, et al. (2025) Optimizing encephalomyocarditis virus VP1 protein assembly on pseudorabies virus envelope via US9 protein anchoring. Virulence, 16(1), 2445235.

Kusumoto K, et al. (2025) Multispanning membrane protein SIDT2 increases knockdown activity of gapmer antisense oligonucleotides. Scientific reports, 15(1), 586.

Colinet D, et al. (2025) Functional Carbohydrate-Active Enzymes Acquired by Horizontal Gene Transfer from Plants in the Whitefly *Bemisia tabaci*. Genome biology and evolution, 17(2).

Gonsalvez A, et al. (2025) Insights into platypus crural gland transcriptomics - venom and beyond. BMC genomics, 26(1), 1105.

Le Moigne D, et al. (2025) Functional study of *Phaeodactylum tricornutum* Seipin highlights specificities of lipid droplets biogenesis in diatoms. The New phytologist, 247(5), 2245.

Kollmar M, et al. (2025) Investigating the bHLH transcription factor TSARL1 as marker and regulator of saponin biosynthesis in *Chenopodium quinoa*. Journal of the science of food and agriculture, 105(13), 7329.

Karagöl T, et al. (2025) Co-evolution of alpha-helical transmembrane protein residues: large-scale variant profiling and complete mutational landscape of 2277 known PDB entries representing 504 unique human protein sequences. Journal of molecular evolution, 93(5), 581.

Fridman CM, et al. (2025) A new class of type VI secretion system effectors can carry two toxic domains and are recognized through the WHIX motif for export. PLoS biology, 23(3), e3003053.

Hsu FY, et al. (2025) Sertm2 is a conserved micropeptide that promotes GDNF-mediated motor neuron subtype specification. EMBO reports, 26(8), 2013.