

Resource Summary Report

Generated by [nidm-terms](#) on Sep 22, 2026

ConceptMapper

RRID:SCR_006548

Type: Tool

Proper Citation

ConceptMapper (RRID:SCR_006548)

Resource Information

URL: <http://code.google.com/p/google-refine/>

Proper Citation: ConceptMapper (RRID:SCR_006548)

Description: Software tool that stores definitions of views of data, along with the ontology concepts they represent. This is a part of the Neuroscience Information Framework (NIF) code stack.

Abbreviations: Concept Mapper

Resource Type: software resource

Keywords: resource:google refine

Funding: NIH

Resource Name: ConceptMapper

Resource ID: SCR_006548

Alternate IDs: nlx_157720

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260919T195113+0000

Ratings and Alerts

No rating or validation information has been found for ConceptMapper.

No alerts have been found for ConceptMapper.

Data and Source Information

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

Chen J, et al. (2024) Integration of background knowledge for automatic detection of inconsistencies in gene ontology annotation. *Bioinformatics (Oxford, England)*, 40(Suppl 1), i390.

Chen J, et al. (2022) Exploring automatic inconsistency detection for literature-based gene ontology annotation. *Bioinformatics (Oxford, England)*, 38(Suppl 1), i273.

Fujiwara T, et al. (2022) Advances in the development of PubCaseFinder, including the new application programming interface and matching algorithm. *Human mutation*, 43(6), 734.

Fujiwara T, et al. (2018) PubCaseFinder: A Case-Report-Based, Phenotype-Driven Differential-Diagnosis System for Rare Diseases. *American journal of human genetics*, 103(3), 389.

Galeota E, et al. (2017) Ontology-based annotations and semantic relations in large-scale (epi)genomics data. *Briefings in bioinformatics*, 18(3), 403.

Funk CS, et al. (2016) Gene Ontology synonym generation rules lead to increased performance in biomedical concept recognition. *Journal of biomedical semantics*, 7(1), 52.

Funk CS, et al. (2015) Evaluating a variety of text-mined features for automatic protein function prediction with GOstruct. *Journal of biomedical semantics*, 6, 9.

Nagalingum NS, et al. (2015) Continental scale patterns and predictors of fern richness and phylogenetic diversity. *Frontiers in genetics*, 6, 132.

Richardet R, et al. (2015) Large-scale extraction of brain connectivity from the neuroscientific literature. *Bioinformatics (Oxford, England)*, 31(10), 1640.

Collier N, et al. (2015) Concept selection for phenotypes and diseases using learn to rank. *Journal of biomedical semantics*, 6, 24.

Spasi?? I, et al. (2015) KneeTex: an ontology-driven system for information extraction from MRI reports. *Journal of biomedical semantics*, 6, 34.