

Resource Summary Report

Generated by [NIF](#) on Aug 23, 2026

CateGORizer

RRID:SCR_005737

Type: Tool

Proper Citation

CateGORizer (RRID:SCR_005737)

Resource Information

URL: <http://www.animalgenome.org/bioinfo/tools/catego/>

Proper Citation: CateGORizer (RRID:SCR_005737)

Description: CateGORizer takes batch input of GO term IDs in a list format or unformatted plain text file, allows users to choose one of the available classifications such as GO_slim, GOA, EGAD, MGI_GO_slim, GO-ROOT, or a self-defined classification list, find its parental branch and performs an accumulative classification count, and returns the results in a sorted table of counts, percentages, and a pie chart (if it takes longer than standard time out period, it will email the user with a URL link to the results). This tool is comprised with a set of perl CGI programs coupled with a MySQL DBMS that stores the GO terms DAG data. Platform: Online tool

Abbreviations: CateGORizer

Synonyms: GO Terms Classifications Counter

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

Keywords: gene ontology, statistical analysis, slimmer-type tool, go term classification, classification, analysis, go slim

Availability: Free for academic use

Resource Name: CateGORizer

Resource ID: SCR_005737

Alternate IDs: nlx_149197

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260821T042654+0000

Ratings and Alerts

No rating or validation information has been found for CateGORizer.

No alerts have been found for CateGORizer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 85 mentions in open access literature.

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

Lefebvre V, et al. (2026) Micropropagation of Cannabis sativa: genetic and epigenetic stability assessment over multiple generations. Journal of cannabis research, 8(1).

Hashikawa K, et al. (2026) Esr1-dependent signaling and transcriptional maturation in the medial preoptic area of the hypothalamus shape the development of mating behavior during adolescence. eLife, 14.

Hemmati R, et al. (2026) Draft genome sequence of Talaromyces trachyspermus, a biocontrol fungus isolated from broomrape. G3 (Bethesda, Md.), 16(4).

López A, et al. (2025) Evaluating restriction enzyme selection for reduced representation sequencing in conservation genomics. Molecular ecology resources, 25(5), e13865.

Xu LA, et al. (2025) Automated analysis of C. elegans behavior by LabGym: an open-source, AI-powered platform. bioRxiv : the preprint server for biology.

Dong Z, et al. (2025) Distinct Co-methylation Patterns in African and European Populations and Their Genetic Associations. Genomics, proteomics & bioinformatics, 23(5).

Otero-Albiol D, et al. (2024) Hypoxia-induced immortalization of primary cells depends on Tfcp2L1 expression. Cell death & disease, 15(2), 177.

Raymond BB, et al. (2024) Snow alga Sanguina aurantia as revealed through de novo genome assembly and annotation. G3 (Bethesda, Md.), 14(10).

Ritz M, et al. (2023) Comparative Genome-Wide Analysis of Two Caryopteris x Candonensis Cultivars: Insights on the Biosynthesis of Volatile Terpenoids. Plants (Basel, Switzerland), 12(3).

Cappe B, et al. (2023) Systematic compositional analysis of exosomal extracellular vesicles produced by cells undergoing apoptosis, necroptosis and ferroptosis. Journal of extracellular vesicles, 12(10), e12365.

Wei FJ, et al. (2021) Construction of a reference transcriptome for the analysis of male sterility in sugi (*Cryptomeria japonica* D. Don) focusing on MALE STERILITY 1 (MS1). *PloS one*, 16(2), e0247180.

Marisaldi L, et al. (2021) De novo transcriptome assembly, functional annotation and characterization of the Atlantic bluefin tuna (*Thunnus thynnus*) larval stage. *Marine genomics*, 58, 100834.

Cano I, et al. (2021) Evidence of Transcriptional Shutoff by Pathogenic Viral Haemorrhagic Septicaemia Virus in Rainbow Trout. *Viruses*, 13(6).

Hollander-Cohen L, et al. (2021) Differential Regulation of Gonadotropins as Revealed by Transcriptomes of Distinct LH and FSH Cells of Fish Pituitary. *International journal of molecular sciences*, 22(12).

McCorison CB, et al. (2020) The wheat pathogen *Zymoseptoria tritici* senses and responds to different wavelengths of light. *BMC genomics*, 21(1), 513.

Maor-Landaw K, et al. (2020) Symbiotic lifestyle triggers drastic changes in the gene expression of the algal endosymbiont *Breviolum minutum* (Symbiodiniaceae). *Ecology and evolution*, 10(1), 451.

Ham TH, et al. (2020) Increasing Coverage of Proteome Identification of the Fruiting Body of *Agaricus bisporus* by Shotgun Proteomics. *Foods (Basel, Switzerland)*, 9(5).

Seneca F, et al. (2020) Gene expression kinetics of *Exaerptasia pallida* innate immune response to *Vibrio parahaemolyticus* infection. *BMC genomics*, 21(1), 768.

Félix AS, et al. (2020) Forebrain Transcriptional Response to Transient Changes in Circulating Androgens in a Cichlid Fish. *G3 (Bethesda, Md.)*, 10(6), 1971.

Meron D, et al. (2020) The Complexity of the Holobiont in the Red Sea Coral *Euphyllia paradivisa* under Heat Stress. *Microorganisms*, 8(3).