

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

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: 20250422T055028+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 [NIF](#).

Fang H, et al. (2023) Functional Characterization of Lycopene β - and γ -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).

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.

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).

- 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.
- Zhang Y, et al. (2019) NaCl-responsive ROS scavenging and energy supply in alkaligrass callus revealed from proteomic analysis. *BMC genomics*, 20(1), 990.
- 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).
- 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.
- 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).
- Bossi F, et al. (2017) Systematic discovery of novel eukaryotic transcriptional regulators using sequence homology independent prediction. *BMC genomics*, 18(1), 480.
- 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.
- Yin Z, et al. (2017) Bicarbonate Induced Redox Proteome Changes in Arabidopsis Suspension Cells. *Frontiers in plant science*, 8, 58.