Resource Summary Report

Generated by RRID on Aug 4, 2026

GENEWEAVER

RRID:SCR_009202
Type: Tool

Proper Citation

GENEWEAVER (RRID:SCR_009202)

Resource Information

URL: http://www.geneweaveronline.com/

Proper Citation: GENEWEAVER (RRID:SCR_009202)

Description: Software application for charting family medical/health history (entry from Genetic Analysis Software), THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GENEWEAVER

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, ms-windows, (95/98/2000/nt/xp)

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GENEWEAVER

Resource ID: SCR_009202

Alternate IDs: nlx_154343

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260801T191055+0000

Ratings and Alerts

No rating or validation information has been found for GENEWEAVER.

No alerts have been found for GENEWEAVER.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

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.

Castaneda EU, et al. (2025) Influence of multi-species data on gene-disease associations in substance use disorder using random walk with restart models. PloS one, 20(6), e0325201.

Roy TA, et al. (2024) Discovery and validation of genes driving drug-intake and related behavioral traits in mice. Genes, brain, and behavior, 23(1), e12875.

Hagenauer MH, et al. (2024) Resource: A curated database of brain-related functional gene sets (Brain.GMT). MethodsX, 13, 102788.

Hagenauer MH, et al. (2024) Resource: A Curated Database of Brain-Related Functional Gene Sets (Brain.GMT). bioRxiv : the preprint server for biology.

Grady SK, et al. (2024) A graph theoretical approach to experimental prioritization in genome-scale investigations. Mammalian genome : official journal of the International Mammalian Genome Society, 35(4), 724.

Philip VM, et al. (2023) Gene expression genetics of the striatum of Diversity Outbred mice. bioRxiv : the preprint server for biology.

Booher WC, et al. (2023) Hippocampal RNA sequencing in mice selectively bred for high and low activity. Genes, brain, and behavior, 22(2), e12832.

Smith ML, et al. (2023) Identification of candidate genes for nicotine withdrawal in C57BL/6J × DBA/2J recombinant inbred mice. Genes, brain, and behavior, 22(2), e12844.

Philip VM, et al. (2023) Gene expression genetics of the striatum of Diversity Outbred mice. Scientific data, 10(1), 522.

Yan L, et al. (2023) CSF1R regulates schizophrenia-related stress response and vascular association of microglia/macrophages. BMC medicine, 21(1), 286.

Ghanbarzehi A, et al. (2023) Disclosing common biological signatures and predicting new therapeutic targets in schizophrenia and obsessive-compulsive disorder by integrated bioinformatics analysis. BMC psychiatry, 23(1), 40.

Brasher MS, et al. (2023) Testing associations between human anxiety and genes previously implicated by mouse anxiety models. Genes, brain, and behavior, 22(6), e12851.

Roy TA, et al. (2023) DISCOVERY AND VALIDATION OF GENES DRIVING DRUG-INTAKE AND RELATED BEHAVIORAL TRAITS IN MICE. bioRxiv : the preprint server for biology.

Baranger DAA, et al. (2023) Multi-omics cannot replace sample size in genome-wide association studies. Genes, brain, and behavior, 22(6), e12846.

Wotton JM, et al. (2022) Identifying genetic determinants of inflammatory pain in mice using a large-scale gene-targeted screen. Pain, 163(6), 1139.

Sepehrinezhad A, et al. (2021) A Computational-Based Drug Repurposing Method Targeting SARS-CoV-2 and its Neurological Manifestations Genes and Signaling Pathways. Bioinformatics and biology insights, 15, 11779322211026728.

Palmer RHC, et al. (2021) Multi-omic and multi-species meta-analyses of nicotine consumption. Translational psychiatry, 11(1), 98.

Zhang Y, et al. (2021) Differential expression analysis in ovarian cancer: A functional genomics and systems biology approach. Saudi journal of biological sciences, 28(7), 4069.

Weston RM, et al. (2021) Transcriptome analysis of chloride intracellular channel knockdown in Drosophila identifies oxidation-reduction function as possible mechanism of altered sensitivity to ethanol sedation. PloS one, 16(7), e0246224.