

Resource Summary Report

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CateGORizer

RRID:SCR_005737

Type: Tool

Proper Citation

CateGORizer (RRID:SCR_005737)

Resource Information

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

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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: data analysis service, service resource, analysis service resource, production 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: 20260804T043246+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 81 mentions in open access literature.

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

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*.

Otero-Albiol D, et al. (2024) Hypoxia-induced immortalization of primary cells depends on Tfcpl2L1 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 Clandonensis* 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 *Exaerchilia pallida* innate immune response to *Vibrio parahaemolyticus* infection. *BMC genomics*, 21(1), 768.

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

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

Bracamonte SE, et al. (2019) Gene expression response to a nematode parasite in novel and native eel hosts. *Ecology and evolution*, 9(23), 13069.

Nomura A, et al. (2019) Unique primed status of microglia under the systemic autoimmune condition of lupus-prone mice. *Arthritis research & therapy*, 21(1), 303.

Dunislawska A, et al. (2019) Transcriptome modulation by in ovo delivered *Lactobacillus* synbiotics in a range of chicken tissues. *Gene*, 698, 27.

Bertke MM, et al. (2019) A deficiency in SUMOylation activity disrupts multiple pathways leading to neural tube and heart defects in *Xenopus* embryos. *BMC genomics*, 20(1), 386.