

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/>

Proper Citation: Cello2Go (RRID:SCR_019042)

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: software resource, web service, data access protocol

Defining Citation: [PMID:24911789](#)

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

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

Availability: Free, Freely available

Resource Name: Cello2Go

Resource ID: SCR_019042

Record Creation Time: 20220129T080343+0000

Record Last Update: 20260821T043038+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 [ASWG](#).

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).

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.

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.

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).

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

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).

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.

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.

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.