

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: 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: 20260805T044428+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 59 mentions in open access literature.

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

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.

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.

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.

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

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).

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.

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.
- Ghorbel M, et al. (2022) Identification and Expression Profiling of Two Saudi Arabia Catalase Genes from Wheat and Barley in Response to Abiotic and Hormonal Stresses. *Antioxidants* (Basel, Switzerland), 11(11).
- Chiang MH, et al. (2022) Proteomic Network of Antibiotic-Induced Outer Membrane Vesicles Released by Extensively Drug-Resistant *Elizabethkingia anophelis*. *Microbiology spectrum*, 10(4), e0026222.
- Ullah A, et al. (2022) An integrative reverse vaccinology, immunoinformatic, docking and simulation approaches towards designing of multi-epitopes based vaccine against monkeypox virus. *Journal of biomolecular structure & dynamics*, 1.
- Alshammari A, et al. (2022) Novel Chimeric Vaccine Candidate Development against *Leptotrichia buccalis*. *International journal of environmental research and public health*, 19(17).
- Pant S, et al. (2022) Genome-wide studies of PAL genes in sorghum and their responses to aphid infestation. *Scientific reports*, 12(1), 22537.
- Sabir IA, et al. (2022) MYB transcription factor family in sweet cherry (*Prunus avium* L.): genome-wide investigation, evolution, structure, characterization and expression patterns. *BMC plant biology*, 22(1), 2.
- Wang D, et al. (2022) In Silico Approach Gives Insights into Ig-like Fold Containing Proteins in *Vibrio parahaemolyticus*: A Focus on the Fibrillar Adhesins. *Toxins*, 14(2).
- Dhurve G, et al. (2022) Outer Membrane Vesicles of *Acinetobacter baumannii* DS002 Are Selectively Enriched with TonB-Dependent Transporters and Play a Key Role in Iron Acquisition. *Microbiology spectrum*, 10(2), e0029322.
- Tavares CS, et al. (2022) Composition and abundance of midgut surface proteins in the Asian citrus psyllid, *Diaphorina citri*. *Journal of proteomics*, 261, 104580.