

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

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: 20260829T182614+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 49 mentions in open access literature.

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

Xu Z, et al. (2026) Analysis of the TIL gene family in Brassicaceae species and functional study of BrTIL1 in cold tolerance. *Frontiers in plant science*, 17, 1794987.

Fan Z, et al. (2026) Genome-wide identification, evolution, and expression pattern analysis of the LEA gene family in Tartary Buckwheat (*Fagopyrum tataricum*). *BMC genomics*, 27(1).

Xing Q, et al. (2026) Blue light as an eco-elicitor effectively enhances flavonoid biosynthesis and antioxidant capacity in dandelion revealed by integrated metabolomic and transcriptomic analyses. *BMC plant biology*, 26(1), 286.

Niu E, et al. (2026) Comprehensive Analysis of the AP2/ERF Superfamily Identifies Key Genes Related to Various Stress Responses in Olive Tree (*Olea europaea* L.). *Current issues in molecular biology*, 48(2).

Hessami A, et al. (2026) Design of a novel proteome-derived scaffold presenting epitopes of *Pseudomonas aeruginosa* in native conformation. *Scientific reports*, 16(1).

Zhao X, et al. (2026) Genome-wide analysis and characterization of the rice OsFBA family provides insights into its responses to ABA and cold stress. *BMC plant biology*, 26(1).

Jin W, et al. (2026) Genome-wide identification, structural characterization, and gene expression analysis of the MYB transcription factor family in faba bean (*Vicia faba* L.). *BMC plant biology*, 26(1), 251.

Rahimi-Farsi N, et al. (2026) Immunoinformatic-driven design of a multi-epitope vaccine against *Helicobacter pylori*. *Biochemistry and biophysics reports*, 45, 102498.

Chen R, et al. (2026) Genome-wide characterization of the LAC gene family in five fern species reveals evolutionary diversification and putative roles in lignin biosynthesis in *Alsophila spinulosa*. *BMC plant biology*, 26(1).

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*.

- 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.
- Xu J, et al. (2025) Target screening and optimization of candidate compounds for breast cancer treatment using bioinformatics and computational chemistry approaches. *Frontiers in pharmacology*, 16, 1467504.
- Ma H, et al. (2025) Multi-Time Point Transcriptome Analysis and Functional Validation Revealed Bol4CL41 Negatively Regulates Black Rot Resistance in Cabbage. *International journal of molecular sciences*, 26(13).
- Bullo E, et al. (2025) Coevolution of Drosophila-type timeless with partner clock proteins. *iScience*, 28(5), 112338.
- 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).
- Xu J, et al. (2025) Transcriptome-wide identification and characterization of WUSCHEL-related homeobox (WOX) gene family in *Pinus yunnanensis*. *BMC genomics*, 26(1), 99.
- Silva IRM, et al. (2025) Evaluation of binding activities of a putative lipoprotein LIC_13355 of *Leptospira* spp. *FEBS open bio*, 15(3), 447.
- 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.
- 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.
- 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.