

Resource Summary Report

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PhenoGen Informatics

RRID:SCR_001613

Type: Tool

Proper Citation

PhenoGen Informatics (RRID:SCR_001613)

Resource Information

URL: <https://phenogen.org>

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Description: Website for analyzing microarray data. Software toolbox for storing, analyzing and integrating microarray data and related genotype and phenotype data. The site is particularly suited for combining QTL and microarray data to search for candidate genes contributing to complex traits. In addition, the site allows, if desired by the investigators, sharing of the data. Investigators can conduct in-silico microarray experiments using their own and/or shared data. There are five major sections of the site: Genome/Transcriptome Data Browser, Microarray Analysis Tools, Gene List Analysis Tools, QTL Tools, and Downloads. The genome/transcriptome data browser combines a genome browser with all the microarray, RNA-Seq, and Genomic Sequencing data. This provides an effective platform to view all of this data side by side. Source code is available on GitHub.

Abbreviations: PhenoGen

Synonyms: PhenoGen Informatics - The site for quantitative genetics of the transcriptome.

Resource Type: data analysis service, data or information resource, data repository, storage service resource, data access protocol, service resource, source code, data set, production service resource, software resource, analysis service resource, application programming interface

Defining Citation: [PMID:17760997](#)

Keywords: genome, transcription, microarray, gene, quantitative trait loci, analysis, complex trait, genotype, phenotype, high-throughput, rna-seq, snp, genomic marker, region, data sharing, normalize, statistics, gene list, pathway, expression value, expression, correlation, exon, annotation, promoter, homolog, brain, heart, liver, adipose, candidate gene, genetics, transcriptome, eqtl, genome browser, inbred panel

Funding: NIAAA R24 AA013162;
NIAAA R01 AA13162;
NIAAA U01 AA013524

Availability: Free, Freely available

Resource Name: PhenoGen Informatics

Resource ID: SCR_001613

Alternate IDs: rid_000093, nlx_153879, r3d100011596

Alternate URLs: <https://github.com/TabakoffLab/PhenogenCloud>,
<https://doi.org/10.17616/R3WS7F>

Old URLs: <http://phenogen.ucdenver.edu>, <http://phenogen.uchsc.edu>

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260801T042507+0000

Ratings and Alerts

No rating or validation information has been found for PhenoGen Informatics.

No alerts have been found for PhenoGen Informatics.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Allayee H, et al. (2023) Systems genetics approaches for understanding complex traits with relevance for human disease. eLife, 12.

Gao J, et al. (2023) Transcriptome analysis reveals the neuroprotective effect of Dlg4 against fastigial nucleus stimulation-induced ischemia/reperfusion injury in rats. BMC neuroscience, 24(1), 40.

Saba LM, et al. (2021) A long non-coding RNA (Lrap) modulates brain gene expression and levels of alcohol consumption in rats. Genes, brain, and behavior, 20(2), e12698.

Lusk R, et al. (2021) Aptardi predicts polyadenylation sites in sample-specific transcriptomes using high-throughput RNA sequencing and DNA sequence. Nature communications, 12(1), 1652.

- Neuman MG, et al. (2020) Alcoholic-Hepatitis, Links to Brain and Microbiome: Mechanisms, Clinical and Experimental Research. *Biomedicines*, 8(3).
- Kordas G, et al. (2019) Insight into genetic regulation of miRNA in mouse brain. *BMC genomics*, 20(1), 849.
- Vestal B, et al. (2018) miRNA-regulated transcription associated with mouse strains predisposed to hypnotic effects of ethanol. *Brain and behavior*, 8(6), e00989.
- Rudra P, et al. (2018) Predictive modeling of miRNA-mediated predisposition to alcohol-related phenotypes in mouse. *BMC genomics*, 19(1), 639.
- Lyu Y, et al. (2018) Condition-adaptive fused graphical lasso (CFGL): An adaptive procedure for inferring condition-specific gene co-expression network. *PLoS computational biology*, 14(9), e1006436.
- Shimoyama M, et al. (2017) Rat Genome and Model Resources. *ILAR journal*, 58(1), 42.
- Abdelmagid N, et al. (2016) Von Willebrand Factor Gene Variants Associate with Herpes simplex Encephalitis. *PloS one*, 11(5), e0155832.
- Harrall KK, et al. (2016) Uncovering the liver's role in immunity through RNA co-expression networks. *Mammalian genome : official journal of the International Mammalian Genome Society*, 27(9-10), 469.
- Ma L, et al. (2015) Association of brain immune genes with social behavior of inbred mouse strains. *Journal of neuroinflammation*, 12, 75.
- Hermesen R, et al. (2015) Genomic landscape of rat strain and substrain variation. *BMC genomics*, 16(1), 357.
- Ru Y, et al. (2014) The multiMiR R package and database: integration of microRNA-target interactions along with their disease and drug associations. *Nucleic acids research*, 42(17), e133.
- Hoffman PL, et al. (2014) Genetics of gene expression characterizes response to selective breeding for alcohol preference. *Genes, brain, and behavior*, 13(8), 743.
- Klein JD, et al. (2014) A snapshot of the hepatic transcriptome: ad libitum alcohol intake suppresses expression of cholesterol synthesis genes in alcohol-preferring (P) rats. *PloS one*, 9(12), e110501.
- Vanderlinden LA, et al. (2013) Whole brain and brain regional coexpression network interactions associated with predisposition to alcohol consumption. *PloS one*, 8(7), e68878.
- Saba LM, et al. (2011) A systems genetic analysis of alcohol drinking by mice, rats and men: influence of brain GABAergic transmission. *Neuropharmacology*, 60(7-8), 1269.
- Hoffman PL, et al. (2011) Using the Phenogen website for 'in silico' analysis of morphine-induced analgesia: identifying candidate genes. *Addiction biology*, 16(3), 393.