

Resource Summary Report

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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 application, software resource

Keywords: gene, genetic, genomic

Resource Name: PHASE

Resource ID: SCR_009327

Alternate IDs: nlx_154533

Record Creation Time: 20220129T080252+0000

Record Last Update: 20260805T044221+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 590 mentions in open access literature.

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

Chen W, et al. (2025) Identification of new major histocompatibility complex-B haplotypes in chinese broilers. *Poultry science*, 104(12), 106045.

Silver LW, et al. (2025) Temporal Loss of Genome-Wide and Immunogenetic Diversity in a Near-Extinct Parrot. *Molecular ecology*, 34(9), e17746.

Schraven AL, et al. (2025) Boost or Bust? The Impact of Supplementation on Functional Genetic Diversity and Selective Processes in Tasmanian Devils. *Molecular ecology*, 34(24), e70188.

Fouet C, et al. (2025) Standing genetic variation underlies divergence of nicotinic acetylcholine receptor subunits among cryptic species of the *Anopheles gambiae* complex. *bioRxiv : the preprint server for biology*.

Teodoro-Paulo J, et al. (2025) Suppression of Plant Resistance May Be a Common Trait Among Adapted Herbivores. *Ecology and evolution*, 15(7), e71706.

Zhang J, et al. (2025) A cohort of GFPT1 related congenital myasthenic syndrome in China: high frequency of c.331 c > t variant. *Orphanet journal of rare diseases*, 20(1), 259.

Luzum JA, et al. (2025) The Beta-Blocker Pharmacogenetic Puzzle: More Pieces of Evidence for Pharmacodynamic Candidate Variants. *Clinical and translational science*, 18(5), e70239.

Møller HI, et al. (2025) Investigations of HLA-F and HLA-G 3'UTR Polymorphisms in Preeclampsia and Fetal Growth Restriction Indicate a Possible Role of HLA-F-HLA-G Haplotypes and Diplotypes. *HLA*, 106(1), e70293.

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.

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.

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

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

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.

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.

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.

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.