

Resource Summary Report

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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: 20250420T014334+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

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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

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

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.