Resource Summary Report

Generated by kravitz2 on Sep 4, 2026

MultiPhen

RRID:SCR_003498
Type: Tool

Proper Citation

MultiPhen (RRID:SCR_003498)

Resource Information

URL: http://cran.r-project.org/web/packages/MultiPhen/

Proper Citation: MultiPhen (RRID:SCR_003498)

Description: Software package that performs genetic association tests between SNPs (one-at-a-time) and multiple phenotypes (separately or in joint model).

Synonyms: MultiPhen: a package for the genetic association testing of multiple phenotypes

Resource Type: software resource

Defining Citation: PMID:22567092

Keywords: standalone software, r, bio.tools

Availability: GNU General Public License, v2

Resource Name: MultiPhen

Resource ID: SCR_003498

Alternate IDs: biotools:multiphen, OMICS_04397

Alternate URLs: https://bio.tools/multiphen

Record Creation Time: 20220129T080219+0000

Record Last Update: 20260903T234623+0000

Ratings and Alerts

No rating or validation information has been found for MultiPhen.

No alerts have been found for MultiPhen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Li RY, et al. (2026) A novel machine learning-based algorithm for eQTL identification reveals complex pleiotropic effects in the MHC region. Briefings in bioinformatics, 27(3).

Chindelevitch L, et al. (2026) ReverseGWAS identifies combined phenotypes associated with a genotype in GWA studies. Bioinformatics (Oxford, England), 42(3).

De T, et al. (2025) Dosage effect of copy number variation in epilepsy and ten regions of the human brain. Scientific reports, 15(1), 45726.

De T, et al. (2025) Plasma metabolomic signatures for copy number variants and COVID-19 risk loci in Northern Finland populations. Scientific reports, 15(1), 13172.

Cao X, et al. (2024) A novel method for multiple phenotype association studies based on genotype and phenotype network. PLoS genetics, 20(5), e1011245.

Liang X, et al. (2022) HCLC-FC: A novel statistical method for phenome-wide association studies. PloS one, 17(11), e0276646.

Mbye H, et al. (2022) Plasmodium falciparum merozoite invasion ligands, linked antimalarial resistance loci and ex vivo responses to antimalarials in The Gambia. The Journal of antimicrobial chemotherapy, 77(11), 2946.

Vilor-Tejedor N, et al. (2021) Multivariate Analysis and Modelling of multiple Brain endOphenotypes: Let's MAMBO! Computational and structural biotechnology journal, 19, 5800.

De T, et al. (2021) Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. iScience, 24(8), 102893.

Liu D, et al. (2021) Impact of low-frequency coding variants on human facial shape. Scientific reports, 11(1), 748.

Fu L, et al. (2021) A Novel Approach Integrating Hierarchical Clustering and Weighted Combination for Association Study of Multiple Phenotypes and a Genetic Variant. Frontiers in genetics, 12, 654804.

Klimentidis YC, et al. (2020) Phenotypic and Genetic Characterization of Lower LDL Cholesterol and Increased Type 2 Diabetes Risk in the UK Biobank. Diabetes, 69(10), 2194.

van der Meer D, et al. (2020) Understanding the genetic determinants of the brain with MOSTest. Nature communications, 11(1), 3512.

Zhang X, et al. (2019) Detecting potential pleiotropy across cardiovascular and neurological diseases using univariate, bivariate, and multivariate methods on 43,870 individuals from the eMERGE network. Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, 24, 272.

Schmid AB, et al. (2019) Genetic components of human pain sensitivity: a protocol for a genome-wide association study of experimental pain in healthy volunteers. BMJ open, 9(4), e025530.

Chung J, et al. (2019) Comparison of methods for multivariate gene-based association tests for complex diseases using common variants. European journal of human genetics : EJHG, 27(5), 811.

Truong DT, et al. (2019) Multivariate genome-wide association study of rapid automatised naming and rapid alternating stimulus in Hispanic American and African-American youth. Journal of medical genetics, 56(8), 557.

Ganesamoorthy D, et al. (2018) GtTR: Bayesian estimation of absolute tandem repeat copy number using sequence capture and high throughput sequencing. BMC bioinformatics, 19(1), 267.

Chibnik LB, et al. (2018) Susceptibility to neurofibrillary tangles: role of the PTPRD locus and limited pleiotropy with other neuropathologies. Molecular psychiatry, 23(6), 1521.

Kaakinen M, et al. (2017) A rare-variant test for high-dimensional data. European journal of human genetics : EJHG, 25(8), 988.