

Resource Summary Report

Generated by T1D on Sep 5, 2026

PhenStat

RRID:SCR_021317

Type: Tool

Proper Citation

PhenStat (RRID:SCR_021317)

Resource Information

URL: <https://bioconductor.org/packages/release/bioc/html/PhenStat.html>

Proper Citation: PhenStat (RRID:SCR_021317)

Description: Software R package for statistical analysis of phenotypic data. Tool kit for standardized analysis of high throughput phenotypic data.

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:26147094](https://pubmed.ncbi.nlm.nih.gov/26147094/)

Keywords: Statistical analysis, phenotypic data, standardized analysis, bio.tools, Bioconductor

Funding: NHGRI U54 HG006370;
Wellcome Trust

Availability: Free, Available for download, Freely available

Resource Name: PhenStat

Resource ID: SCR_021317

Alternate IDs: biotools:phenstat

Alternate URLs: <https://bio.tools/phenstat>

License: Apache License

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260903T235714+0000

Ratings and Alerts

No rating or validation information has been found for PhenStat.

No alerts have been found for PhenStat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Cox RM, et al. (2026) A protein interactome for the last eukaryotic common ancestor illuminates the biochemical basis of modern genetic diseases. *Cell genomics*, 6(6), 101254.

Sun JL, et al. (2026) Ferroptotic tumor cells reprogram tumor-associated macrophage antigen presentation to enhance the efficacy of immune checkpoint blockade. *Cell reports. Medicine*, 7(5), 102774.

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.

Manrique-Rinc??n AJ, et al. (2025) Simulating CD8 T cell exhaustion: A comprehensive approach. *iScience*, 28(7), 112897.

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.

Garrett L, et al. (2024) Co-expression of prepulse inhibition and Schizophrenia genes in the mouse and human brain. *Neuroscience applied*, 3, 104075.

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*.

Sabik OL, et al. (2021) A computational approach for identification of core modules from a co-expression network and GWAS data. *STAR protocols*, 2(3), 100768.

Sabik OL, et al. (2020) Identification of a Core Module for Bone Mineral Density through the Integration of a Co-expression Network and GWAS Data. *Cell reports*, 32(11), 108145.

Ngan CY, et al. (2020) Chromatin interaction analyses elucidate the roles of PRC2-bound silencers in mouse development. *Nature genetics*, 52(3), 264.

Meehan TF, et al. (2017) Disease model discovery from 3,328 gene knockouts by The International Mouse Phenotyping Consortium. *Nature genetics*, 49(8), 1231.