Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 23, 2025

ngLOC

RRID:SCR_003150
Type: Tool

Proper Citation

ngLOC (RRID:SCR_003150)

Resource Information

URL: http://genome.unmc.edu/ngLOC/index.html

Proper Citation: ngLOC (RRID:SCR_003150)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 5, 2023.An n-gram-based Bayesian classifier that predicts subcellular localization of proteins both in prokaryotes and eukaryotes. The downloadable version of this software with source code is freely available for academic use under the GNU General Public License.

Abbreviations: ngLOC

Synonyms: ngLOC - A Bayesian method for predicting protein subcellular localization

Resource Type: analysis service resource, data analysis service, software resource, production service resource, service resource

Defining Citation: PMID:22780965, PMID:17472741

Keywords: subcellular localization, protein, eukaryote, prokaryote, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ngLOC

Resource ID: SCR_003150

Alternate IDs: OMICS_01629, biotools:ngloc

Alternate URLs: https://bio.tools/ngloc

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250423T060114+0000

Ratings and Alerts

No rating or validation information has been found for ngLOC.

No alerts have been found for ngLOC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Bappy MNI, et al. (2024) Screening of Novel Drug Targets and Drug Design for Bordetella pertussis: A Subtractive Proteomics Approach. Current research in microbial sciences, 7, 100291.

Huangfu Y, et al. (2021) Genome-wide identification of PTI1 family in Setaria italica and salinity-responsive functional analysis of SiPTI1-5. BMC plant biology, 21(1), 319.

di Rienzo V, et al. (2021) Functional conservation of the grapevine candidate gene INNER NO OUTER for ovule development and seed formation. Horticulture research, 8(1), 29.

Suo J, et al. (2020) Na2CO3-responsive Photosynthetic and ROS Scavenging Mechanisms in Chloroplasts of Alkaligrass Revealed by Phosphoproteomics. Genomics, proteomics & bioinformatics, 18(3), 271.

Li Y, et al. (2020) Integrated Analysis of mRNA and microRNA Elucidates the Regulation of Glycyrrhizic Acid Biosynthesis in Glycyrrhiza uralensis Fisch. International journal of molecular sciences, 21(9).

Ahmad A, et al. (2020) A Genome-Scale Metabolic Model of Thalassiosira pseudonana CCMP 1335 for a Systems-Level Understanding of Its Metabolism and Biotechnological Potential. Microorganisms, 8(9).

Cao S, et al. (2019) Genome-wide characterization of aspartic protease (AP) gene family in Populus trichocarpa and identification of the potential PtAPs involved in wood formation.

BMC plant biology, 19(1), 276.

Chhajed S, et al. (2019) Chemodiversity of the Glucosinolate-Myrosinase System at the Single Cell Type Resolution. Frontiers in plant science, 10, 618.

Mahmud A, et al. (2019) Identification of novel drug targets for humans and potential vaccine targets for cattle by subtractive genomic analysis of Brucella abortus strain 2308. Microbial pathogenesis, 137, 103731.

Hisham Y, et al. (2018) Identification of Cross-Protective Potential Antigens against Pathogenic Brucella spp. through Combining Pan-Genome Analysis with Reverse Vaccinology. Journal of immunology research, 2018, 1474517.

Yin Z, et al. (2017) Bicarbonate Induced Redox Proteome Changes in Arabidopsis Suspension Cells. Frontiers in plant science, 8, 58.

Ushijima T, et al. (2017) Light Controls Protein Localization through Phytochrome-Mediated Alternative Promoter Selection. Cell, 171(6), 1316.

Ünsald? E, et al. (2017) Proteome-wide alterations in an industrial clavulanic acid producing strain of Streptomyces clavuligerus. Synthetic and systems biotechnology, 2(1), 39.

Gamberucci A, et al. (2017) GLUT10-Lacking in Arterial Tortuosity Syndrome-Is Localized to the Endoplasmic Reticulum of Human Fibroblasts. International journal of molecular sciences, 18(8).

Sigloch FC, et al. (2017) Proteomic analysis of lung metastases in a murine breast cancer model reveals divergent influence of CTSB and CTSL overexpression. Journal of Cancer, 8(19), 4065.

Lande NV, et al. (2017) Dissecting the chloroplast proteome of chickpea (Cicer arietinum L.) provides new insights into classical and non-classical functions. Journal of proteomics, 165, 11.

Wei S, et al. (2017) Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae Dunaliella salina Revealed by Quantitative Proteomics and Phosphoproteomics. Frontiers in plant science, 8, 810.

Yin Z, et al. (2016) Water deficit mechanisms in perennial shrubs Cerasus humilis leaves revealed by physiological and proteomic analyses. Proteome science, 15, 9.

Meng X, et al. (2016) Chilling-responsive mechanisms in halophyte Puccinellia tenuiflora seedlings revealed from proteomics analysis. Journal of proteomics, 143, 365.

Ariani P, et al. (2016) Genome-wide characterisation and expression profile of the grapevine ATL ubiquitin ligase family reveal biotic and abiotic stress-responsive and development-related members. Scientific reports, 6, 38260.