

# Resource Summary Report

Generated by [NIF](#) on Aug 31, 2026

## 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>

**Proper Citation:** Ontodog: A Web-based Ontology View Generator (RRID:SCR\_005061)

**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 ;  
NIAID R01AI081062;  
NIGMS 5R01GM93132-1

**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:** 20260829T182842+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 [NIF](#) .

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.
- Pathak A, et al. (2016) Comparative Genomics and Metabolic Analysis Reveals Peculiar Characteristics of *Rhodococcus opacus* Strain M213 Particularly for Naphthalene Degradation. *PloS one*, 11(8), e0161032.
- Wang L, et al. (2016) Genome-Wide Identification of MicroRNAs and Their Targets in the Leaves and Fruits of *Eucommia ulmoides* Using High-Throughput Sequencing. *Frontiers in plant science*, 7, 1632.
- Török A, et al. (2016) The cnidarian *Hydractinia echinata* employs canonical and highly adapted histones to pack its DNA. *Epigenetics & chromatin*, 9(1), 36.
- Fiscella K, et al. (2015) Activation of persons living with HIV for treatment, the great study. *BMC public health*, 15, 1056.
- Diner BA, et al. (2015) The functional interactome of PYHIN immune regulators reveals IFIX is a sensor of viral DNA. *Molecular systems biology*, 11(1), 787.
- Pombert JF, et al. (2015) The *Ordospora colligata* genome: Evolution of extreme reduction in microsporidia and host-to-parasite horizontal gene transfer. *mBio*, 6(1).
- Feng J, et al. (2015) High-throughput deep sequencing reveals that microRNAs play important roles in salt tolerance of euhalophyte *Salicornia europaea*. *BMC plant biology*, 15, 63.
- Howe JR, et al. (2013) BMPR1A mutations in juvenile polyposis affect cellular localization. *The Journal of surgical research*, 184(2), 739.
- 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.
- Putku M, et al. (2011) Novel polymorphic AluYb8 insertion in the WNK1 gene is associated with blood pressure variation in Europeans. *Human mutation*, 32(7), 806.
- Bergeault K, et al. (2010) Low level of polymorphism in two putative NPR1 homologs in the Vitaceae family. *Biology direct*, 5, 9.