

Resource Summary Report

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Cello2Go

RRID:SCR_019042

Type: Tool

Proper Citation

Cello2Go (RRID:SCR_019042)

Resource Information

URL: <http://cello.life.nctu.edu.tw/cello2go/>

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Description: Web server for protein subcellular localization prediction with functional gene ontology annotation. Web based system for screening various properties of targeted protein and its subcellular localization.

Synonyms: subCELLular LOcalization prediction with functional Gene Ontology annotation

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

Defining Citation: [PMID:24911789](#)

Keywords: Protein subcellular localization, localization prediction, functional gene ontology annotation, targeted protein properties screening

Funding: China Medical University of Taiwan ;
National Chiao Tung University and Ministry of Education of Taiwan ;
National Science Council of Taiwan

Availability: Free, Freely available

Resource Name: Cello2Go

Resource ID: SCR_019042

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260903T235520+0000

Ratings and Alerts

No rating or validation information has been found for Cello2Go.

No alerts have been found for Cello2Go.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 79 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hessami A, et al. (2026) Design of a novel proteome-derived scaffold presenting epitopes of *Pseudomonas aeruginosa* in native conformation. Scientific reports, 16(1).

Han X, et al. (2026) The FoPLT Gene of *Fusarium oxysporum* Affects Conidial Development and Pathogenicity. Journal of fungi (Basel, Switzerland), 12(3).

Zhao S, et al. (2025) Characterization and Anti-Inflammatory Effects of *Akkermansia muciniphila*-Derived Extracellular Vesicles. Microorganisms, 13(2).

Maurastoni M, et al. (2025) Protein landscape of the brush border membrane of first instar larvae of *Frankliniella occidentalis*, the western flower thrips. PloS one, 20(6), e0326260.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. iScience, 28(3), 112081.

Basmenj ER, et al. (2025) Computational epitope-based vaccine design with bioinformatics approach; a review. Heliyon, 11(1), e41714.

Sohail S, et al. (2025) Druggable proteins of *Alistipes* reveal promising antimicrobial targets against chronic intestinal inflammation. Frontiers in pharmacology, 16, 1555062.

Yasin N, et al. (2024) Metabolic Proteins Expression Up-Regulated in Blood-Borne Extensively Drug-Resistant *Salmonella Typhi* Isolates from Pakistan. Medicina (Kaunas, Lithuania), 60(9).

Ahmad W, et al. (2024) Computational proteomics analysis of *Taphrina deformans* for the identification of antifungal drug targets and validation with commercial fungicides. Frontiers in plant science, 15, 1429890.

Urta G, et al. (2024) From Proteome to Potential Drugs: Integration of Subtractive Proteomics and Ensemble Docking for Drug Repurposing against *Pseudomonas aeruginosa* RND Superfamily Proteins. International journal of molecular sciences, 25(15).

Upadhyay A, et al. (2023) Deciphering Target Protein Cascade in *Salmonella typhi* Biofilm using Genomic Data Mining, and Protein-protein Interaction. Current genomics, 24(2), 100.

Ayu Eka Pitaloka D, et al. (2023) Bioinformatics Analysis to Uncover the Potential Drug Targets Responsible for Mycobacterium tuberculosis Peptidoglycan and Lysine Biosynthesis. *Bioinformatics and biology insights*, 17, 11779322231171774.

Zribi I, et al. (2023) Genome-Wide Identification and Expression Profiling of Pathogenesis-Related Protein 1 (PR-1) Genes in Durum Wheat (*Triticum durum* Desf.). *Plants* (Basel, Switzerland), 12(10).

Hussain MA, et al. (2023) Potential Therapeutic Target and Vaccines for SARS-CoV-2. *Pathogens* (Basel, Switzerland), 12(7).

Yoon J, et al. (2023) Quantitative Proteomic Analysis Deciphers the Molecular Mechanism for Endosperm Nuclear Division in Early Rice Seed Development. *Plants* (Basel, Switzerland), 12(21).

Jiang Z, et al. (2023) Identification and Evaluation of Novel Antigen Candidates against *Salmonella Pullorum* Infection Using Reverse Vaccinology. *Vaccines*, 11(4).

Zhan H, et al. (2023) Genome-Wide Identification and Expression Analysis of the bHLH Transcription Factor Family and Its Response to Abiotic Stress in Mongolian Oak (*Quercus mongolica*). *Current issues in molecular biology*, 45(2), 1127.

Aiman S, et al. (2023) Vaccinomics-aided next-generation novel multi-epitope-based vaccine engineering against multidrug resistant *Shigella Sonnei*: Immunoinformatics and chemoinformatics approaches. *PloS one*, 18(11), e0289773.

Afzal M, et al. (2023) Genomic landscape of the emerging XDR *Salmonella Typhi* for mining druggable targets *clpP*, *hisH*, *folP* and *gpml* and screening of novel TCM inhibitors, molecular docking and simulation analyses. *BMC microbiology*, 23(1), 25.

Jimenez-Vasquez V, et al. (2023) In-silico identification of linear B-cell epitopes in specific proteins of *Bartonella bacilliformis* for the serological diagnosis of Carrion's disease. *PLoS neglected tropical diseases*, 17(5), e0011321.