

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: 20260801T190258+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 [dkNET](#) .

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.

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

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

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.