Resource Summary Report

Generated by dkNET on May 21, 2025

BaCelLo

RRID:SCR_011965
Type: Tool

Proper Citation

BaCelLo (RRID:SCR_011965)

Resource Information

URL: http://gpcr.biocomp.unibo.it/bacello/

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Description: A predictor for the subcellular localization of proteins in eukaryotes that is based on a decision tree of several support vector machines (SVMs). It classifies up to four localizations for Fungi and Metazoan proteins and five localizations for Plant ones. BaCelLo's predictions are balanced among different classes and all the localizations are considered as equiprobable.

Abbreviations: BaCelLo

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: PMID:16873501

Keywords: protein, data set, proteome

Funding:

Resource Name: BaCelLo

Resource ID: SCR_011965

Alternate IDs: OMICS_01616

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250521T061413+0000

Ratings and Alerts

No rating or validation information has been found for BaCelLo.

No alerts have been found for BaCelLo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Zhou Y, et al. (2024) Genome-wide analysis of bZIP gene family members in Pleurotus ostreatus, and potential roles of PobZIP3 in development and the heat stress response. Microbial biotechnology, 17(2), e14413.

Sedaghatkish A, et al. (2023) Characterization of a virulence factor in Plasmodiophora brassicae, with molecular markers for identification. PloS one, 18(9), e0289842.

Rodrigues JL, et al. (2022) Challenges in the Heterologous Production of Furanocoumarins in Escherichia coli. Molecules (Basel, Switzerland), 27(21).

Naqvi STQ, et al. (2021) Designing of Potential Polyvalent Vaccine Model for Respiratory Syncytial Virus by System Level Immunoinformatics Approaches. BioMed research international, 2021, 9940010.

Sharma B, et al. (2021) Genome-wide analysis of HECT E3 ubiquitin ligase gene family in Solanum lycopersicum. Scientific reports, 11(1), 15891.

V?ela?ová L, et al. (2021) Auxin Metabolome Profiling in the Arabidopsis Endoplasmic Reticulum Using an Optimised Organelle Isolation Protocol. International journal of molecular sciences, 22(17).

Wang Y, et al. (2021) Decipher the Helicobacter pylori Protein Targeting in the Nucleus of Host Cell and their Implications in Gallbladder Cancer: An insilico approach. Journal of Cancer, 12(23), 7214.

Raghavendra KP, et al. (2021) Genome-wide identification and expression analysis of the plant specific LIM genes in Gossypium arboreum under phytohormone, salt and pathogen stress. Scientific reports, 11(1), 9177.

Wang G, et al. (2020) Expression profiling of Cordyceps DnaJ protein family in Tolypocladium guangdongense during developmental and temperature stress processes.

Gene, 743, 144563.

Gu X, et al. (2020) Molecular characterization and serodiagnostic potential of two serpin proteins in Psoroptes ovis var. cuniculi. Parasites & vectors, 13(1), 620.

Zámocký M, et al. (2020) Hybrid Heme Peroxidases from Rice Blast Fungus Magnaporthe oryzae Involved in Defence against Oxidative Stress. Antioxidants (Basel, Switzerland), 9(8).

Safavi A, et al. (2020) Exploring the out of sight antigens of SARS-CoV-2 to design a candidate multi-epitope vaccine by utilizing immunoinformatics approaches. Vaccine, 38(48), 7612.

Chatterjee A, et al. (2020) MAPK cascade gene family in Camellia sinensis: In-silico identification, expression profiles and regulatory network analysis. BMC genomics, 21(1), 613.

Tang Y, et al. (2019) Molecular identification and expression of sesquiterpene pathway genes responsible for patchoulol biosynthesis and regulation in Pogostemon cablin. Botanical studies, 60(1), 11.

Liu Y, et al. (2019) Molecular characterisation and expression analysis of two heat-shock proteins in Taenia multiceps. Parasites & vectors, 12(1), 93.

Shan X, et al. (2019) Genome-Wide Analysis of Basic Helix-Loop-Helix Superfamily Members Reveals Organization and Chilling-Responsive Patterns in Cabbage (Brassica oleracea var. capitata L.). Genes, 10(11).

Armbruster L, et al. (2019) The Recovery from Sulfur Starvation Is Independent from the mRNA Degradation Initiation Enzyme PARN in Arabidopsis. Plants (Basel, Switzerland), 8(10).

Bartholomew ES, et al. (2019) Comprehensive Analysis of the Chitinase Gene Family in Cucumber (Cucumis sativus L.): From Gene Identification and Evolution to Expression in Response to Fusarium oxysporum. International journal of molecular sciences, 20(21).

Wang S, et al. (2019) Cytological and Proteomic Analysis of Wheat Pollen Abortion Induced by Chemical Hybridization Agent. International journal of molecular sciences, 20(7).

Orioli T, et al. (2019) Benchmarking subcellular localization and variant tolerance predictors on membrane proteins. BMC genomics, 20(Suppl 8), 547.