Resource Summary Report

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ToppGene Suite

RRID:SCR_005726
Type: Tool

Proper Citation

ToppGene Suite (RRID:SCR_005726)

Resource Information

URL: http://toppgene.cchmc.org/

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Description: ToppGene Suite is a one-stop portal for gene list enrichment analysis and candidate gene prioritization based on functional annotations and protein interactions network. ToppGene Suite is a one-stop portal for (i) gene list functional enrichment, (ii) candidate gene prioritization using either functional annotations or network analysis and (iii) identification and prioritization of novel disease candidate genes in the interactome. Functional annotation-based disease candidate gene prioritization uses a fuzzy-based similarity measure to compute the similarity between any two genes based on semantic annotations. The similarity scores from individual features are combined into an overall score using statistical meta-analysis.

Synonyms: ToppGene

Resource Type: analysis service resource, data analysis service, data or information resource, database, portal, production service resource, resource, service resource

Defining Citation: PMID:19465376

Keywords: gene portal, enrichment analysis, functional annotation, gene prioritization, protein interaction, bio.tools, FASEB list

Funding: State of Ohio Computational Medicine Center ODD TECH 04-042;
NIDDK 1U01DK70219;
NIDDK P30DK078392

Availability: Free for academic use

Resource Name: ToppGene Suite

Resource ID: SCR_005726

Alternate IDs: nlx_149183, biotools:toppgene_suite

Alternate URLs: https://bio.tools/toppgene_suite

Record Creation Time: 20220129T080232+0000

Record Last Update: 20260919T195058+0000

Ratings and Alerts

No rating or validation information has been found for ToppGene Suite .

No alerts have been found for ToppGene Suite .

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1131 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Norouzi M, et al. (2026) DNA-PKcs promotes therapy resistance and metastatic recurrence in neuroblastoma. Cancer letters, 646, 218383.

Amoruso F, et al. (2026) Nanoplastics Impair GnRH Neuron Migration and Neuroendocrine Function: Emerging Players in the Pathogenesis of Reproductive Disorders. Small (Weinheim an der Bergstrasse, Germany), 22(15), e06171.

Grotzinger AD, et al. (2026) Mapping the genetic landscape across 14 psychiatric disorders. Nature, 649(8096), 406.

Rao Z, et al. (2026) A Novel Longitudinal Proteomic Aging Index Predicts Mortality, Multimorbidity, and Frailty in Older Adults. Aging cell, 25(1), e70317.

Wu S, et al. (2026) GABRB3 Gene Polymorphisms Influences the Analgesic Response to Acupuncture Treatment in Patients With Chronic Knee Pain: A Randomized Controlled Neuroimaging Transcriptomics Study. FASEB journal : official publication of the Federation of American Societies for Experimental Biology, 40(8), e71779.

Barali? K, et al. (2026) A Network Toxicology Framework for Identification of Immune System Disruption by Per- and Polyfluoroalkyl Substance (PFAS) Mixture: In Silico Analysis. Journal of xenobiotics, 16(3).

Liu L, et al. (2026) Risperidone reduces individualized morphometric similarity deviation in schizophrenia and associates with cortical transcriptomic patterns. Schizophrenia (Heidelberg, Germany), 12(1), 19.

Zhang L, et al. (2026) Phosphorylation Protects Oncogenic RAS from LZTR1-Mediated Degradation. bioRxiv : the preprint server for biology.

Preziosa P, et al. (2026) Spatial gene expression and functional network abnormalities in multiple sclerosis: exploring biological influence on brain functional reorganization. Translational psychiatry, 16(1).

Ren P, et al. (2026) Imaging-based organ-specific aging clock predicts human diseases and mortality. NPJ digital medicine, 9(1).

Sun SH, et al. (2026) Single-Cell Transcriptomic Analysis of Macaque LGN Neurons Reveals Novel Subpopulations. Molecular neurobiology, 63(1), 449.

Mirfakhar FS, et al. (2026) A pathogenic Tau mutation drives autophagy-lysosome dysfunction that limits Tau degradation in a model of frontotemporal dementia. Nature communications, 17(1).

Wallen TE, et al. (2026) Plasma Regulates Homeostatic Pulmonary Endothelial Signaling to Mitigate Vascular Leak Following Polytrauma and Hemorrhagic Shock. Shock (Augusta, Ga.), 66(1), 218.

Tally DG, et al. (2026) Clustering Digestive Tract Tumors Using Transcriptomic and Mutation Data. Cancers, 18(9).

Fang M, et al. (2026) Multimodal integration of neuroimaging, transcriptomics and single-cell analysis reveals molecular correlates linking osteoporosis to brain abnormalities. Frontiers in immunology, 17, 1817475.

Graesser C, et al. (2026) Prolonged Inflammation Associates With Greater Infarct Size and Poor Outcome After ST-Segment Elevation Myocardial Infarction. JACC. Basic to translational science, 11(7), 101563.

Is?yel M, et al. (2026) Bioinformatics-Based Discovery of Therapeutic Targets in Cadmium-Induced Lung Adenocarcinoma: The Role of Oxyresveratrol. Biological trace element research, 204(2), 1068.

Giacomel A, et al. (2026) Transcriptome-informed brain cartography of polygenic risk and association with brain structure in major psychiatric disorders. Molecular psychiatry, 31(7), 3965.

Feng L, et al. (2026) The neural, neurotransmitter, and transcriptomic mechanisms underlying dispositional greed: exploring its link to negative psychopathology. Behavioral and brain functions : BBF, 22(1).

Qiu Y, et al. (2026) Osimertinib activates TFEB to trigger hepatocyte cytoplasmic vacuolation-associated cell death. Cell communication and signaling : CCS, 24(1).