

Resource Summary Report

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OWLTools

RRID:SCR_005732

Type: Tool

Proper Citation

OWLTools (RRID:SCR_005732)

Resource Information

URL: <http://code.google.com/p/owltools/>

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Description: OWLTools (aka OWL2LS - OWL2 Life Sciences) is a java API for accessing ontologies in either OBO or OWL. OWLTools provides a bio-ontologies friendly wrapper on top of the Manchester OWL API. It provides many features, including: * convenience methods for OBO-like properties such as synonyms, textual definitions, obsolescence, replaced_by * simple graph-like operations over ontologies * visualization using the QuickGO graphs libraries Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: OWLTools

Synonyms: OWL2LS - OWL2 Life Sciences, OWL Tools

Resource Type: software resource

Keywords: software library, ontology

Availability: Open unspecified license - Free for academic use

Resource Name: OWLTools

Resource ID: SCR_005732

Alternate IDs: nlx_149192

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260725T190611+0000

Ratings and Alerts

No rating or validation information has been found for OWLTools.

No alerts have been found for OWLTools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Shefchek K, et al. (2025) Development of self-phenotyping tools to empower patients and improve diagnostics. *EBioMedicine*, 121, 105965.

Alqassar JD, et al. (2025) WntA expression and wing transcriptomics illuminate the evolution of stripe patterns in skipper butterflies. *Biology open*, 14(11).

Callahan TJ, et al. (2024) An open source knowledge graph ecosystem for the life sciences. *Scientific data*, 11(1), 363.

Alegria Terrazas R, et al. (2022) Defining Composition and Function of the Rhizosphere Microbiota of Barley Genotypes Exposed to Growth-Limiting Nitrogen Supplies. *mSystems*, 7(6), e0093422.

Vinje MA, et al. (2021) Description and functional analysis of the transcriptome from malting barley. *Genomics*, 113(5), 3310.

Konopka T, et al. (2021) Diffusion enables integration of heterogeneous data and user-driven learning in a desktop knowledge-base. *PLoS computational biology*, 17(8), e1009283.

Henningsen EC, et al. (2021) Identification of Candidate Susceptibility Genes to Puccinia graminis f. sp. tritici in Wheat. *Frontiers in plant science*, 12, 657796.

Haas JC, et al. (2021) Candidate regulators and target genes of drought stress in needles and roots of Norway spruce. *Tree physiology*, 41(7), 1230.

Entrambasaguas L, et al. (2021) Gene body DNA methylation in seagrasses: inter- and intraspecific differences and interaction with transcriptome plasticity under heat stress. *Scientific reports*, 11(1), 14343.

Gouveia D, et al. (2020) Combining proteogenomics and metaproteomics for deep taxonomic and functional characterization of microbiomes from a non-sequenced host. *NPJ biofilms and microbiomes*, 6(1), 23.

Hinderer EW, et al. (2020) GOcats: A tool for categorizing Gene Ontology into subgraphs of user-defined concepts. *PloS one*, 15(6), e0233311.

Wang R, et al. (2019) Regulation of Intronic Polyadenylation by PCF11 Impacts mRNA Expression of Long Genes. *Cell reports*, 26(10), 2766.

Hinderer EW, et al. (2019) Advances in gene ontology utilization improve statistical power of annotation enrichment. *PloS one*, 14(8), e0220728.

Kiyama R, et al. (2018) Genome sequence of the cauliflower mushroom *Sparassis crispa* (Hanabiratake) and its association with beneficial usage. *Scientific reports*, 8(1), 16053.

Li Z, et al. (2017) Single-Copy Genes as Molecular Markers for Phylogenomic Studies in Seed Plants. *Genome biology and evolution*, 9(5), 1130.

Meehan TF, et al. (2017) Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. *Nature genetics*, 49(8), 1231.

Buttigieg PL, et al. (2016) The environment ontology in 2016: bridging domains with increased scope, semantic density, and interoperation. *Journal of biomedical semantics*, 7(1), 57.

Robinson PN, et al. (2014) Improved exome prioritization of disease genes through cross-species phenotype comparison. *Genome research*, 24(2), 340.