Resource Summary Report

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YLoc

RRID:SCR_002464
Type: Tool

Proper Citation

YLoc (RRID:SCR_002464)

Resource Information

URL: http://abi.inf.uni-tuebingen.de/Services/YLoc/webloc.cgi

Proper Citation: YLoc (RRID:SCR_002464)

Description: An interpretable web server for predicting subcellular localization. In addition to the predicted location, YLoc gives a reasoning why this prediction was made and which biological properties of the protein sequence lead to this prediction. Moreover, a confidence estimate helps users to rate predictions as trustworthy. YLoc+ is able to predict the location of multiple-targeted proteins with high accuracy. The YLoc webserver is also accessible via SOAP.

Abbreviations: YLoc

Synonyms: Yloc - Interpretable Subcellular Localization Prediction

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

Defining Citation: PMID:20507917, PMID:20299325

Keywords: subcellular localization, protein

Funding:

Availability: Acknowledgement requested

Resource Name: YLoc

Resource ID: SCR_002464

Alternate IDs: OMICS_01638

Record Creation Time: 20220129T080213+0000

Record Last Update: 20250403T060210+0000

Ratings and Alerts

No rating or validation information has been found for YLoc.

No alerts have been found for YLoc.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Fang H, et al. (2023) Functional Characterization of Lycopene ?- and ?-Cyclases from a Lutein-Enriched Green Microalga Chlorella sorokiniana FZU60. Marine drugs, 21(7).

Bhattacharya O, et al. (2023) The tomato chloroplast stromal proteome compendium elucidated by leveraging a plastid protein-localization prediction Atlas. Frontiers in plant science, 14, 1020275.

Vasu K, et al. (2022) Analysis of nested alternate open reading frames and their encoded proteins. NAR genomics and bioinformatics, 4(4), lqac076.

Ingle S, et al. (2022) Discovery and initial characterization of YloC, a novel endoribonuclease in Bacillus subtilis. RNA (New York, N.Y.), 28(2), 227.

Liu W, et al. (2021) The Papain-like Cysteine Protease HpXBCP3 from Haematococcus pluvialis Involved in the Regulation of Growth, Salt Stress Tolerance and Chlorophyll Synthesis in Microalgae. International journal of molecular sciences, 22(21).

Hou L, et al. (2021) Genome-Wide Identification of CYP72A Gene Family and Expression Patterns Related to Jasmonic Acid Treatment and Steroidal Saponin Accumulation in Dioscorea zingiberensis. International journal of molecular sciences, 22(20).

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.

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.

Ali N, et al. (2020) Ectopic Expression of AhGLK1b (GOLDEN2-like Transcription Factor) in Arabidopsis Confers Dual Resistance to Fungal and Bacterial Pathogens. Genes, 11(3).

Moreno-Córdova EN, et al. (2020) Molecular characterization and expression analysis of the chicken-type and goose-type lysozymes from totoaba (Totoaba macdonaldi). Developmental and comparative immunology, 113, 103807.

De Rosa A, et al. (2020) Genome-wide identification and characterisation of Aquaporins in Nicotiana tabacum and their relationships with other Solanaceae species. BMC plant biology, 20(1), 266.

Armbruster L, et al. (2019) The Recovery from Sulfur Starvation Is Independent from the mRNA Degradation Initiation Enzyme PARN in Arabidopsis. Plants (Basel, Switzerland), 8(10).

Li S, et al. (2019) Heat-Responsive Proteomics of a Heat-Sensitive Spinach Variety. International journal of molecular sciences, 20(16).

Zhang Y, et al. (2019) NaCl-responsive ROS scavenging and energy supply in alkaligrass callus revealed from proteomic analysis. BMC genomics, 20(1), 990.

Zuma B, et al. (2018) Prolonged Expression of a Putative Invertase Inhibitor in Micropylar Endosperm Suppressed Embryo Growth in Arabidopsis. Frontiers in plant science, 9, 61.

Bossi F, et al. (2017) Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. BMC genomics, 18(1), 480.

Jia Q, et al. (2017) Genome-Wide Analyses of the Soybean F-Box Gene Family in Response to Salt Stress. International journal of molecular sciences, 18(4).

Vuorinen EM, et al. (2017) Search for KPNA7 cargo proteins in human cells reveals MVP and ZNF414 as novel regulators of cancer cell growth. Biochimica et biophysica acta. Molecular basis of disease, 1863(1), 211.

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.

Hernández-Sánchez IE, et al. (2017) In vivo evidence for homo- and heterodimeric interactions of Arabidopsis thaliana dehydrins AtCOR47, AtERD10, and AtRAB18. Scientific reports, 7(1), 17036.