

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

Gene Ontology For Functional Analysis (GOFFA)

RRID:SCR_006484

Type: Tool

Proper Citation

Gene Ontology For Functional Analysis (GOFFA) (RRID:SCR_006484)

Resource Information

URL: <http://www.fda.gov/ScienceResearch/BioinformaticsTools/Arraytrack/default.htm>

Proper Citation: Gene Ontology For Functional Analysis (GOFFA) (RRID:SCR_006484)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 23, 2023. Software tool developed for ArrayTrack that takes a list of genes and identifies terms in Gene Ontology associated with those genes. GOFFA provides tools to view/access the following: GO term hierarchy, full listing of GO terms annotated with the genes associated with a given term, Fisher's exact test p-value providing the probability of identifying that many genes for a given term by chance alone, and relative enrichment factor (E-value) giving the enrichment of a GO term for genes in the submitted list relative to the frequency of genes assigned to that term from the full set of GOFFA annotated genes for a particular species.

Abbreviations: GOFFA

Synonyms: Gene Ontology For Functional Analysis

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

Defining Citation: [PMID:17118145](#)

Keywords: gene ontology, proteomic, visualization, fisher's exact test, browser, search engine, term enrichment, text mining, ontology browser, annotation browser, ontology visualization, annotation visualization, database, data warehouse, software, identify term

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Gene Ontology For Functional Analysis (GOFFA)

Resource ID: SCR_006484

Alternate IDs: nlx_149101

Alternate URLs: <http://edkb.fda.gov/webstart/arraytrack/>

Record Creation Time: 20220129T080236+0000

Record Last Update: 20260905T132554+0000

Ratings and Alerts

No rating or validation information has been found for Gene Ontology For Functional Analysis (GOFFA).

No alerts have been found for Gene Ontology For Functional Analysis (GOFFA).

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Pan M, et al. (2023) Identification of an Imidazopyridine-based Compound as an Oral Selective Estrogen Receptor Degradar for Breast Cancer Therapy. Cancer research communications, 3(7), 1378.

Lee J, et al. (2022) Exercise Promotes Pro-Apoptotic Ceramide Signaling in a Mouse Melanoma Model. Cancers, 14(17).

An N, et al. (2022) Interferon-inducible SAMHD1 restricts viral replication through downregulation of lipid synthesis. Frontiers in immunology, 13, 1007718.

Suo L, et al. (2018) Transcriptome profiling of human oocytes experiencing recurrent total fertilization failure. Scientific reports, 8(1), 17890.

Zhang H, et al. (2018) Targeting CDK9 Reactivates Epigenetically Silenced Genes in Cancer. Cell, 175(5), 1244.

Gates KC, et al. (2017) Effect of proline rich 15-deficiency on trophoblast viability and survival. PloS one, 12(4), e0174976.

Zhao W, et al. (2014) Cellular intrinsic mechanism affecting the outcome of AML treated with Ara-C in a syngeneic mouse model. PloS one, 9(10), e109198.

Kwekel JC, et al. (2013) Sex differences in kidney gene expression during the life cycle of F344 rats. Biology of sex differences, 4(1), 14.

Pointon AV, et al. (2010) Doxorubicin in vivo rapidly alters expression and translation of myocardial electron transport chain genes, leads to ATP loss and caspase 3 activation. PloS one, 5(9), e12733.