

Resource Summary Report

Generated by [dkNET](#) on Jul 30, 2026

Psort

RRID:SCR_007038

Type: Tool

Proper Citation

Psort (RRID:SCR_007038)

Resource Information

URL: <http://www.psort.org>

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Description: Portal to the PSORT family of computer programs for the prediction of protein localization sites in cells, as well as other datasets and resources relevant to localization prediction. The standalone versions are available for download for larger analyses.

Abbreviations: PSORT

Synonyms: Psort.org, PSORT: Prediction of Protein Sorting Signals and Localization Sites in Amino Acid Sequences

Resource Type: software application, service resource, data set, data analysis software, data or information resource, data analysis service, data processing software, software resource, production service resource, analysis service resource, topical portal, portal

Keywords: subcellular, localization, prediction, gram, gram-positive, gram-negative, sequence, fasta, protein, protein localization, cell, motif, profile, amino acid, subcellular localization

Resource Name: Psort

Resource ID: SCR_007038

Alternate IDs: OMICS_01634, nif-0000-31883

Alternate URLs: <http://psort.hgc.jp/>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260729T044142+0000

Ratings and Alerts

No rating or validation information has been found for Psort.

No alerts have been found for Psort.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 209 mentions in open access literature.

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

Dai R, et al. (2025) Overexpression MsJAR1 gene increased lateral branches and plant height in alfalfa (*Medicago sativa* L.). *Scientific reports*, 15(1), 16956.

Castillo G, et al. (2025) Genome Sequencing Reveals the Potential of *Enterobacter* sp. Strain UNJFSC003 for Hydrocarbon Bioremediation. *Genes*, 16(1).

Blanchard AM, et al. (2025) In vitro determination of essential genes required by *Streptococcus uberis* to grow in a complex biological media relating to intramammary infection. *Microbial genomics*, 11(6).

Yuan Y, et al. (2025) Genomic identification of a pair of multidrug-resistant but non-pathogenic *Salmonella enterica* serovar Goldcoast isolates in southeast China. *Frontiers in microbiology*, 16, 1540843.

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.

Kiguchi Y, et al. (2025) Giant extrachromosomal element "Inocle" potentially expands the adaptive capacity of the human oral microbiome. *Nature communications*, 16(1), 7397.

Mikitova V, et al. (2025) Complex transcription regulation of acidic chitinase suggests fine-tuning of digestive processes in *Drosera binata*. *Planta*, 261(2), 32.

Yang X, et al. (2025) Nuclear entry of AS160 as a transcriptional regulator of satellite cells for muscle regeneration. *Nature communications*, 16(1), 9162.

Yang X, et al. (2025) TBC1D1 functions as a negative regulator of satellite cells for muscle regeneration. *Nature communications*, 16(1), 10091.

Gonsalvez A, et al. (2025) Insights into platypus crural gland transcriptomics - venom and beyond. *BMC genomics*, 26(1), 1105.

Mas-Ud MA, et al. (2025) Comprehensive genome-wide identification and analysis of MYB transcription factors related to abiotic and biotic stress regulation in rice. *Scientific reports*, 15(1), 44024.

Froschauer K, et al. (2025) Complementary Ribo-seq approaches map the translome and provide a small protein census in the foodborne pathogen *Campylobacter jejuni*. *Nature communications*, 16(1), 3078.

Gong X, et al. (2024) Genomic insight into the diversity of *Glaesserella parasuis* isolates from 19 countries. *mSphere*, 9(9), e0023124.

Li X, et al. (2023) RPG interacts with E3-ligase CERBERUS to mediate rhizobial infection in *Lotus japonicus*. *PLoS genetics*, 19(2), e1010621.

Yan W, et al. (2023) Genome-wide characterization of the wall-associated kinase-like (WAKL) family in sesame (*Sesamum indicum*) identifies a SiWAKL6 gene involved in resistance to *Macrophomina Phaseolina*. *BMC plant biology*, 23(1), 624.

Ma X, et al. (2023) Genome-wide identification and expression analysis of the SAUR gene family in foxtail millet (*Setaria italica* L.). *BMC plant biology*, 23(1), 31.

Tarracchini C, et al. (2023) Genetic strategies for sex-biased persistence of gut microbes across human life. *Nature communications*, 14(1), 4220.

Carlton JD, et al. (2023) Expansion of *Armatimonadota* through marine sediment sequencing describes two classes with unique ecological roles. *ISME communications*, 3(1), 64.

Gao S, et al. (2023) Ectopic Expression of Sugarcane ScAMT1.1 Has the Potential to Improve Ammonium Assimilation and Grain Yield in Transgenic Rice under Low Nitrogen Stress. *International journal of molecular sciences*, 24(2).

Zhang T, et al. (2023) The Screening of the Protective Antigens of *Aeromonas hydrophila* Using the Reverse Vaccinology Approach: Potential Candidates for Subunit Vaccine Development. *Vaccines*, 11(7).