## **Resource Summary Report**

Generated by dkNET on May 8, 2025

# 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: 20250508T065904+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 57 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

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.

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.

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).

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

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.

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.

Tavares CS, et al. (2022) Composition and abundance of midgut surface proteins in the Asian citrus psyllid, Diaphorina citri. Journal of proteomics, 261, 104580.

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.

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.

Pant S, et al. (2022) Genome-wide studies of PAL genes in sorghum and their responses to aphid infestation. Scientific reports, 12(1), 22537.

Alshammari A, et al. (2022) Novel Chimeric Vaccine Candidate Development against Leptotrichia buccalis. International journal of environmental research and public health, 19(17).

Mosby CA, et al. (2022) Interaction with mammalian enteric viruses alters outer membrane vesicle production and content by commensal bacteria. Journal of extracellular vesicles, 11(1), e12172.

Ma X, et al. (2022) Characterizations of a Class-I BASIC PENTACYSTEINE Gene Reveal Conserved Roles in the Transcriptional Repression of Genes Involved in Seed Development. Current issues in molecular biology, 44(9), 4059.