Resource Summary Report

Generated by dkNET on Jul 30, 2026

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, service resource, data analysis service, production 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: 20260728T043136+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 5 mentions in open access literature.

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

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

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.