

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

GO Online SQL Environment (GOOSE)

RRID:SCR_006174

Type: Tool

Proper Citation

GO Online SQL Environment (GOOSE) (RRID:SCR_006174)

Resource Information

URL: <http://www.berkeleybop.org/goose/>

Proper Citation: GO Online SQL Environment (GOOSE) (RRID:SCR_006174)

Description: A web utility providing a direct interface to perform SQL queries directly on the GO database, allowing users to run custom queries without having to install a copy of the GO database locally. GOOSE includes many sample queries to aid novice users and allows results to be retrieved as a web page or as tab-delimited text. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: GOOSE

Synonyms: GO Online SQL Environment

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

Defining Citation: [PMID:19033274](#)

Keywords: database, gene ontology, sql, database or data warehouse

Availability: Open unspecified license - Free for academic use

Resource Name: GO Online SQL Environment (GOOSE)

Resource ID: SCR_006174

Alternate IDs: nlx_151682

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260904T000207+0000

Ratings and Alerts

No rating or validation information has been found for GO Online SQL Environment (GOOSE).

No alerts have been found for GO Online SQL Environment (GOOSE).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Hussain S, et al. (2023) A novel hybrid methodology to secure GOOSE messages against cyberattacks in smart grids. Scientific reports, 13(1), 1857.

Ko?? I, et al. (2017) The natural history of molecular functions inferred from an extensive phylogenomic analysis of gene ontology data. PloS one, 12(5), e0176129.

Galhardo M, et al. (2014) Integrated analysis of transcript-level regulation of metabolism reveals disease-relevant nodes of the human metabolic network. Nucleic acids research, 42(3), 1474.

Jaime MD, et al. (2012) Identification of yeast genes that confer resistance to chitosan oligosaccharide (COS) using chemogenomics. BMC genomics, 13, 267.

, et al. (2012) The Gene Ontology: enhancements for 2011. Nucleic acids research, 40(Database issue), D559.

Tkach JM, et al. (2012) Dissecting DNA damage response pathways by analysing protein localization and abundance changes during DNA replication stress. Nature cell biology, 14(9), 966.

Blackman RK, et al. (2012) Mitochondrial electron transport is the cellular target of the oncology drug elesclomol. PloS one, 7(1), e29798.

Chooneea D, et al. (2010) Elucidation of the outer membrane proteome of Salmonella enterica serovar Typhimurium utilising a lipid-based protein immobilization technique. BMC microbiology, 10, 44.

Barrell D, et al. (2009) The GOA database in 2009--an integrated Gene Ontology Annotation resource. Nucleic acids research, 37(Database issue), D396.

, et al. (2008) The Gene Ontology project in 2008. Nucleic acids research, 36(Database issue), D440.