

Resource Summary Report

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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

Resource Name: MedGene

Resource ID: SCR_008122

Alternate IDs: nif-0000-20869

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260905T132618+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 [Kravitz](#) .

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.