Resource Summary Report

Generated by dkNET on Apr 16, 2025

PHASE

RRID:SCR_009327
Type: Tool

Proper Citation

PHASE (RRID:SCR_009327)

Resource Information

URL: http://www.stat.washington.edu/stephens/software.html

Proper Citation: PHASE (RRID:SCR_009327)

Description: Software program that implements a new statistical method for reconstructing haplotypes from population genotype data (entry from Genetic Analysis Software)

Abbreviations: PHASE

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: PHASE

Resource ID: SCR_009327

Alternate IDs: nlx_154533

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063544+0000

Ratings and Alerts

No rating or validation information has been found for PHASE.

No alerts have been found for PHASE.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 582 mentions in open access literature.

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

Hämäläinen K, et al. (2024) Non-targeted metabolomics for the identification of plasma metabolites associated with organic anion transporting polypeptide 1B1 function. Clinical and translational science, 17(3), e13773.

Kulski JK, et al. (2024) Regulatory SVA retrotransposons and classical HLA genotyped-transcripts associated with Parkinson's disease. Frontiers in immunology, 15, 1349030.

Clarke DN, et al. (2024) Fluorescent proteins generate a genetic color polymorphism and counteract oxidative stress in intertidal sea anemones. Proceedings of the National Academy of Sciences of the United States of America, 121(11), e2317017121.

Silva VDC, et al. (2024) ADRB2 and ADCY9 Sequence Variations in Brazilian Asthmatic Patients. Current issues in molecular biology, 46(7), 6951.

Gallego A, et al. (2024) Study protocol for a three-arm randomized controlled trial investigating the effectiveness, cost-utility, and physiological effects of a fully self-guided digital Acceptance and Commitment Therapy for Spanish patients with fibromyalgia. Digital health, 10, 20552076241239177.

Sanchez-Flores M, et al. (2024) Novel genotype-phenotype correlations, differential cerebellar allele-specific methylation, and a common origin of the (ATTTC)n insertion in spinocerebellar ataxia type 37. Human genetics, 143(3), 211.

Parker HG, et al. (2024) Genome-wide analyses reveals an association between invasive urothelial carcinoma in the Shetland sheepdog and NIPAL1. NPJ precision oncology, 8(1), 112.

Wickramasinghe DN, et al. (2024) Variations in candidalysin amino acid sequence influence toxicity and host responses. mBio, 15(8), e0335123.

Huynh S, et al. (2023) Whole-genome Analyses Reveal Past Population Fluctuations and Low Genetic Diversities of the North Pacific Albatrosses. Molecular biology and evolution, 40(7).

Liu Y, et al. (2023) GC heterogeneity reveals sequence-structures evolution of angiosperm ITS2. BMC plant biology, 23(1), 608.

Mangó K, et al. (2023) Association between CYP2B6 genetic variability and

cyclophosphamide therapy in pediatric patients with neuroblastoma. Scientific reports, 13(1), 11770.

Bu R, et al. (2023) Identification and characterization of ATM founder mutation in BRCA-negative breast cancer patients of Arab ethnicity. Scientific reports, 13(1), 20924.

Lehtisalo M, et al. (2023) A comprehensive pharmacogenomic study indicates roles for SLCO1B1, ABCG2 and SLCO2B1 in rosuvastatin pharmacokinetics. British journal of clinical pharmacology, 89(1), 242.

Dieter C, et al. (2023) Polymorphisms in TIE2 and ANGPT-1 genes are associated with protection against diabetic retinopathy in a Brazilian population. Archives of endocrinology and metabolism, 67(5), e000624.

Siraj AK, et al. (2023) PALB2 germline mutations in a large cohort of Middle Eastern breast-ovarian cancer patients. Scientific reports, 13(1), 7666.

Jablonski D, et al. (2023) A new, rare, small-ranged, and endangered mountain snake of the genus Elaphe from the Southern Levant. Scientific reports, 13(1), 4839.

Thawornwattana Y, et al. (2023) Major patterns in the introgression history of Heliconius butterflies. eLife, 12.

Casale F, et al. (2022) Genomic prediction of the recombination rate variation in barley - A route to highly recombinogenic genotypes. Plant biotechnology journal, 20(4), 676.

Mestiri S, et al. (2022) New Insight into the human genetic diversity in North African populations by genotyping of SNPs in DRD3, CSMD1 and NRG1 genes. Molecular genetics & genomic medicine, 10(3), e1871.

de Melo IB, et al. (2022) TRPA1 Polymorphisms Modify the Hypotensive Responses to Propofol with No Change in Nitrite or Nitrate Levels. Current issues in molecular biology, 44(12), 6333.