

Resource Summary Report

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

PheWAS R Package

RRID:SCR_003512

Type: Tool

Proper Citation

PheWAS R Package (RRID:SCR_003512)

Resource Information

URL: <http://knowledgemap.mc.vanderbilt.edu/research/content/phewas-r-package>

Proper Citation: PheWAS R Package (RRID:SCR_003512)

Description: Software package contains methods for performing Phenome-Wide Association Study.

Synonyms: Phenome-Wide Association Study

Resource Type: software resource

Defining Citation: [PMID:20335276](#)

Keywords: bio.tools

Availability: Free

Resource Name: PheWAS R Package

Resource ID: SCR_003512

Alternate IDs: OMICS_00242, biotools:phewas

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

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260903T234623+0000

Ratings and Alerts

No rating or validation information has been found for PheWAS R Package.

No alerts have been found for PheWAS R Package.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Khan Y, et al. (2026) Transdiagnostic and Disorder-Level Genome-Wide Association Studies Enhance Precision of Substance Use and Psychiatric Genetic Risk Profiles in African and European Ancestries. *Biological psychiatry*, 99(1), 68.

Harutyunyan AS, et al. (2019) H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. *Nature communications*, 10(1), 1262.

Karikari B, et al. (2019) Genome-Wide Detection of Major and Epistatic Effect QTLs for Seed Protein and Oil Content in Soybean Under Multiple Environments Using High-Density Bin Map. *International journal of molecular sciences*, 20(4).

Bhaskaran N, et al. (2018) Identification of Casz1 as a Regulatory Protein Controlling T Helper Cell Differentiation, Inflammation, and Immunity. *Frontiers in immunology*, 9, 184.

Pashos EE, et al. (2017) Large, Diverse Population Cohorts of hiPSCs and Derived Hepatocyte-like Cells Reveal Functional Genetic Variation at Blood Lipid-Associated Loci. *Cell stem cell*, 20(4), 558.

Friedemann G, et al. (2016) Multidimensional differentiation in foraging resource use during breeding of two sympatric top predators. *Scientific reports*, 6, 35031.

Liao M, et al. (2015) Analyzing large-scale samples confirms the association between rs16892766 polymorphism and colorectal cancer susceptibility. *Scientific reports*, 5, 7957.