

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

GeneNetwork

RRID:SCR_002388

Type: Tool

Proper Citation

GeneNetwork (RRID:SCR_002388)

Resource Information

URL: <http://www.genenetwork.org/>

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Description: Web platform that provides access to data and tools to study complex networks of genes, molecules, and higher order gene function and phenotypes. Sequence data (SNPs) and transcriptome data sets (expression genetic or eQTL data sets). Quantitative trait locus (QTL) mapping module that is built into GN is optimized for fast on-line analysis of traits that are controlled by combinations of gene variants and environmental factors. Used to study humans, mice (BXD, AXB, LXS, etc.), rats (HXB), Drosophila, and plant species (barley and Arabidopsis). Users are welcome to enter their own private data.

Abbreviations: GeneNetwork, WebQTL

Synonyms: GeneNetwork and WebQTL, GeneNetwork / WebQTL, www.genenetwork.org, GeneNetwork WebQTL, The GeneNetwork / WebQTL

Resource Type: data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:8043953](#), [PMID:11737945](#), [PMID:15043217](#), [PMID:15114364](#), [PMID:15043220](#), [PMID:15043219](#), [PMID:15711545](#), [PMID:18368372](#), [PMID:27933521](#)

Keywords: Variation, trait, vertebrate trait ontology, phenotype, systems genetics, quantitative trait, gene mapping, experimental precision medicine network analysis, causal modeling, genomic location, genotype, inbred strain, sex, heterogeneous stock, phenome, phenotype, QTL, expression QTL, genetic reference population, single nucleotide polymorphism, RNA expression, protein expression, metabolite expression, metagenomics, epigenomics, gene-by-environmental interaction, epistasis, FAIR data standards, open source software, FASEB list

Funding: NCI U01 CA105417;
NCRR U24 RR021760;
NIAAA U01 AA014425;
NIAAA U01 AA016662;
NIAAA U01 AA13499;
NIAAA U24 AA13513;
NIA R01 AG043930;
NIDA P20 DA21131;
NIGMS R01 GM123489

Availability: Restricted

Resource Name: GeneNetwork

Resource ID: SCR_002388

Alternate IDs: nif-0000-00380

License: GNU Affero General Public License, v3, GNU General Public License

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260903T234528+0000

Ratings and Alerts

No rating or validation information has been found for GeneNetwork.

No alerts have been found for GeneNetwork.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 499 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kim M, et al. (2026) Identification of susceptibility loci using a novel murine model for triple-negative breast cancer. G3 (Bethesda, Md.), 16(2).

Yin Q, et al. (2026) Genetic landscape of morphine response in BXD recombinant inbred mice. HGG advances, 7(1), 100535.

Saxena S, et al. (2026) Cannabidiol dose modulates behavioral response to acute and repeated administration of ??9-Tetrahydrocannabinol by strain and sex. bioRxiv : the preprint server for biology.

Ninoyu Y, et al. (2026) Novel candidate genes for vestibular function identified through GWAS in the hybrid mouse diversity panel. *BMC genomics*, 27(1).

Durante GL, et al. (2026) Meta-analysis of genetic mapping studies in mice reveals candidate epilepsy modifier genes that are outside the current drug development landscape. *Epilepsia*, 67(3), 1421.

Arcego DM, et al. (2026) Sex-specific interaction effects of Syntaxin 1A coexpression network and childhood trauma on adult depressive symptoms. *EBioMedicine*, 123, 106062.

Maassen WTK, et al. (2026) A multidisciplinary RNA-guided approach to complement genomic analysis of unsolved patients with an inborn error of immunity. *Frontiers in immunology*, 17, 1829883.

Laezza F, et al. (2026) Identifying new targets in the fight against opioids. *eLife*, 15.

Yang Z, et al. (2025) Morc4 is a novel functional gene associated with lipid metabolism in BXD recombinant inbred population. *Frontiers in cardiovascular medicine*, 12, 1570729.

Jones BC, et al. (2025) Epigenetic study of the long-term effects of gulf War illness. *Frontiers in genetics*, 16, 1553410.

Rogers WD, et al. (2025) Identification of ethanol analgesia quantitative trait loci and candidate genes in BXD recombinant inbred mouse lines. *Addiction biology*, 30(2), e70013.

Li L, et al. (2025) Genetic modulation of protein expression in rat brain. *iScience*, 28(3), 112079.

King CP, et al. (2025) Genetic Loci Influencing Cue-Reactivity in Heterogeneous Stock Rats. *Genes, brain, and behavior*, 24(2), e70018.

Haydar S, et al. (2025) A Genome-Wide Association Study of Taste Liking in the Danish Population. *The Journal of nutrition*, 155(8), 2591.

Chowdhury T, et al. (2025) Evaluation of Choline Metabolic Genes in the Liver of the Dam as Candidates for Mediating Choline's Efficacy in Mitigating Ethanol-Induced Cell Death in the Neural Tube: A Preliminary Analysis. *Genes*, 17(1).

Lian Y, et al. (2025) System biology analysis reveals that Grm6 is associated with glutamate accumulation-induced scotopic vision impairment in diabetic mice. *Molecular vision*, 31, 440.

Arends D, et al. (2025) Genetic Modulation of Lifespan: Dynamic Effects, Sex Differences, and Body Weight Trade-offs. *bioRxiv : the preprint server for biology*.

Villani F, et al. (2025) Pangenome reconstruction in rats enhances genotype-phenotype mapping and variant discovery. *iScience*, 28(2), 111835.

Sharp BM, et al. (2025) Inbred rat heredity and sex affect oral oxycodone self-administration and augmented intake in long sessions: correlations with anxiety and novelty-seeking. *PloS one*, 20(3), e0314777.

Bajpai AK, et al. (2025) Atad1 Is a Potential Candidate Gene for Prepulse Inhibition. *Genes*, 16(10).