Resource Summary Report

Generated by NIF on Apr 17, 2025

MedGene

RRID:SCR_008122
Type: Tool

Proper Citation

MedGene (RRID:SCR_008122)

Resource Information

URL: http://medgene.med.harvard.edu/MEDGENE/

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Description: An algorithm that generates lists of genes associated with a gene or one or more disorders. The algorithm can be used in high-throughput screening experiments, can create disease-specific micro-arrays, and can sort the results of gene profiling data. Based on the co-citations of all Medline records, MedGene can retrieve the following relationships: 1. A list of human genes associated with a particular human disease in ranking order 2. A list of human genes associated with multiple human diseases in ranking order 3. A list of human diseases associated with a particular human gene in ranking order 4. A list of human genes associated with a particular human gene in ranking order 5. The sorted gene list from other disease related high-throughput experiments, such as micro-array 6. The sorted gene list from other gene related high-throughput experiments, such as micro-array

Synonyms: MedGene

Resource Type: software resource

Keywords: gene, disease, human order, microarray

Funding:

Resource Name: MedGene

Resource ID: SCR_008122

Alternate IDs: nif-0000-20869

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250410T065709+0000

Ratings and Alerts

No rating or validation information has been found for MedGene.

No alerts have been found for MedGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

González-González M, et al. (2021) Tracking the Antibody Immunome in Sporadic Colorectal Cancer by Using Antigen Self-Assembled Protein Arrays. Cancers, 13(11).

Yuan C, et al. (2021) PEDV infection in neonatal piglets through the nasal cavity is mediated by subepithelial CD3+ T cells. Veterinary research, 52(1), 26.

Marín M, et al. (2019) An integrative methodology based on protein-protein interaction networks for identification and functional annotation of disease-relevant genes applied to channelopathies. BMC bioinformatics, 20(1), 565.

Li Y, et al. (2018) An alternative pathway of enteric PEDV dissemination from nasal cavity to intestinal mucosa in swine. Nature communications, 9(1), 3811.