

Resource Summary Report

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Human Gene Connectome Server

RRID:SCR_002627

Type: Tool

Proper Citation

Human Gene Connectome Server (RRID:SCR_002627)

Resource Information

URL: <http://hgc.rockefeller.edu/>

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Description: An interactive web server that enables researchers to prioritize any list of genes by their biological proximity to defined core genes (i.e. genes that are known to be associated with the phenotype), and to predict novel gene pathways.

Abbreviations: HGCS

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:23509278](#)

Keywords: gene, disease, phenotype, genome, connectome, bio.tools

Availability: Free

Resource Name: Human Gene Connectome Server

Resource ID: SCR_002627

Alternate IDs: nlx_156049, biotools:hgcs

Alternate URLs: <https://bio.tools/hgcs>

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260905T133118+0000

Ratings and Alerts

No rating or validation information has been found for Human Gene Connectome Server.

No alerts have been found for Human Gene Connectome Server.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Mosquera-Heredia MI, et al. (2024) Long Non-Coding RNAs and Alzheimer's Disease: Towards Personalized Diagnosis. International journal of molecular sciences, 25(14).

Fallerini C, et al. (2022) Common, low-frequency, rare, and ultra-rare coding variants contribute to COVID-19 severity. Human genetics, 141(1), 147.

Salazar-Tortosa DF, et al. (2022) Novel brown adipose tissue candidate genes predicted by the human gene connectome. Scientific reports, 12(1), 7614.

Varzari A, et al. (2022) Candidate genes and sequence variants for susceptibility to mycobacterial infection identified by whole-exome sequencing. Frontiers in genetics, 13, 969895.

Kong XF, et al. (2018) Disruption of an antimycobacterial circuit between dendritic and helper T cells in human SPPL2a deficiency. Nature immunology, 19(9), 973.

Leiva-Torres GA, et al. (2017) Discovery of Variants Underlying Host Susceptibility to Virus Infection Using Whole-Exome Sequencing. Methods in molecular biology (Clifton, N.J.), 1656, 209.

Itan Y, et al. (2015) Novel primary immunodeficiency candidate genes predicted by the human gene connectome. Frontiers in immunology, 6, 142.

Itan Y, et al. (2014) HGCS: an online tool for prioritizing disease-causing gene variants by biological distance. BMC genomics, 15, 256.