

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Ontologizer

RRID:SCR_005801

Type: Tool

Proper Citation

Ontologizer (RRID:SCR_005801)

Resource Information

URL: <http://compbio.charite.de/contao/index.php/ontologizer2.html>

Proper Citation: Ontologizer (RRID:SCR_005801)

Description: The Ontologizer is a Java webstart application for GO term enrichment analysis that provides browsing and graph visualization capabilities. The Ontologizer allows users to analyze data with the standard Fisher exact test and also the parent-child method and topology methods. The tool can be started directly from the web using Java webstart. For graph visualizations, users need to install the GraphViz library. The tool is freely available to all, and source code is available at SourceForge. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: Ontologizer

Synonyms: The Ontologizer

Resource Type: analysis service resource, data analysis service, data processing software, production service resource, service resource, software application, software resource, source code

Defining Citation: [PMID:18511468](#), [PMID:17848398](#)

Keywords: high-throughput, biological data, gene ontology, statistical analysis, fisher exact test, visualization, graph, java, annotation, parent-child, topology

Funding: DFG SFB 760

Availability: Free for academic use

Resource Name: Ontologizer

Resource ID: SCR_005801

Alternate IDs: nlx_149289

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260905T132542+0000

Ratings and Alerts

No rating or validation information has been found for Ontologizer.

No alerts have been found for Ontologizer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 124 mentions in open access literature.

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

Bajunaid W, et al. (2026) A bacterial family of fatty acid acyltransferases related to the Shigella effector IcsB. mBio, 17(4), e0389025.

Hassan N, et al. (2026) Optimizing bio-orthogonal non-canonical amino acid tagging (BONCAT) for low-disruption labeling of Arabidopsis proteins in vivo. Plant physiology, 201(1).

Weinheimer EI, et al. (2025) Differential gene reactions reveal drought response strategies in African acacias. The Plant journal : for cell and molecular biology, 123(3), e70385.

Grubb LE, et al. (2025) Quantitative Proteomic Analysis of Brassica Napus Reveals Intersections Between Nutrient Deficiency Responses. Plant, cell & environment, 48(2), 1409.

Bai M, et al. (2025) Genome sequencing of three Polyscias species reveals common features in terpene synthase gene family evolution in these species. The plant genome, 18(1), e20563.

Pazzaglia J, et al. (2025) Handling the heat: ocean acidification mitigates the effects of marine heatwaves on Posidonia oceanica seedlings. Journal of experimental botany, 76(22), 6958.

Bickels Nuri R, et al. (2024) Acanthamoeba polyphaga de novo transcriptome and its dynamics during Mimivirus infection. Scientific reports, 14(1), 25894.

Baijal K, et al. (2024) Polyphosphate kinase regulates LPS structure and polymyxin resistance during starvation in E. coli. PLoS biology, 22(3), e3002558.

Demko V, et al. (2024) Regulation of developmental gatekeeping and cell fate transition by the calpain protease DEK1 in Physcomitrium patens. Communications biology, 7(1), 261.

Baijal K, et al. (2023) Proteomics analysis reveals a role for *E. coli* polyphosphate kinase in membrane structure and polymyxin resistance during starvation. *bioRxiv : the preprint server for biology*.

Kobayashi S, et al. (2023) DNA sequencing in the classroom: complete genome sequence of two earwig (Dermaptera; Insecta) species. *Biological research*, 56(1), 6.

Žárský V, et al. (2023) Contrasting outcomes of genome reduction in mikrocytids and microsporidians. *BMC biology*, 21(1), 137.

Rondeau EB, et al. (2023) Insights from a chum salmon (*Oncorhynchus keta*) genome assembly regarding whole-genome duplication and nucleotide variation influencing gene function. *G3 (Bethesda, Md.)*, 13(8).

Kui L, et al. (2023) A chromosome-level genome assembly for *Erianthus fulvus* provides insights into its biofuel potential and facilitates breeding for improvement of sugarcane. *Plant communications*, 4(4), 100562.

Rodriguez Gallo MC, et al. (2023) Quantitative Time-Course Analysis of Osmotic and Salt Stress in *Arabidopsis thaliana* Using Short Gradient Multi-CV FAIMSpro BoxCar DIA. *Molecular & cellular proteomics : MCP*, 22(11), 100638.

Tuschl K, et al. (2022) Loss of *slc39a14* causes simultaneous manganese hypersensitivity and deficiency in zebrafish. *Disease models & mechanisms*, 15(6).

Ren J, et al. (2022) Deletion of all three MAP kinase genes results in severe defects in stress responses and pathogenesis in *Fusarium graminearum*. *Stress biology*, 2(1), 6.

Couvillion M, et al. (2022) Transcription elongation is finely tuned by dozens of regulatory factors. *eLife*, 11.

McCarthy L, et al. (2022) Ddp1 Cooperates with Ppx1 to Counter a Stress Response Initiated by Nonvacuolar Polyphosphate. *mBio*, 13(4), e0039022.

Karlebach G, et al. (2022) Betacoronavirus-specific alternate splicing. *Genomics*, 114(2), 110270.