

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: analysis service resource, data analysis service, production service resource, 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: 20260905T133201+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 95 mentions in open access literature.

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

Mao W, et al. (2026) Genome-Wide Analysis of Heat Shock Transcription Factors (HSFs) in Kelp (*Saccharina japonica*) and Analysis of Their Expression in Response to Abiotic Stresses. *Plants* (Basel, Switzerland), 15(3).

Xiong X, et al. (2026) Combined Transcriptomic and Metabolomic Analyses of Low-Temperature Adaptation in *Bursaphelenchus xylophilus*. *International journal of molecular sciences*, 27(3).

Mao Y, et al. (2026) Genome to single-cell characterization of the MAPK family in bighead carp (*Hypophthalmichthys nobilis*) spleen during *Aeromonas hydrophila* challenge. *Frontiers in immunology*, 17, 1777786.

Zhang S, et al. (2026) Comprehensive Genomic Analysis and Expression Profiling of the C2H2-Type Zinc Finger Protein Family Under Abiotic Stresses in Watermelon. *Genes*, 17(5).

Ren R, et al. (2026) Genome-Wide Analysis Reveals the Roles of FAR1/FHY3 Genes in *Fragaria ananassa* Under Abiotic/Biotic Stresses and Highlights Their Potential Functions in Anthocyanin Biosynthesis During Fruit Development. *International journal of molecular sciences*, 27(12).

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

Lin D, et al. (2025) Genome-Wide Identification, Phylogenetic Analysis, and Expression Pattern of Polyamine Biosynthesis Gene Family in Pepper. *International journal of molecular sciences*, 26(17).

Zhang Z, et al. (2025) Genome-Wide Analysis of the PERK Gene Family in *Brassica napus* L. and Their Potential Roles in Clubroot Disease. *International journal of molecular sciences*, 26(6).

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

- 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.
- 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.
- Chen F, et al. (2025) Genome-wide identification and comprehensive analysis of the COI1 gene family in *Medicago sativa*. *Frontiers in plant science*, 16, 1712214.
- 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).
- Liu H, et al. (2025) Genome-Wide Characterization of the ANN Gene Family in *Corydalis saxicola* Bunting and the Role of CsANN1 in Dehydrocavidine Biosynthesis. *Plants (Basel, Switzerland)*, 14(13).
- 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.
- Teng L, et al. (2025) Genome-wide identification and analysis of expression of pathogenesis-related protein 1 (PR-1) gene family in brown algae. *Frontiers in plant science*, 16, 1754480.
- Lu M, et al. (2025) Functional characterization of cutinase genes NsCut1-NsCut4 in *Neostagonosporella sichuanensis* and their effects on fishscale bamboo. *Frontiers in plant science*, 16, 1564651.
- Rehmani MBI, et al. (2025) Computational design of an mRNA vaccine targeting antifungal-resistant *Lomentospora prolificans*. *Scientific reports*, 15(1), 34157.
- Xu Q, et al. (2025) Genome-Wide Identification and Characterization of Isoflavone Synthase (IFS) Gene Family, and Analysis of GgARF4-GgIFS9 Regulatory Module in *Glycyrrhiza glabra*. *International journal of molecular sciences*, 26(21).
- Duan C, et al. (2025) Evolutionary Dynamics and Functional Bifurcation of the C2H2 Gene Family in Basidiomycota. *Journal of fungi (Basel, Switzerland)*, 11(7).