

Resource Summary Report

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Gene Ontology Tools

RRID:SCR_006941

Type: Tool

Proper Citation

Gene Ontology Tools (RRID:SCR_006941)

Resource Information

URL: <http://geneontology.org/docs/tools-overview/>

Proper Citation: Gene Ontology Tools (RRID:SCR_006941)

Description: Collection of tools developed by GO Consortium and by third parties. Tools are listed by category or alphabetically and continue to be improved and expanded.

Abbreviations: GO Tools

Resource Type: database, catalog, software resource, software repository, data or information resource

Keywords: registry, annotation browser, annotation search engine, annotation visualization, ontology, annotation editor, database, data warehouse, software library, statistical analysis, slimmer-type tool, term enrichment, text mining, protein interaction, functional similarity, semantic similarity, analysis, annotation, visualization, editor

Availability: Free, Freely available

Resource Name: Gene Ontology Tools

Resource ID: SCR_006941

Alternate IDs: nlx_146273

Alternate URLs: https://neuinfo.org/mynif/search.php?q=*&t=indexable&nif=nlx_146273-1

Old URLs: <http://www.geneontology.org/GO.tools.shtml>

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260728T043241+0000

Ratings and Alerts

No rating or validation information has been found for Gene Ontology Tools.

No alerts have been found for Gene Ontology Tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Chang J, et al. (2025) Antagonistic roles for MITF and TFE3 in melanoma plasticity. Cell reports, 44(4), 115474.

Kunath N, et al. (2021) DNA repair enzyme NEIL3 enables a stable neural representation of space by shaping transcription in hippocampal neurons. iScience, 24(12), 103470.

Guerra SL, et al. (2020) A Deregulated HOX Gene Axis Confers an Epigenetic Vulnerability in KRAS-Mutant Lung Cancers. Cancer cell, 37(5), 705.

Ross KG, et al. (2018) SoxB1 Activity Regulates Sensory Neuron Regeneration, Maintenance, and Function in Planarians. Developmental cell, 47(3), 331.

Ugras S, et al. (2018) Induction of the Immunoproteasome Subunit Lmp7 Links Proteostasis and Immunity in ??-Synuclein Aggregation Disorders. EBioMedicine, 31, 307.

Sandoval IT, et al. (2017) A metabolic switch controls intestinal differentiation downstream of Adenomatous polyposis coli (APC). eLife, 6.

Wang J, et al. (2015) Pathway and network approaches for identification of cancer signature markers from omics data. Journal of Cancer, 6(1), 54.

, et al. (2013) Gene Ontology annotations and resources. Nucleic acids research, 41(Database issue), D530.

Tabas-Madrid D, et al. (2012) GeneCodis3: a non-redundant and modular enrichment analysis tool for functional genomics. Nucleic acids research, 40(Web Server issue), W478.

Mi H, et al. (2011) Ontologies and standards in bioscience research: for machine or for human. Frontiers in physiology, 2, 5.

Skrzypek MS, et al. (2011) Using the Saccharomyces Genome Database (SGD) for analysis of genomic information. Current protocols in bioinformatics, Chapter 1, 1.20.1.

Park YR, et al. (2011) GOChase-II: correcting semantic inconsistencies from Gene Ontology-based annotations for gene products. BMC bioinformatics, 12 Suppl 1(Suppl 1),

S40.

Huntley RP, et al. (2009) QuickGO: a user tutorial for the web-based Gene Ontology browser. Database : the journal of biological databases and curation, 2009, bap010.

Lovering RC, et al. (2009) Improvements to cardiovascular gene ontology. Atherosclerosis, 205(1), 9.

Zhang DY, et al. (2009) Proteomics, pathway array and signaling network-based medicine in cancer. Cell division, 4, 20.

Carvalho PC, et al. (2009) GO Explorer: A gene-ontology tool to aid in the interpretation of shotgun proteomics data. Proteome science, 7, 6.

Lovering RC, et al. (2008) Access to immunology through the Gene Ontology. Immunology, 125(2), 154.

Soreq L, et al. (2008) Advanced microarray analysis highlights modified neuro-immune signaling in nucleated blood cells from Parkinson's disease patients. Journal of neuroimmunology, 201-202, 227.

Zhang C, et al. (2008) An emerging cyberinfrastructure for biodefense pathogen and pathogen-host data. Nucleic acids research, 36(Database issue), D884.

Schirra HJ, et al. (2008) Altered metabolism of growth hormone receptor mutant mice: a combined NMR metabonomics and microarray study. PloS one, 3(7), e2764.