

Resource Summary Report

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Gene Weaver

RRID:SCR_003009

Type: Tool

Proper Citation

Gene Weaver (RRID:SCR_003009)

Resource Information

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

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Description: Freely accessible phenotype-centered database with integrated analysis and visualization tools. It combines diverse data sets from multiple species and experiment types, and allows data sharing across collaborative groups or to public users. It was conceived of as a tool for the integration of biological functions based on the molecular processes that subserved them. From these data, an empirically derived ontology may one day be inferred. Users have found the system valuable for a wide range of applications in the arena of functional genomic data integration.

Synonyms: GeneWeaver, GeneWeaver - A system for the integration of functional genomics experiments, Ontological Discovery Environment, GeneWeaver.org

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

Defining Citation: [PMID:22080549](#), [PMID:19733230](#)

Keywords: phenotype, microarray, gene, genome, functional genomics, process, pathway, function, gene set, genomic data integration, analysis, visualization

Funding: Integrative Neuroscience Initiative on Alcoholism ;
NIAAA R01 AA18776;
NIAAA U01 AA13499;
NIAAA U24 AA13513

Availability: Free, Freely available

Resource Name: Gene Weaver

Resource ID: SCR_003009

Alternate IDs: r3d100012464, OMICS_02232, nif-0000-00517

Alternate URLs: <http://ontologicaldiscovery.org/>, <https://doi.org/10.17616/R3248T>

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Record Creation Time: 20220129T080216+0000

Record Last Update: 20260912T200009+0000

Ratings and Alerts

No rating or validation information has been found for Gene Weaver.

No alerts have been found for Gene Weaver.

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 [SPARC SAWG](#) .

Tatom Z, et al. (2026) Fifteen years of the Diversity Outbred mouse model: a review. Mammalian genome : official journal of the International Mammalian Genome Society, 37(1), 28.

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.

Schoenrock SA, et al. (2025) Genetic mapping in collaborative cross mouse strains identifies loci that affect initial sensitivity to cocaine. Psychopharmacology.

Wolstenholme JT, et al. (2025) Variation of Myelin-associated Gene Expression and Ndr1 within the Prefrontal Cortex as Determinants for Initial Level of Response to Alcohol. bioRxiv : the preprint server for biology.

Shan H, et al. (2024) Combination of transcriptome and Mendelian inheritance reveals novel prognostic biomarker of CTLA-4-related lncRNAs and protective role of nitrogen metabolism pathway in lung adenocarcinoma development. BMC cancer, 24(1), 1009.

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). *bioRxiv : the preprint server for biology*.

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

Oviya IR, et al. (2024) Comorbidity-Guided Text Mining and Omics Pipeline to Identify Candidate Genes and Drugs for Alzheimer's Disease. *Genes*, 15(5).

Ghanbarzahi 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.

Kearney SK, et al. (2023) Aon: a service to augment Alliance Genome Resource data with additional species. *BMC research notes*, 16(1), 297.

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*.

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.

Dolan ME, et al. (2020) Investigation of COVID-19 comorbidities reveals genes and pathways coincident with the SARS-CoV-2 viral disease. *bioRxiv : the preprint server for biology*.

Dolan ME, et al. (2020) Investigation of COVID-19 comorbidities reveals genes and pathways coincident with the SARS-CoV-2 viral disease. *Scientific reports*, 10(1), 20848.

Sharma A, et al. (2020) Common genetic signatures of Alzheimer's disease in Down Syndrome. *F1000Research*, 9, 1299.

Chunduri A, et al. (2020) Narcolepsy in Parkinson's disease with insulin resistance. *F1000Research*, 9, 1361.

Bubier JA, et al. (2020) Discovery of a Role for Rab3b in Habituation and Cocaine Induced Locomotor Activation in Mice Using Heterogeneous Functional Genomic Analysis. *Frontiers in neuroscience*, 14, 721.