Resource Summary Report

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HARDY

RRID:SCR_009107
Type: Tool

Proper Citation

HARDY (RRID:SCR_009107)

Resource Information

URL: http://www.stat.washington.edu/thompson/Genepi/Hardy.shtml

Proper Citation: HARDY (RRID:SCR_009107)

Description: Markov chain Monte Carlo program for association in two-dimensional contingency tables, and for testing Hardy-Weinberg equilibrium. (entry from Genetic Analysis Software)

Abbreviations: HARDY

Synonyms: PANGAEA

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, c, unix, (dec-unix/..)

Resource Name: HARDY

Resource ID: SCR_009107

Alternate IDs: nlx_154205

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260727T040444+0000

Ratings and Alerts

No rating or validation information has been found for HARDY.

No alerts have been found for HARDY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7329 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Le SV, et al. (2026) Signature of Selection Analysis Reveals Candidate Genes Related to Climate Adaptation and Production Traits in Lao Native Goats. Journal of animal breeding and genetics = Zeitschrift fur Tierzuchtung und Zuchtungsbiologie, 143(1), 152.

Morales-González E, et al. (2025) Maintenance of genetic diversity in subdivided populations using genomic coancestry matrices. Molecular ecology resources, 25(5), e13781.

López A, et al. (2025) Evaluating restriction enzyme selection for reduced representation sequencing in conservation genomics. Molecular ecology resources, 25(5), e13865.

Kaabi AM, et al. (2025) Association between factor I fibrinogen (rs6050) and factor XI plasma thromboplastin (rs4253417) genetic polymorphisms and recurrent spontaneous miscarriage in Saudi women. Saudi medical journal, 46(2), 150.

Godina E, et al. (2025) Prediction of success in sports based on assumed individual genetic predisposition: lack of association with the C > T variant in the ACTN3 gene. Journal of physiological anthropology, 44(1), 6.

Komiyama T, et al. (2025) Association of adenylate cyclase activity in vasopressor-type neurally mediated syncope based on the ?2b-AR gene. PloS one, 20(2), e0317817.

He J, et al. (2025) Constructing a potential HLA haplo-homozygous induced pluripotent stem cell haplobank using data from an umbilical cord blood bank. Stem cell research & therapy, 16(1), 42.

Sarömba JA, et al. (2025) Solanidine-derived CYP2D6 phenotyping elucidates phenoconversion in multimedicated geriatric patients. British journal of clinical pharmacology, 91(6), 1842.

Zimmermann H, et al. (2025) Mixed Parentage Broods Indicate Group Spawning in the Brood Parasitic Cuckoo Catfish. Molecular ecology, 34(6), e17692.

Sampaio AL, et al. (2025) Frequency of TNFalpha, IL17RA, and Act1 Genetic Polymorphisms in a Population with Psoriasis Compared with Healthy Individuals: Results in a Multiracial Population in Rio de Janeiro, Brazil. Acta dermato-venereologica, 105, adv42017.

Lee SB, et al. (2025) Impact of genetic markers related to hyper-HDL cholesterol on the prevalence of myocardial infarction: a KoGES study. Journal of lipid research, 66(4), 100777.

Breddels EM, et al. (2025) Brain morphology mediating the effects of common genetic risk variants on Alzheimer's disease. Journal of Alzheimer's disease reports, 9, 25424823251328300.

Gálvez-Montosa F, et al. (2025) Polymorphisms within autophagy-related genes as susceptibility biomarkers for pancreatic cancer: A meta-analysis of three large European cohorts and functional characterization. International journal of cancer, 156(2), 339.

Mukiibi R, et al. (2025) Integrated functional genomic analysis identifies regulatory variants underlying a major QTL for disease resistance in European sea bass. BMC biology, 23(1), 75.

Inoue S, et al. (2025) The influence of hypertensive disorders of pregnancy on the development of long-term postpartum type 2 diabetes mellitus. Endocrine journal, 72(6), 727.

Özkaraca M?, et al. (2025) Divide and conquer approach for genome-wide association studies. Genetics, 229(4).

Mei S, et al. (2025) Comprehensive elucidation on the genetic profile of the Hezhou Han population via an efficient InDel panel. Forensic sciences research, 10(1), owae021.

Luo C, et al. (2025) Risk Allele rs117026326-Mediated Alternative Splicing of GTF2I Promotes B Cell Proliferation in Primary Sjögren's Syndrome. Journal of immunology research, 2025, 4821639.

Goeury T, et al. (2025) Evidence for Pathogen-Driven Selection Acting on HLA-DPB1 in Response to Plasmodium falciparum Malaria in West Africa. Ecology and evolution, 15(2), e70933.

Abdalfatah MF, et al. (2025) The Association of VDR/FokI Gene Polymorphism and Protein Expression With Histopathological Alterations in Patients With Thyroid Colloid Nodule. Analytical cellular pathology (Amsterdam), 2025, 6796922.