Resource Summary Report

Generated by NIF on May 4, 2025

PSORT II

RRID:SCR_018772

Type: Tool

Proper Citation

PSORT II (RRID:SCR_018772)

Resource Information

URL: http://www.genscript.com/psort/psort2.html

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Description: Web tool for prediction of protein sorting signals and localization sites in amino acid sequencies. Recommended for animal/yeast sequences. Analyzes input sequence by applying stored rules for various sequence features of known protein sorting signals to report possiblity for input protein to be localized at each candidate site with additional information.

Synonyms: prediction of protein sorting signals and localization sites in amino acid sequencies, psort2, psort II

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

Keywords: Protein sorting signal prediction, protein localization site, localization site prediction, amino acid sequence, sequence analysis, protein sorting signal

Funding:

Availability: Free, Freely available

Resource Name: PSORT II

Resource ID: SCR_018772

Alternate URLs: https://psort.hgc.jp/, https://www.psort.org/

Record Creation Time: 20220129T080341+0000

Record Last Update: 20250503T060822+0000

Ratings and Alerts

No rating or validation information has been found for PSORT II.

No alerts have been found for PSORT II.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Liang X, et al. (2025) Genome-Wide Identification of GmPIF Family and Regulatory Pathway Analysis of GmPIF3g in Different Temperature Environments. International journal of molecular sciences, 26(2).

Van't Hof AE, et al. (2024) Zygosity-based sex determination in a butterfly drives hypervariability of Masculinizer. Science advances, 10(18), eadj6979.

Song W, et al. (2024) Genome-wide profiling of WRKY genes involved in flavonoid biosynthesis in Erigeron breviscapus. Frontiers in plant science, 15, 1412574.

Xiong R, et al. (2024) Genome-wide identification, structural characterization and gene expression analysis of the WRKY transcription factor family in pea (Pisum sativum L.). BMC plant biology, 24(1), 113.

Zhang D, et al. (2024) APC mutations disrupt ?-catenin destruction complex condensates organized by Axin phase separation. Cellular and molecular life sciences: CMLS, 81(1), 57.

Vincek A, et al. (2024) The N-terminus of the Aspergillus fumigatus group III hybrid histidine kinase TcsC is essential for its physiological activity and targets the protein to the nucleus. mBio, 15(7), e0118424.

Alves de Castro P, et al. (2024) Aspergillus fumigatus mitogen-activated protein kinase MpkA is involved in gliotoxin production and self-protection. Nature communications, 15(1), 33.

Jia Y, et al. (2024) Clindamycin Derivatives: Unveiling New Prospects as Potential Antitumor Agents. Pharmaceuticals (Basel, Switzerland), 17(3).

Jia Y, et al. (2023) Structure-Activity Relationship Target Prediction Studies of Clindamycin Derivatives with Broad-Spectrum Bacteriostatic Antibacterial Properties. Molecules (Basel, Switzerland), 28(21).

Wang C, et al. (2023) Mutations in CCNB3 affect its location thus causing a multiplicity of phenotypes in human oocytes maturation by aberrant CDK1 activity and APC/C activity at different stages. Journal of ovarian research, 16(1), 178.

Gao Q, et al. (2023) WDR38, a novel equatorial segment protein, interacts with the GTPase protein RAB19 and Golgi protein GM130 to play roles in acrosome biogenesis. Acta biochimica et biophysica Sinica, 55(10), 1561.

Wang F, et al. (2023) Increased TCP11 gene expression can inhibit the proliferation, migration and promote apoptosis of cervical cancer cells. BMC cancer, 23(1), 853.

Li J, et al. (2023) Genome-Wide Analysis of bHLH Family Genes and Identification of Members Associated with Cold/Drought-Induced Photoinhibition in Kandelia obovata. International journal of molecular sciences, 24(21).

Okuda EK, et al. (2020) Nucleolar localization of the yeast RNA exosome subunit Rrp44 hints at early pre-rRNA processing as its main function. The Journal of biological chemistry, 295(32), 11195.