

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

Human Gene Connectome

RRID:SCR_002628

Type: Tool

Proper Citation

Human Gene Connectome (RRID:SCR_002628)

Resource Information

URL: <http://lab.rockefeller.edu/casanova/HGC>

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Description: Data set containing a gene-specific connectome file for each human gene and computer programs for ranking lists of genes within a gene-specific connectome, clustering and plotting the genes by the functional genomic alignment (FGA) approach, and generating gene-specific connectomes. The programs were developed and tested on Mac and Linux systems. The external software required for running these programs is open-source and free of charge. The HGC is the set of all biologically plausible routes, distances, and degrees of separation between all pairs of human genes. A gene-specific connectome contains the set of all available human genes sorted on the basis of their predicted biological proximity to the specific gene of interest. The HGC is a powerful approach for human genotype-phenotype high-throughput studies, for which it can be used to rank any list of genes within a gene-specific connectome for an experimentally validated core gene. Functional genomic alignment (FGA) is equivalent to traditional multiple sequence alignment (MSA), except that it clusters genes in trees on the basis of the functional biological distance between them predicted by HGC, rather than on the basis of molecular evolutionary genetic distance. This method is therefore more suitable for disease and phenotypic studies.

Abbreviations: HGC

Resource Type: data or information resource, data set, software resource

Defining Citation: [PMID:23509278](#)

Keywords: gene, disease, phenotype, genome, connectome, functional genomic alignment

Funding: NCATS 8 UL1 TR000043

Availability: Free

Resource Name: Human Gene Connectome

Resource ID: SCR_002628

Alternate IDs: nlx_156050

Record Creation Time: 20220129T080214+0000

Record Last Update: 20260905T133038+0000

Ratings and Alerts

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

No alerts have been found for Human Gene Connectome.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Tran GB, et al. (2023) Caffeine supplementation and FOXM1 inhibition enhance the antitumor effect of statins in neuroblastoma. Cancer research.

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

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. (2015) Evolutionary Genomics. Evolutionary bioinformatics online, 11(Suppl 2), 53.

, et al. (2014) Esid 2014 oral presentations. Journal of clinical immunology, 34 Suppl 2(Suppl 2), 139.

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