

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 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: 20260905T132504+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 [Kravitz](#) .

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.