Resource Summary Report

Generated by NIF on Apr 21, 2025

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: resource, data or information resource, portal, service resource, data analysis service, analysis service resource, database, production 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: 20250421T053515+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 930 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

McCool JL, et al. (2025) CD206+ Trem2+ macrophage accumulation in the murine knee joint after injury is associated with protection against post-traumatic osteoarthritis in MRL/MpJ mice. PloS one, 20(1), e0312587.

Afshari MK, et al. (2025) The Transcriptomic and Gene Fusion Landscape of Pleomorphic Salivary Gland Adenomas. Genes, chromosomes & cancer, 64(1), e70023.

Bell MB, et al. (2025) Brain Transcriptome Changes Associated With an Acute Increase of Protein O-GlcNAcylation and Implications for Neurodegenerative Disease. Journal of neurochemistry, 169(1), e16302.

Wang F, et al. (2025) Human epicardial organoids from pluripotent stem cells resemble fetal stage with potential cardiomyocyte- transdifferentiation. Cell & bioscience, 15(1), 4.

Rajeeve AD, et al. (2025) Elucidating the potential of EGFR mutated NSCLC and identifying its multitargeted inhibitors. Scientific reports, 15(1), 3649.

Peterson JM, et al. (2025) A window into intracellular events in myositis through subcellular

proteomics. Inflammation research : official journal of the European Histamine Research Society ... [et al.], 74(1), 31.

Yamaguchi K, et al. (2025) PLASMA: Partial LeAst Squares for Multiomics Analysis. Cancers, 17(2).

Gabriel GC, et al. (2025) Mitotic block and epigenetic repression underlie neurodevelopmental defects and neurobehavioral deficits in congenital heart disease. Nature communications, 16(1), 469.

Gleason C, et al. (2025) An integrated approach for the accurate detection of HERV-K HML-2 transcription and protein synthesis. Nucleic acids research, 53(2).

Makhani K, et al. (2025) Single-Cell Multi-Omics Profiling of Immune Cells Isolated from Atherosclerotic Plaques in Male ApoE Knockout Mice Exposed to Arsenic. Environmental health perspectives, 133(1), 17007.

Choi J, et al. (2024) Molecular targets of glucocorticoids that elucidate their therapeutic efficacy in aggressive lymphomas. Cancer cell, 42(5), 833.

Hunt EG, et al. (2024) Acetyl-CoA carboxylase obstructs CD8+ T cell lipid utilization in the tumor microenvironment. Cell metabolism.

Vogel JW, et al. (2024) Deciphering the functional specialization of whole-brain spatiomolecular gradients in the adult brain. Proceedings of the National Academy of Sciences of the United States of America, 121(25), e2219137121.

Barali? K, et al. (2024) Deciphering the molecular landscape of ionising radiation-induced eye damage with the help of genomic data mining. Arhiv za higijenu rada i toksikologiju, 75(2), 91.

Rajalingam A, et al. (2024) Identification of common genetic factors and immune-related pathways associating more than two autoimmune disorders: implications on risk, diagnosis, and treatment. Genomics & informatics, 22(1), 10.

Hughes BW, et al. (2024) NPAS4 supports cocaine-conditioned cues in rodents by controlling the cell type-specific activation balance in the nucleus accumbens. Nature communications, 15(1), 5971.

Wang Y, et al. (2024) Comparative Analysis of Human-Chimpanzee Divergence in Brain Connectivity and its Genetic Correlates. bioRxiv : the preprint server for biology.

Wang PS, et al. (2024) Long noncoding RNA ABHD11-AS1 interacts with SART3 and regulates CD44 RNA alternative splicing to promote lung carcinogenesis. Environment international, 185, 108494.

Medina-Dols A, et al. (2024) Role of PATJ in stroke prognosis by modulating endothelial to mesenchymal transition through the Hippo/Notch/PI3K axis. Cell death discovery, 10(1), 85.

Grice ASB, et al. (2024) Transient peripheral blood transcriptomic response to ketamine

treatment in children with ADNP syndrome. medRxiv : the preprint server for health sciences.