Resource Summary Report

Generated by dkNET on May 20, 2025

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, production service resource, data analysis service, data analysis software, topical portal, data processing software, data set, analysis service resource, data or information resource, portal, software resource

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

Funding:

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: 20250519T203456+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 199 mentions in open access literature.

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

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

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

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

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.

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

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.

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.

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).

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).

Lau WYV, et al. (2023) Pathogen-associated gene discovery workflows for novel antivirulence therapeutic development. EBioMedicine, 88, 104429.

Gao P, et al. (2023) Genomic insight of sulfate reducing bacterial genus Desulfofaba reveals their metabolic versatility in biogeochemical cycling. BMC genomics, 24(1), 209.

De Marco Verissimo C, et al. (2023) Glycan Complexity and Heterogeneity of Glycoproteins in Somatic Extracts and Secretome of the Infective Stage of the Helminth Fasciola hepatica. Molecular & cellular proteomics : MCP, 22(12), 100684.

Imai T, et al. (2022) Group II truncated haemoglobin YjbI prevents reactive oxygen species-induced protein aggregation in Bacillus subtilis. eLife, 11.

Rajapaksha LGTG, et al. (2022) In silico detection and characterization of novel virulence proteins of the emerging poultry pathogen Gallibacterium anatis. Genomics & informatics, 20(4), e41.

Smedile F, et al. (2022) Adaptations to high pressure of Nautilia sp. strain PV-1, a piezophilic Campylobacterium (aka Epsilonproteobacterium) isolated from a deep-sea hydrothermal vent. Environmental microbiology, 24(12), 6164.

Al-Shayeb B, et al. (2022) Borgs are giant genetic elements with potential to expand metabolic capacity. Nature, 610(7933), 731.

Cao Y, et al. (2022) Knockout of the lignin pathway gene BnF5H decreases the S/G lignin compositional ratio and improves Sclerotinia sclerotiorum resistance in Brassica napus. Plant, cell & environment, 45(1), 248.

Dash A, et al. (2022) Genome-wide in silico characterization and stress induced expression analysis of BcL-2 associated athanogene (BAG) family in Musa spp. Scientific reports, 12(1), 625.

Yu Q, et al. (2022) Characterization of the ABC Transporter G Subfamily in Pomegranate and Function Analysis of PgrABCG14. International journal of molecular sciences, 23(19).