Resource Summary Report

Generated by NIF on May 21, 2025

GeneMANIA

RRID:SCR_005709
Type: Tool

Proper Citation

GeneMANIA (RRID:SCR_005709)

Resource Information

URL: http://genemania.org/

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Description: Data analysis service to predict the function of your favorite genes and gene sets. Indexing 1,421 association networks containing 266,984,699 interactions mapped to 155,238 genes from 7 organisms. GeneMANIA interaction networks are available for download in plain text format. GeneMANIA finds other genes that are related to a set of input genes, using a very large set of functional association data. Association data include protein and genetic interactions, pathways, co-expression, co-localization and protein domain similarity. You can use GeneMANIA to find new members of a pathway or complex, find additional genes you may have missed in your screen or find new genes with a specific function, such as protein kinases. Your question is defined by the set of genes you input. If members of your gene list make up a protein complex, GeneMANIA will return more potential members of the protein complex. If you enter a gene list, GeneMANIA will return connections between your genes, within the selected datasets. GeneMANIA suggests annotations for genes based on Gene Ontology term enrichment of highly interacting genes with the gene of interest. GeneMANIA is also a gene recommendation system. GeneMANIA is also accessible via a Cytoscape plugin, designed for power users. Platform: Online tool, Windows compatible, Mac OS X compatible, Linux compatible, Unix compatible

Abbreviations: GeneMANIA

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

Defining Citation: PMID:20576703, PMID:18613948, PMID:20926419

Keywords: gene, association data, protein interaction, genetic interaction, pathway, co-expression, co-localization, protein, software library, statistical analysis, term enrichment, analysis, browser, gene ontology, gene predicting, gene prioritization, database or data warehouse, other analysis, interaction browser, protein-protein interaction, interaction, FASEB list

Funding: Genome Canada ;
Ontario Ministry of Research and Innovation 2007-OGI-TD-05

Availability: Open unspecified license, Free for academic use

Resource Name: GeneMANIA

Resource ID: SCR_005709

Alternate IDs: nlx_149159

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250521T061039+0000

Ratings and Alerts

No rating or validation information has been found for GeneMANIA.

No alerts have been found for GeneMANIA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2739 mentions in open access literature.

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

Bouzid A, et al. (2025) Whole exome sequencing identifies ABHD14A and MRNIP as novel candidate genes for developmental language disorder. Scientific reports, 15(1), 367.

Shuang L, et al. (2025) Downregulation of Gldc attenuates myocardial ischemia reperfusion injury in vitro by modulating Akt and NF-?B signalings. Scientific reports, 15(1), 268.

Husami SF, et al. (2025) Corporate genome screening India (CoGsI) identified genetic variants association with T2D in young Indian professionals. Scientific reports, 15(1), 506.

Mayyas A, et al. (2025) Deciphering the Anti-Diabetic Potential of Gymnema Sylvestre Using Integrated Computer-Aided Drug Design and Network Pharmacology. Journal of cellular and

molecular medicine, 29(1), e70349.

Wei M, et al. (2025) Identification of a novel disulfidptosis-related gene signature in osteoarthritis using bioinformatics analysis and experimental validation. Scientific reports, 15(1), 1339.

Yang X, et al. (2025) Prolyl 4-hydroxylase ?-subunit family regulation of type I collagen deposition and IL17RB/c-Jun activation synergistically mediate choline dehydrogenase promotion of colorectal cancer metastasis. MedComm, 6(1), e70007.

Huang F, et al. (2025) Comprehensive bioinformatics analysis of metabolism?related microRNAs in high myopia in young and old adults with age?related cataracts. Molecular medicine reports, 31(2).

Wan J, et al. (2025) Exploration of the shared gene signatures and comorbidity mechanisms of primary aldosteronism and atrial fibrillation. Endocrine connections, 14(1).

Xiao H, et al. (2025) Assessing the causal effect of inflammation-related genes on myocarditis: A Mendelian randomization study. ESC heart failure, 12(1), 271.

Hashemi Karoii D, et al. (2025) Identification of novel cytoskeleton protein involved in spermatogenic cells and sertoli cells of non-obstructive azoospermia based on microarray and bioinformatics analysis. BMC medical genomics, 18(1), 19.

Qi S, et al. (2025) Ethyl Acetate Extract of Cichorium glandulosum Activates the P21/Nrf2/HO-1 Pathway to Alleviate Oxidative Stress in a Mouse Model of Alcoholic Liver Disease. Metabolites, 15(1).

Wang C, et al. (2025) Unveiling novel biomarkers for platinum chemoresistance in ovarian cancer. Open medicine (Warsaw, Poland), 20(1), 20241084.

Rafiepoor H, et al. (2025) Diagnostic Power of MicroRNAs in Melanoma: Integrating Machine Learning for Enhanced Accuracy and Pathway Analysis. Journal of cellular and molecular medicine, 29(2), e70367.

Deng Z, et al. (2025) Pan-cancer analysis shows that TNFSF4 is a potential prognostic and immunotherapeutic biomarker for multiple cancer types including liver cancer. BMC cancer, 25(1), 100.

Lee H, et al. (2025) Adaptation responses to salt stress in the gut of Poecilia reticulata. Animal cells and systems, 29(1), 84.

Wu S, et al. (2025) Comprehensive bioinformatics analysis identifies hub genes associated with immune cell infiltration in early-onset schizophrenia. BMC psychiatry, 25(1), 55.

Yoon JH, et al. (2025) NKX6.3 modulation of mitotic dynamics and genomic stability in gastric carcinogenesis. Cell communication and signaling : CCS, 23(1), 35.

Chen Z, et al. (2025) Genetic variation reveals the therapeutic potential of BRSK2 in idiopathic pulmonary fibrosis. BMC medicine, 23(1), 22.

Fan W, et al. (2025) Mendelian randomization analysis of plasma proteins reveals potential novel tumor markers for gastric cancer. Scientific reports, 15(1), 3537.

Lu R, et al. (2025) A novel regulatory axis of MSI2-AGO2/miR-30a-3p-CGRRF1 drives cancer chemoresistance by upregulating the KRAS/ERK pathway. Neoplasia (New York, N.Y.), 59, 101082.