Resource Summary Report

Generated by NIF on Aug 10, 2026

SignalP

RRID:SCR_015644
Type: Tool

Proper Citation

SignalP (RRID:SCR_015644)

Resource Information

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

Proper Citation: SignalP (RRID:SCR_015644)

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: web application, software resource

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: 20260808T190239+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10033 mentions in open access literature.

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

Chen L, et al. (2026) Mycobacterial metallophosphatase MmpE acts as a nucleomodulin to regulate host gene expression and promote intracellular survival. eLife, 14.

Pohto A, et al. (2026) Uncovering Sequence and Structural Characteristics of Fungal Expansin-Related Proteins With Potential to Drive Substrate Targeting. Proteins, 94(2), 547.

Ste-Croix DT, et al. (2026) The genome and stage-specific transcriptomes of the carrot weevil, Listronotus oregonensis, reveal adaptive mechanisms for host specialisation and symbiotic interactions. Insect molecular biology, 35(2), 126.

Hua Y, et al. (2026) Proteomic Portrait of Degranulation Program in Human Circulating Neutrophils Upon Multi-Inflammatory and Infectious Activation. Molecular & cellular proteomics : MCP, 25(1), 101078.

Kim D, et al. (2026) Requirement of group I lytic polysaccharide monooxygenase for turnover of chitinous cuticle during moulting in two forest pest beetles, Monochamus alternatus and Psacothea hilaris. Insect molecular biology, 35(2), 115.

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).

Rahimi M, et al. (2026) Systematic Evaluation of Vector Sequence Elements in Isogenic CHO Cells for Improved Antibody Production. ACS synthetic biology, 15(1), 342.

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).

Wong ELY, et al. (2026) Historical comparative genomics to track the evolution of fungal pathogens: a proof of concept. BMC genomics, 27(1), 164.

Wang H-Q, et al. (2026) Structural and functional insights into Uly1040, an ulvan lyase from polysaccharide lyase family 40. Applied and environmental microbiology, 92(2), e0210125.

Zaccaron AZ, et al. (2026) The poplar pathogen Sphaerulina musiva has a dynamic genome architecture marked by chromosomal inversions and changes in transposable element abundance. Microbial genomics, 12(1).

Fu E, et al. (2026) Assembly of Macromolecular Complexes in the Whole-Cell Model of a Minimal Cell. The journal of physical chemistry. B, 130(1), 11.

Ferreira GC, et al. (2026) The WAK/WAKL gene family in Phaseolus vulgaris: genomic characterization and expression under Colletotrichum lindemuthianum infection. BMC genomics, 27(1), 210.

Cresens C, et al. (2026) Deciphering Stiffness-Driven Changes in Colorectal Cancer by Proteomics. Molecular & cellular proteomics : MCP, 25(3), 101515.

Ha HT, et al. (2026) Development and evaluation of recombinant dense granule 14 for serological diagnosis of Toxoplasma gondii infection in domestic cats. Scientific reports, 16(1).

Nixon A, et al. (2026) Borrelia BBJ25 is a plasmid-encoded Omp85-family protein associated with a potential export system. Bioscience reports, 46(2).

Liu CP, et al. (2026) A brain-gut excitatory peptide/CCHamide homolog regulates satiation and motivational state transitions in the Aplysia feeding circuit. The Journal of biological chemistry, 302(3), 111257.

Armbruster KM, et al. (2026) Identification and characterization of the functional LolB ortholog in Bacteroides. bioRxiv : the preprint server for biology.

Lai D, et al. (2026) Branched-chain amino acid specialization drove diversification within Calditenuaceae (Caldarchaeia) and enables their cultivation. Nature communications, 17(1).

Kabir M, et al. (2026) A machine learning classifier to identify and prioritise genes associated with murine cardiac development. PLoS genetics, 22(2), e1011489.