

Resource Summary Report

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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 sequences. Recommended for animal/yeast sequences. Analyzes input sequence by applying stored rules for various sequence features of known protein sorting signals to report possibility 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 sequences, psort2, psort II

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

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

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: 20260801T190624+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 21 mentions in open access literature.

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

Bullo E, et al. (2025) Coevolution of Drosophila-type timeless with partner clock proteins. *iScience*, 28(5), 112338.

Liu Z, et al. (2025) Genome-wide identification of GmEDS1 gene family members in soybean and expression analysis in response to biotic and abiotic stresses. *Frontiers in plant science*, 16, 1554399.

Raman P, et al. (2025) Dynamic evolution of EZHIP, an inhibitor of the Polycomb Repressive Complex 2 in mammals. *bioRxiv : the preprint server for biology*.

Li Z, et al. (2025) Evolutionary and functional insights into HSF gene family underpin thermal adaptation in the plateau plant *Anisodus tanguticus*. *BMC plant biology*, 25(1), 1452.

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).

Silva IRM, et al. (2025) Evaluation of binding activities of a putative lipoprotein LIC_13355 of *Leptospira* spp. *FEBS open bio*, 15(3), 447.

Li H, et al. (2025) Genome-wide identification and gene expression pattern analysis of the carotenoid cleavage oxygenase gene family in *Fagopyrum tataricum*. *BMC plant biology*, 25(1), 466.

Zhou X, et al. (2025) Genome-wide identification of the MADS-box gene family and their role in the formation of faba bean (*Vicia faba* L.) growth habits. *BMC plant biology*, 25(1), 1510.

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

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 β -catenin destruction complex condensates organized by Axin phase separation. *Cellular and molecular life sciences : CMLS*, 81(1), 57.

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

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

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.

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.

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).

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).

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.

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.