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: data analysis service, data or information resource, portal, database, service resource, resource, production service resource, analysis 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: 20260801T190301+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 1030 mentions in open access literature.

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

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

Nomura J, et al. (2025) ESC models of autism with copy-number variations reveal cell-type-specific translational vulnerability. Cell genomics, 5(6), 100877.

Ayabe H, et al. (2025) Cellular crosstalk mediated by TGF-? drives epithelial-mesenchymal transition in patient-derived multi-compartment biliary organoids. Nature communications, 16(1), 6575.

Rodriques A, et al. (2025) Probing the CaV1.2 interactome in heart failure identifies a positive modulator of inotropy and lusitropy. bioRxiv : the preprint server for biology.

Zang W, et al. (2025) Kinesin-related genes stratified the prognosis and immune responses of clear cell renal cell carcinoma. European journal of medical research, 30(1), 621.

Yu K, et al. (2025) Inhibition of AhR improves cortical bone and skeletal muscle function via preservation of neuromuscular junctions. JCI insight, 10(16).

Namestnikov M, et al. (2025) Human fetal kidney organoids model early human nephrogenesis and Notch-driven cell fate. The EMBO journal, 44(17), 4681.

Ding H, et al. (2025) Polyamine Metabolism Promotes the Progression of Thyroid Carcinoma by Regulating the Immune Phenotype of Tumor Associated Macrophages. Smart medicine, 4(2), e70009.

Pei X, et al. (2025) Transcriptomic analysis of the anti-tumor effects of leflunomide in prolactinoma. Scientific reports, 15(1), 11703.

Liu Y, et al. (2025) Mechanism of the Traditional Chinese Medicine Simiao Biejia Decoction Improves the Diabetes Mellitus-Induced Erectile Dysfunction in Rats. Drug design, development and therapy, 19, 2609.

Qiao J, et al. (2025) Contribution of leukocyte telomere length to cardiovascular disease onset from genome-wide cross-trait analysis. Nature communications, 16(1), 8677.

Reid LV, et al. (2025) Influenza-induced microRNA-155 expression is altered in extracellular vesicles derived from the COPD epithelium. Frontiers in cellular and infection microbiology, 15, 1560700.

Teerikorpi N, et al. (2025) Ciliary biology intersects autism and congenital heart disease. Development (Cambridge, England), 152(12).

Mori Y, et al. (2025) Genome-wide association and multi-omics analyses provide insights into the disease mechanisms of central serous chorioretinopathy. Scientific reports, 15(1), 9158.

Revilla SA, et al. (2025) Tumor-derived colorectal cancer organoids induce a unique Treg cell population by directing CD4+ T cell differentiation. iScience, 28(2), 111827.

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.

Yin Q, et al. (2025) Proteomic analysis of human follicular fluid based on the 4D label free method to identify proteins that may affect oocyte quality in hyperandrogenic PCOS patients. Frontiers in endocrinology, 16, 1579469.

Li D, et al. (2025) Imputation disparities driven by recent selection and their impact on disease risk estimation in East and Southeast Asian populations. Communications biology, 8(1), 1822.

Ma W, et al. (2025) 3D4 cells exhibit transcriptional features inconsistent with alveolar macrophage identity. Veterinary research, 56(1), 201.