

Resource Summary Report

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CELLO

RRID:SCR_011968

Type: Tool

Proper Citation

CELLO (RRID:SCR_011968)

Resource Information

URL: <http://cello.life.nctu.edu.tw/>

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Description: A subCELLular Localization predictor based on a multi-class support vector machine (SVM) classification system. CELLO uses 4 types of sequence coding schemes: the amino acid composition, the di-peptide composition, the partitioned amino acid composition and the sequence composition based on the physico-chemical properties of amino acids. They combine votes from these classifiers and use the jury votes to determine the final assignment.

Abbreviations: CELLO

Synonyms: CELLO: subCELLular LLocalization predictor

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

Defining Citation: [PMID:15096640](#)

Keywords: dna, protein, proteomic, genomic

Availability: Acknowledgement requested

Resource Name: CELLO

Resource ID: SCR_011968

Alternate IDs: OMICS_01618

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260806T054538+0000

Ratings and Alerts

No rating or validation information has been found for CELLO.

No alerts have been found for CELLO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 957 mentions in open access literature.

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

Ansari F, et al. (2026) Characterisation of a Novel Jumbo Lytic *Aeromonas dhakensis* Bacteriophage P19 and Its Endolysin. *Microbial biotechnology*, 19(1), e70289.

De Coninck T, et al. (2025) OsAPSE modulates non-covalent interactions between arabinogalactan protein O-glycans and pectin in rice cell walls. *Frontiers in plant science*, 16, 1588802.

Kotsovolos N, et al. (2025) Sequence- and structure-based bioinformatic screening for potential *Theileria parva* transport-related proteins. *Computational biology and chemistry*, 120(Pt 1), 108653.

Xiong Y, et al. (2025) DUSP4 inhibited tumor cell proliferation by downregulating glycolysis via p-ERK/p-PGK1 signaling in ovarian cancer. *Cancer cell international*, 25(1), 87.

Wu Z, et al. (2025) PcNAC25, a NAC transcription factor of *Pugionium cornutum*(L.) Gaertn conferring enhanced drought and salt stress tolerances in *Arabidopsis*. *Scientific reports*, 15(1), 1501.

Yolcu S, et al. (2025) Deciphering melatonin biosynthesis pathway in *Chenopodium quinoa*: genome-wide analysis and expression levels of the genes under salt and drought. *Planta*, 262(1), 23.

Yuan Z, et al. (2025) Membrane Vesicles of *Enterococcus faecalis*: In Vitro Composition Analysis and Macrophage Inflammatory Response Under Different pH Conditions. *Microorganisms*, 13(6).

Fang H, et al. (2025) Unveiling the Role of GhP5CS1 in Cotton Salt Stress Tolerance: A Comprehensive Genomic and Functional Analysis of P5CS Genes. *Plants (Basel, Switzerland)*, 14(2).

Yuan J, et al. (2025) OSaMPle workflow for salivary metaproteomics analysis reveals dysbiosis in inflammatory bowel disease patients. *NPJ biofilms and microbiomes*, 11(1), 63.

Sun M, et al. (2025) MeCP2 Lactylation Protects against Ischemic Brain Injury by Transcriptionally Regulating Neuronal Apoptosis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(21), e2415309.

Wei J, et al. (2025) Genome-wide identification of the P4ATPase gene family and its response to biotic and abiotic stress in soybean (*Glycine max* L.). *BMC genomics*, 26(1), 277.

Naz H, et al. (2025) Utilizing the subtractive proteomics approach to design ensemble vaccine against *Candida lusitanae* for immune response stimulation; a bioinformatics study. *PloS one*, 20(2), e0316264.

Wang JL, et al. (2025) Chromosome-level genome assembly of *Pontederia cordata* L. provides insights into its rapid adaptation and variation of flower colours. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(2).

Meng X, et al. (2025) Genome-wide analyses of the NAC transcription factor gene family in *Acer palmatum* provide valuable insights into the natural process of leaf senescence. *PeerJ*, 13, e18817.

Guo Z, et al. (2025) Comparative analysis of HKT genes in *Ipomoea pes-caprae* unveils conserved Na⁺/K⁺ symporter functions within the gene family. *Frontiers in plant science*, 16, 1538669.

Moradkasani S, et al. (2025) Development of a multi-epitope vaccine from outer membrane proteins and identification of novel drug targets against *Francisella tularensis*: an In Silico approach. *Frontiers in immunology*, 16, 1479862.

Zhang S, et al. (2025) Genome-wide identification and functional analysis of R2R3-MYB genes in *Acer pseudosieboldianum*: insights into low temperature stress response and anthocyanin biosynthesis. *BMC plant biology*, 25(1), 795.

Liu J, et al. (2025) Genome-wide systematic characterization of PHT gene family and its member involved in phosphate uptake in *Orychophragmus violaceus*. *BMC genomics*, 26(1), 876.

Shen X, et al. (2025) Transcriptomic and Proteomic Insights Into Buffalo Milk Fat Synthesis and the Role of IGFBP4 in BMECs. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*, 39(16), e70971.

Punniyamoorthy D, et al. (2025) Whole genome sequencing reveals transcriptional and translational elements potentially regulating biotic and abiotic stress responses in cowpea. *Scientific reports*, 15(1), 32913.