

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/>

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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: production service resource, web service, data access protocol, software resource, service resource, 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: 20260815T182505+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 553 mentions in open access literature.

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

Heininger H, et al. (2026) BACE1 regulates sleep-wake cycle through both enzymatic and non-enzymatic actions. EMBO reports, 27(1), 50.

Leria L, et al. (2026) Innovations in Silicon Transport Shaped the Rise of Biosilicification and Skeletal Evolution in Sponges. Molecular biology and evolution, 43(3).

Graff van Creveld S, et al. (2026) Induced pathogenicity toward open-ocean diatoms by a filterable bacterium Ekhidna algicida sp. nov. The ISME journal, 20(1).

Gutierrez LJ, et al. (2026) Evidence for an early cadherin-catenin interaction network in ctenophores. Molecular biology and evolution, 43(6).

Rigano G, et al. (2026) Comparative genomics of space-resilient Chroococcidiopsis cyanobacteria reveals a core genetic repertoire supporting extreme tolerance towards desert and non-Earth conditions. FEMS microbes, 7, xtag036.

Leal K, et al. (2026) Exploration of inactive metabolic pathways in Antarctic Pseudogymnoascus australis through elicitation: a genomic and metabolomic approach to investigate its biotechnological potential. IMA fungus, 17, e156018.

Sanyal P, et al. (2026) Sec and Tat Mediated Secretion Safeguards Mycobacterium tuberculosis Membrane Homeostasis. Molecular & cellular proteomics : MCP, 25(4), 101555.

Wang G, et al. (2026) Correlation and expression pattern analyses of immune receptor genes in cotton. BMC genomics, 27(1).

Savelieva EM, et al. (2026) An Unusual Component of the Multistep Phosphorelay from Tea Plant (Camellia sinensis L.). International journal of molecular sciences, 27(10).

Kumar M, et al. (2026) Exploiting evolutionary diversity of cellulose synthase catalytic subunits to generate novel cellulose microfibril structure in Arabidopsis. Journal of experimental botany, 77(6), 1598.

Antony F, et al. (2026) Comparative Evaluation of Solid-phase and Membrane Mimetic Strategies in Membrane Proteome Coverage and Disease-State Analysis. Molecular &

cellular proteomics : MCP, 25(2), 101496.

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

Su H, et al. (2026) Lipid Droplet-Localized Spindle Apparatus Coiled-Coil Protein 1 Regulates Lipid Droplet Distribution. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), e11960.

Saldarriaga-C??rdoba M, et al. (2026) In-Depth Multi-Assembler Venom-Gland Transcriptomics of Three Medically Important Colombian Snakes Highlights Diversity of Accessory, Low-Abundance Protein Families. *Toxins*, 18(3).

Elrashedy A, et al. (2026) Immunoinformatics-based design of artificial chimeric proteins as universal vaccine candidates against foot-and-mouth disease virus serotypes A, O, and SAT2. *Scientific reports*, 16(1).

Griem-Krey H, et al. (2026) Transposable elements hitchhike on Starships across fungal genomes. *Nature communications*, 17(1).

Ma Y, et al. (2026) The hidden Markov model and its applications in bioinformatics analysis. *Genes & diseases*, 13(1), 101729.

Bifolco M, et al. (2026) Comparative proteomics reveals protein signatures shared between and unique to bona fide plant EVs and other plant-derived vesicles. *Plant physiology*, 200(3).

Jackson M, et al. (2026) Exploring the lipoproteome of *Parageobacillus thermoglucosidasius*. *Access microbiology*, 8(4).

Fiesinger A, et al. (2026) The genome of the reef-building coral *Porites harrisoni* from the southern Persian/Arabian Gulf. *GigaByte* (Hong Kong, China), 2026, gigabyte174.