

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

go-moose

RRID:SCR_005666

Type: Tool

Proper Citation

go-moose (RRID:SCR_005666)

Resource Information

URL: <http://geneontology.svn.sourceforge.net/viewvc/geneontology/go-moose/>

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Description: go-moose is intended as a replacement for the aging go-perl and go-db-perl Perl libraries. It is written using the object oriented Moose libraries. It can be used for performing a number of analyses on GO data, including the remapping of GO annotations to a selected subset of GO terms. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: go-moose

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

Keywords: software library, slimmer-type tool, analysis, gene ontology, other analysis

Availability: Free for academic use

Resource Name: go-moose

Resource ID: SCR_005666

Alternate IDs: nlx_149189

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T132539+0000

Ratings and Alerts

No rating or validation information has been found for go-moose.

No alerts have been found for go-moose.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.