

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: analysis service resource, data analysis service, production service resource, 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: 20260821T042856+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 1271 mentions in open access literature.

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

Xin P, et al. (2026) Plasma Proteomics Identifies Thousand-and-One-Amino Acid Kinase 3 as a Potential Biomarker of Rheumatoid Arthritis Activity and a Novel Therapeutic Target. *Arthritis & rheumatology* (Hoboken, N.J.), 78(5), 1045.

Yang X, et al. (2026) Genome-wide identification of the ADF gene family and expression analysis of responses to cold stress in bitter melon. *BMC plant biology*, 26(1).

Fernández-Roldán P, et al. (2026) Genome-Wide Identification and Expression Analysis of Tubby-like Proteins (TLPs) in *Fragaria × ananassa* Reveals Their Role in Abiotic Stress Responses. *Genes*, 17(2).

Koramutla MK, et al. (2026) Genome-wide identification of ethylene receptor protein-coding gene families in wheat and their regulated expression during development and under multiple abiotic stresses. *BMC plant biology*, 26(1), 347.

Tian Y, et al. (2026) Genome-wide analysis of the B3 family in apple (*Malus domestica* Borkh.) and functional identification of MdREM19 involvement in salt stress. *BMC genomics*, 27(1).

Wang H, et al. (2026) Integrated Proteomics and Metabolomics Reveal the Direct Hepatic Protection of Propionate Against Alcoholic Liver Disease via the RGN-PPAR γ Pathway. *Nutrients*, 18(5).

Zhang L, et al. (2026) Tat-HSPE1 suppresses clear cell renal cell carcinoma growth through lysosome-dependent cell death. *Frontiers in pharmacology*, 17, 1822208.

Potts J, et al. (2026) Genome-wide identification and expression profiling of the GYF gene family in *Vanilla planifolia*: insights into fruit development and Cymbidium mosaic virus response. *Frontiers in plant science*, 17, 1795375.

Abdelouahab M, et al. (2026) Pangenomics-Driven Reverse Vaccinology for the Discovery of New Vaccine Candidates Against *Bordetella pertussis*. *Bioinformatics and biology insights*, 20, 11779322261442522.

Nong L, et al. (2026) Unveiling molecular mechanisms and therapeutic targets in HbH-CS disease: a focus on oxidative stress and mitochondrial dysfunction. *Open life sciences*,

21(1), 20251337.

Yang Y, et al. (2026) Integrated multi-omics analysis suggests the involvement of PI3K-Akt/p21 signaling in the anti-colorectal cancer effects of *Diaphragma Juglandis Fructus* extract. *Frontiers in pharmacology*, 17, 1833123.

Ma W, et al. (2026) Genome-Wide Identification and Expression of the Mulberry PLA Family Under Drought and Salinity. *Biology*, 15(12).

Liu C, et al. (2026) Genome-wide identification of the PI4P5K gene family in cotton and role of GhPI4P5K-D04-2 in salt stress tolerance. *Frontiers in plant science*, 17, 1750290.

Ferrari ASA, et al. (2026) Discovery of Novel c-di-GMP-Related Genes in *Leptospira interrogans*. *Pathogens (Basel, Switzerland)*, 15(2).

Ye X, et al. (2026) Systemic serum protein alterations and molecular mechanisms in alcohol dependence. *PeerJ*, 14, e20671.

Wang J, et al. (2026) Full-length transcriptome sequencing analysis and characterization of MADS-box genes in *Rhododendron fortunei*. *BMC plant biology*, 26(1).

Zou D, et al. (2026) Integrated DIA proteomics and transcriptomics unravel molecular mechanisms of uterine prolificacy in Yunshang Black goats during the estrous cycle. *BMC genomics*, 27(1).

Wei L, et al. (2026) Mycosporine-like Amino Acids Biosynthesis in *Asterarcys* sp. Driving by Phosphorus Limitation: Evidence from Physiological and Transcriptomic Analyses. *Marine drugs*, 24(5).

Alanzi AR, et al. (2026) In silico identification and validation of vaccine and drug targets in *Coccidioides posadasii* through integrated genomic, proteomic, and molecular modeling approaches. *Medicine*, 105(23), e49169.

Shi Q, et al. (2026) Identification of HsfB Family in Peanut (*Arachis hypogea*) and Role of AhHsfB1-5A in High-Temperature Stress. *Plants (Basel, Switzerland)*, 15(12).