

Resource Summary Report

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[go-perl](#)

RRID:SCR_005730

Type: Tool

Proper Citation

go-perl (RRID:SCR_005730)

Resource Information

URL: <http://search.cpan.org/~cmungall/go-perl/>

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Description: go-perl is a set of Perl modules for parsing, manipulating and exporting ontologies and annotations. It includes parsers for the OBO and GO gene association file formats. It has a graph-based object model with methods for graph traversal. For more details, see the documentation included with the modules. go-perl comes bundled with XSL (Extensible Stylesheet Language) transforms (which can also be used independently of Perl, provided you have files in OBO-XML format), as well as scripts that can be used as standalone tools. Installation should be simple, provided you have some experience with Perl and CPAN; see the INSTALL file for details. Platform: Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: go-perl

Resource Type: software resource

Keywords: ontology, annotation, software library, slimmer-type tool, parser

Availability: Free for academic use

Resource Name: go-perl

Resource ID: SCR_005730

Alternate IDs: nlx_149190

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260905T132541+0000

Ratings and Alerts

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

No alerts have been found for go-perl.

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 [PRECISE-TBI](#) .

Sun L, et al. (2026) Isolation, Identification, and Genomic Characterization of a Cellulolytic *Bacillus subtilis* A2 from Goose Ileum. *Microorganisms*, 14(6).

Shinzato C, et al. (2014) A snapshot of a coral "holobiont": a transcriptome assembly of the scleractinian coral, *porites*, captures a wide variety of genes from both the host and symbiotic zooxanthellae. *PloS one*, 9(1), e85182.

Sato Y, et al. (2013) RiceFRIEND: a platform for retrieving coexpressed gene networks in rice. *Nucleic acids research*, 41(Database issue), D1214.

Tang X, et al. (2013) Systematically profiling and annotating long intergenic non-coding RNAs in human embryonic stem cell. *BMC genomics*, 14 Suppl 5(Suppl 5), S3.

Petzold A, et al. (2013) The transcript catalogue of the short-lived fish *Nothobranchius furzeri* provides insights into age-dependent changes of mRNA levels. *BMC genomics*, 14, 185.

Sato Y, et al. (2011) Field transcriptome revealed critical developmental and physiological transitions involved in the expression of growth potential in japonica rice. *BMC plant biology*, 11, 10.

Weber CC, et al. (2011) Support for multiple classes of local expression clusters in *Drosophila melanogaster*, but no evidence for gene order conservation. *Genome biology*, 12(3), R23.

Davis MJ, et al. (2010) Automatic, context-specific generation of Gene Ontology slim. *BMC bioinformatics*, 11, 498.

Carbon S, et al. (2009) AmiGO: online access to ontology and annotation data. *Bioinformatics (Oxford, England)*, 25(2), 288.

Chiba H, et al. (2008) Weak correlation between sequence conservation in promoter regions and in protein-coding regions of human-mouse orthologous gene pairs. *BMC genomics*, 9, 152.

Vavouri T, et al. (2007) Parallel evolution of conserved non-coding elements that target a common set of developmental regulatory genes from worms to humans. *Genome biology*,

8(2), R15.