

Resource Summary Report

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SignalP

RRID:SCR_015644

Type: Tool

Proper Citation

SignalP (RRID:SCR_015644)

Resource Information

URL: <http://www.cbs.dtu.dk/services/SignalP/>

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Description: Web application for prediction of the presence and location of signal peptide cleavage sites in amino acid sequences from different organisms. The method incorporates a prediction of cleavage sites and a signal peptide/non-signal peptide prediction based on a combination of several artificial neural networks.

Resource Type: software resource, web application

Defining Citation: [PMID:28451972](#)

Keywords: prediction, signal peptide, cleavage site, amino acid, sequence, artificial neural network

Availability: Freely available, Acknowledgment requested, Free, Available for download, Runs on Windows, Runs on Mac OS

Resource Name: SignalP

Resource ID: SCR_015644

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260804T043612+0000

Ratings and Alerts

No rating or validation information has been found for SignalP.

No alerts have been found for SignalP.

Data and Source Information

Usage and Citation Metrics

We found 9406 mentions in open access literature.

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

Sperschneider J, et al. (2026) The fungal pathogen *Rhizoctonia solani* AG-8 has 2 nuclear haplotypes that differ in abundance. *G3* (Bethesda, Md.), 16(1).

Luo Z, et al. (2026) Host adaptation and genome evolution of the broad host range fungal rust pathogen, *Austropuccinia psidii*. *G3* (Bethesda, Md.), 16(1).

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Zhu W, et al. (2026) Secreted Glycoside Hydrolase BcGH61 From *Botrytis cinerea* Induces Cell Death by the Apoplastic Location and Triggers Intracellular Immune Perception. *Molecular plant pathology*, 27(1), e70199.

Maurstad MF, et al. (2026) The green lacewing venom system and the complex mechanisms underlying its evolution. *Molecular biology and evolution*, 43(1).

Ahmed FH, et al. (2026) Disordered N-termini enhance the thermostability of SGNH-hydrolase family polyesterases. *Protein science : a publication of the Protein Society*, 35(1), e70402.

Pasha AVK, et al. (2026) Immunoinformatics-Based Multi-Epitope Vaccine Targeting *Helicobacter Pylori*. *Cancer reports* (Hoboken, N.J.), 9(1), e70441.

Lima Cunha W, et al. (2026) Molecular mechanisms associated with rootstock-scion interactions in rubber trees. *The plant genome*, 19(1), e70147.

Wang L, et al. (2025) A receptor antagonist counterbalances multiple systemin phytocytokines in tomato. *Cell*.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Krueger T, et al. (2025) Exo-Tox: Identifying Exotoxins from secreted bacterial proteins. *BioData mining*, 18(1), 52.

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

Nobari MB, et al. (2025) The Lpp-OmpA-BtaE fusion protein causes a protective immune response against *Brucella melitensis* in mice. *Scientific reports*, 15(1), 27210.

Mendel HC, et al. (2025) PeptideMiner-neuropeptide discovery across the animal kingdom. *GigaScience*, 14.

Kr??ger T, et al. (2025) Toxin data quality: a critical examination of bacterial exotoxins and animal toxins. *BMC research notes*, 18(1), 418.

Bergheim BG, et al. (2025) Molecular dynamics of the matrisome across sea anemone life history. *eLife*, 14.

Bharti S, et al. (2025) Single-cell transcriptome atlas of adult male and female human hookworm *Ancylostoma ceylanicum*. *iScience*, 28(11), 113846.

Svetlicic E, et al. (2025) Mass Spectrometry-Based Analysis of Surface Proteins in *Staphylococcus aureus* Clinical Strains: Identification of Promising k-mer Targets for Diagnostics. *Journal of proteome research*, 24(9), 4575.