

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

Multi Loc2

RRID:SCR_023013

Type: Tool

Proper Citation

Multi Loc2 (RRID:SCR_023013)

Resource Information

URL: <https://abi-services.informatik.uni-tuebingen.de/multiloc2/webloc.cgi>

Proper Citation: Multi Loc2 (RRID:SCR_023013)

Description: Web application for integrating phylogeny and Gene Ontology terms into subcellular protein colalization prediction.Extensive high performance subcellular protein localization prediction system.

Synonyms: MultiLoc2

Resource Type: software resource, data access protocol, web service

Defining Citation: [PMID:19723330](#)

Keywords: subcellular protein localization, prediction system, integrating phylogeny and Gene Ontology terms, subcellular protein colalization prediction

Availability: Free, Freely available

Resource Name: Multi Loc2

Resource ID: SCR_023013

License: GNU GPL

Record Creation Time: 20221130T050154+0000

Record Last Update: 20260813T055241+0000

Ratings and Alerts

No rating or validation information has been found for Multi Loc2.

No alerts have been found for Multi Loc2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Raiyemo DA, et al. (2025) Chromosome-level assemblies of *Amaranthus palmeri*, *Amaranthus retroflexus*, and *Amaranthus hybridus* allow for genomic comparisons and identification of a sex-determining region. *The Plant journal : for cell and molecular biology*, 121(4), e70027.

Antos-Krzeminska N, et al. (2023) *Acanthamoeba castellanii* Uncoupling Protein: A Complete Sequence, Activity, and Role in Response to Oxidative Stress. *International journal of molecular sciences*, 24(15).

Luo W, et al. (2022) Quantitative proteomic analysis provides insight into the survival mechanism of *Salmonella typhimurium* under high-intensity ultrasound treatment. *Current research in food science*, 5, 1740.

Cheng X, et al. (2022) The genome wide analysis of Tryptophan Aminotransferase Related gene family, and their relationship with related agronomic traits in *Brassica napus*. *Frontiers in plant science*, 13, 1098820.

Babula-Skowrońska D, et al. (2021) Functional divergence of *Brassica napus* BnaABI1 paralogs in the structurally conserved PP2CA gene subfamily of Brassicaceae. *Genomics*, 113(5), 3185.