

Resource Summary Report

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Euk-mPLoc

RRID:SCR_011971

Type: Tool

Proper Citation

Euk-mPLoc (RRID:SCR_011971)

Resource Information

URL: <http://www.csbio.sjtu.edu.cn/bioinf/euk-multi-2/>

Proper Citation: Euk-mPLoc (RRID:SCR_011971)

Description: Data analysis service for predicting subcellular localization of eukaryotic proteins including those with multiple sites. Euk-mPLoc covers 22 eukaryotic subcellular locations.

Abbreviations: Euk-mPLoc

Synonyms: Euk-mPLoc 2.0: Predicting subcellular localization of eukaryotic proteins including those with multiple sites

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

Defining Citation: [PMID:17397210](#)

Keywords: subcellular location

Availability: Acknowledgement requested

Resource Name: Euk-mPLoc

Resource ID: SCR_011971

Alternate IDs: OMICS_01621

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260806T054538+0000

Ratings and Alerts

No rating or validation information has been found for Euk-mPLOC.

No alerts have been found for Euk-mPLOC.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 75 mentions in open access literature.

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

Tang W, et al. (2025) Characterization and enzymatic function of thioredoxin glutathione reductase in *Orientobilharzia turkestanicum* isolated from Xizang. *BMC veterinary research*, 21(1), 517.

Obuobi A, et al. (2025) Unveiling the *Plasmodium* inositol (pyro)phosphate pathway: Highlighting inositol polyphosphate multikinase as a novel therapeutic target for malaria. *PloS one*, 20(12), e0338411.

Li H, et al. (2025) Molecular Characterization, Recombinant Expression, and Functional Analysis of Carboxypeptidase B in *Litopenaeus vannamei*. *Genes*, 16(1).

Xu L, et al. (2025) Functional analysis of NtPDX2 in *Nicotiana tabacum* L. associated with stem development. *Frontiers in plant science*, 16, 1547677.

Guo S, et al. (2025) Genome-Wide Identification of DNA Methyltransferases (Dnmts) in Fish and Its Potential Roles During Sex Change in Blackhead Seabream. *Biomolecules*, 15(6).

Zhou YJ, et al. (2025) Proteomic analysis and functional characterization of excretory-secretory products from adult *Toxocara canis*: insights into parasite-host interactions. *BMC genomics*, 26(1), 806.

Rehmani MBI, et al. (2025) Computational design of an mRNA vaccine targeting antifungal-resistant *Lomentospora prolificans*. *Scientific reports*, 15(1), 34157.

Lu M, et al. (2025) Functional characterization of cutinase genes NsCut1-NsCut4 in *Neostagonospora sichuanensis* and their effects on fishscale bamboo. *Frontiers in plant science*, 16, 1564651.

Jia YL, et al. (2024) Identification of lipid synthesis genes in *Schizochytrium* sp. and their application in improving eicosapentaenoic acid synthesis in *Yarrowia lipolytica*. *Biotechnology for biofuels and bioproducts*, 17(1), 32.

Chen Y, et al. (2024) Identification and expression profiling of the bone morphogenetic protein gene family based on pearl culture in mantle and visceral mass of *Hyriopsis cumingii*. *Frontiers in veterinary science*, 11, 1445594.

Ouali R, et al. (2024) Trypanosoma cruzi reprograms mitochondrial metabolism within the anterior midgut of its vector Rhodnius prolixus during the early stages of infection. Parasites & vectors, 17(1), 381.

Zhang S, et al. (2024) Genome-wide identification and characterization of pectin methylesterase inhibitor gene family members related to abiotic stresses in watermelon. Frontiers in plant science, 15, 1454046.

Teng L, et al. (2024) Exon shuffling and alternative splicing of ROCO genes in brown algae enables a diverse repertoire of candidate immune receptors. Frontiers in plant science, 15, 1445022.

Wang J, et al. (2024) Genome-wide identification of YABBY gene family and its expression pattern analysis in Astragalus mongholicus. Plant signaling & behavior, 19(1), 2355740.

Tang B, et al. (2024) Fertility restorer gene CaRf and PepperSNP50K provide a promising breeding system for hybrid pepper. Horticulture research, 11(10), uhae223.

Zhang Y, et al. (2023) AfLaeA, a Global Regulator of Mycelial Growth, Chlamydospore Production, Pathogenicity, Secondary Metabolism, and Energy Metabolism in the Nematode-Trapping Fungus Arthrobotrys flagrans. Microbiology spectrum, 11(4), e0018623.

Ferreira P, et al. (2023) Post-Transcriptional Gene Silencing of Glucanase Inhibitor Protein in Phytophthora cinnamomi. Plants (Basel, Switzerland), 12(22).

Liu TY, et al. (2023) Functional analysis of differentially expressed circular RNAs in sheep subcutaneous fat. BMC genomics, 24(1), 591.

Wang B, et al. (2023) Characterization of Banana SNARE Genes and Their Expression Analysis under Temperature Stress and Mutualistic and Pathogenic Fungal Colonization. Plants (Basel, Switzerland), 12(8).

Hua Y, et al. (2023) Genome-wide analysis of the HSP20 gene family and its response to heat and drought stress in Coix (Coix lacryma-jobi L.). BMC genomics, 24(1), 478.