

Resource Summary Report

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Ontodog: A Web-based Ontology View Generator

RRID:SCR_005061

Type: Tool

Proper Citation

Ontodog: A Web-based Ontology View Generator (RRID:SCR_005061)

Resource Information

URL: <http://ontodog.hegroup.org/index.php>

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Description: Ontodog is a web-based ontology view generator. It can generate inSubset annotation ontology, user preferred label annotation ontology and subset of source ontology. Simply provide Ontodog input term file (Microsoft Excel file or tab-delimited text file), select one source ontology or enter your own source ontology and SPARQL endpoint, then set the settings for Ontodog output files and get the OWL (RDF/XML) Output files. Ontodog performs the basic ontology modularization-like function, i.e., it automatically extracts all axioms and related terms associated with user-specified signature term(s). In addition, Ontodog includes extra features: (1) extracting all instance data associated with the retrieved class terms and annotations; and (2) recursively extracting all axioms and related terms indirectly associated with signature terms. More features are being added to Ontodog, such as relabeling preferred names for various ontology terms to fit in with the needs from a specific community. The Ontodog input data requires a source ontology and a list of user-specified signature terms in tab-delimited format. Ontodog provides the template files for generating the signature terms as the input terms file to download. There are several output options that the users can choose based on their needs. With more and more ontologies being developed, Ontodog offers a timely web-based package of solutions for ontology view generation. Ontodog provides an efficient approach to promote ontology sharing and interoperability. It is easy to use and does not require knowledge of SPARQL, script programming, and command line operation. Ontodog is developed to serve the ontology community for ontology reuse. It is freely available under the Apache License 2.0. The source code is made available under Apache License 2.0.

Abbreviations: Ontodog

Resource Type: production service resource, service resource, software resource, source code

Keywords: ontology, interoperability

Funding: Rackham Pilot Research ;
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Resource Name: Ontodog: A Web-based Ontology View Generator

Resource ID: SCR_005061

Alternate IDs: nlx_144053

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260821T193730+0000

Ratings and Alerts

No rating or validation information has been found for Ontodog: A Web-based Ontology View Generator.

No alerts have been found for Ontodog: A Web-based Ontology View Generator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Shen YZ, et al. (2025) Exploration potential sepsis-ferroptosis mechanisms through the use of CETSA technology and network pharmacology. Scientific reports, 15(1), 13527.

Sohi MG, et al. (2025) HTS analysis of resistance induction against PPV by four hairpin constructs in Nicotiana benthamiana Domin. Scientific reports, 15(1), 12362.

Aydin S, et al. (2021) Toward Routine Minimally Invasive Ventricular Septal Defect Closure Via Right Lateral Minithoracotomy. Frontiers in pediatrics, 9, 708203.

Singh S, et al. (2021) Comprehensive analysis and identification of drought-responsive candidate NAC genes in three semi-arid tropics (SAT) legume crops. BMC genomics, 22(1), 289.

Chen Y, et al. (2017) Coexpression Analysis of Transcriptome on AIDS and Other Human Disease Pathways by Canonical Correlation Analysis. International journal of genomics, 2017, 9163719.

- Zhang J, et al. (2017) Small RNA and Transcriptome Sequencing Reveal a Potential miRNA-Mediated Interaction Network That Functions during Somatic Embryogenesis in *Lilium pumilum* DC. Fisch. *Frontiers in plant science*, 8, 566.
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- Wan LC, et al. (2012) Identification and characterization of small non-coding RNAs from Chinese fir by high throughput sequencing. *BMC plant biology*, 12, 146.
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