Resource Summary Report

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, production service resource, portal, data or information resource, data analysis service, database, service resource, 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: 20250422T055253+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.

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.

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).

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.

Rangel MV, et al. (2024) Single-cell and spatiotemporal transcriptomic profiling of brain immune infiltration following Venezuelan equine encephalitis virus infection. Frontiers in immunology, 15, 1497839.

Bu L, et al. (2024) Haplotype analysis incorporating ancestral origins identified novel genetic loci associated with chicken body weight using an advanced intercross line. Genetics, selection, evolution : GSE, 56(1), 78.

Sun C, et al. (2024) Lineage tracing of nuclei in skeletal myofibers uncovers distinct transcripts and interplay between myonuclear populations. Nature communications, 15(1), 9372.

Benitez MJ, et al. (2024) Transcriptomic alterations in APP/PS1 mice astrocytes lead to early postnatal axon initial segment structural changes. Cellular and molecular life sciences : CMLS, 81(1), 444.

Desai A, et al. (2024) cAMP driven UCP1 induction in human adipocytes requires ATGL-catalyzed lipolysis. Molecular metabolism, 90, 102051.

Dailamy A, et al. (2024) Charting and probing the activity of ADARs in human development and cell-fate specification. Nature communications, 15(1), 9818.

Butto T, et al. (2024) Characterization of transcriptional profiles associated with stress-induced neuronal activation in Arc-GFP mice. Molecular psychiatry, 29(10), 3010.

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.