

Resource Summary Report

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

GOCat

RRID:SCR_003608

Type: Tool

Proper Citation

GOCat (RRID:SCR_003608)

Resource Information

URL: <http://eagl.unige.ch/GOCat/>

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Description: Software tool that uses a machine learning (ML) approach to classify text, based on the Gene Ontology. It relies on a k-Nearest Neighbours algorithm, a simple algorithm which assigns to a new text the categories that are the most prevalent among the k most similar instances contained in the knowledge base. The ML classifier operates in two steps and combines two components. First, a related article search engine retrieves instances (i.e. abstracts) in the knowledge base that are the most similar to the input text (its nearest neighbours); second, a score computer infers the functional profile from the k most similar instances.

Abbreviations: GOCat

Synonyms: GOCat the Gene Ontology Categorizer, GOCat - the Gene Ontology Categorizer

Resource Type: analysis service resource, data analysis service, production service resource, service resource, software resource

Defining Citation: [PMID:23842461](#)

Keywords: machine learning, classification

Resource Name: GOCat

Resource ID: SCR_003608

Alternate IDs: nlx_157764

Record Creation Time: 20220129T080220+0000

Record Last Update: 20260905T132506+0000

Ratings and Alerts

No rating or validation information has been found for GOCat.

No alerts have been found for GOCat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Miao J, et al. (2015) Generally detected genes in comparative transcriptomics in bivalves: toward the identification of molecular markers of cellular stress response. Environmental toxicology and pharmacology, 39(1), 475.

Gobeill J, et al. (2014) Closing the loop: from paper to protein annotation using supervised Gene Ontology classification. Database : the journal of biological databases and curation, 2014.