

# Resource Summary Report

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

## OwlSim

RRID:SCR\_006819

Type: Tool

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### Proper Citation

OwlSim (RRID:SCR\_006819)

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### Resource Information

**URL:** <http://owlsim.org>

**Proper Citation:** OwlSim (RRID:SCR\_006819)

**Description:** Software package that provides the ability to do a number of standard semantic similarity methods and includes novel methods for combining these with dynamic selection of anonymous grouping classes. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

**Abbreviations:** OwlSim

**Resource Type:** data processing software, software application, software resource

**Defining Citation:** [PMID:19956802](#)

**Keywords:** functional similarity, semantic similarity, ontology, phenotype, annotation, windows, mac os x, linux, unix

**Funding:** Biomedical Information Science and Technology Initiative ;  
National Center for Biomedical Ontology ;  
NHGRI U54 HG004028;  
NHGRI HG002659

**Availability:** Open unspecified license - Free for academic use

**Resource Name:** OwlSim

**Resource ID:** SCR\_006819

**Alternate IDs:** nlx\_149312

**Record Creation Time:** 20220129T080238+0000

**Record Last Update:** 20260905T133042+0000

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## Ratings and Alerts

No rating or validation information has been found for OwlSim.

No alerts have been found for OwlSim.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Tanaka N, et al. (2020) An atlas of evidence-based phenotypic associations across the mouse phenome. Scientific reports, 10(1), 3957.

Wang RL, et al. (2019) Ontology-based semantic mapping of chemical toxicities. Toxicology, 412, 89.

Mungall CJ, et al. (2017) The Monarch Initiative: an integrative data and analytic platform connecting phenotypes to genotypes across species. Nucleic acids research, 45(D1), D712.

Bone WP, et al. (2016) Computational evaluation of exome sequence data using human and model organism phenotypes improves diagnostic efficiency. Genetics in medicine : official journal of the American College of Medical Genetics, 18(6), 608.

Maynard SM, et al. (2013) A knowledge based approach to matching human neurodegenerative disease and animal models. Frontiers in neuroinformatics, 7, 7.