Resource Summary Report

Generated by RRID on Apr 8, 2025

MIGen

RRID:SCR_006959
Type: Tool

Proper Citation

MIGen (RRID:SCR_006959)

Resource Information

URL: http://migen.sourceforge.net/

Proper Citation: MIGen (RRID:SCR_006959)

Description: Standard specification for the information required to report a genotyping experiment, covering: study and experiment design, subject information, genotyping procedure, and data analysis methods. The goal is to set a reporting standard for adoption by the research community to facilitate consistent data interpretation and independent validation/reproduction, and to serve as guidance for database design for storing genotyping experiment data. MIGen is being developed as a collaborative project involving international domain experts and is a registered project under MIBBI: Minimum Information for Biological and Biomedical Investigations.

Abbreviations: MIGen

Synonyms: Minimum Information about a Genotyping Experiment

Resource Type: narrative resource, data or information resource, knowledge environment, standard specification

Keywords: genotyping, genotype, genotyping experiment, data archiving, data management, data sharing, data transfer, data analysis, experiment

Funding:

Availability: The community can contribute to this resource

Resource Name: MIGen

Resource ID: SCR_006959

Alternate IDs: OMICS_01786

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250407T215623+0000

Ratings and Alerts

No rating or validation information has been found for MIGen.

No alerts have been found for MIGen.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Trastulla L, et al. (2024) Distinct genetic liability profiles define clinically relevant patient strata across common diseases. Nature communications, 15(1), 5534.

Hindy G, et al. (2022) Rare coding variants in 35 genes associate with circulating lipid levels-A multi-ancestry analysis of 170,000 exomes. American journal of human genetics, 109(1), 81.

Straniero L, et al. (2022) Role of Lysosomal Gene Variants in Modulating GBA-Associated Parkinson's Disease Risk. Movement disorders : official journal of the Movement Disorder Society, 37(6), 1202.

Zeng L, et al. (2022) Cis-epistasis at the LPA locus and risk of cardiovascular diseases. Cardiovascular research, 118(4), 1088.

Koko M, et al. (2021) Distinct gene-set burden patterns underlie common generalized and focal epilepsies. EBioMedicine, 72, 103588.

Lali R, et al. (2021) Calibrated rare variant genetic risk scores for complex disease prediction using large exome sequence repositories. Nature communications, 12(1), 5852.

Straniero L, et al. (2020) The SPID-GBA study: Sex distribution, Penetrance, Incidence, and Dementia in GBA-PD. Neurology. Genetics, 6(6), e523.

Emdin CA, et al. (2018) Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. Nature communications, 9(1), 1613.

Kaput J, et al. (2017) Propelling the paradigm shift from reductionism to systems nutrition. Genes & nutrition, 12, 3.

Frånberg M, et al. (2017) Fast and general tests of genetic interaction for genome-wide association studies. PLoS computational biology, 13(6), e1005556.

Liu DJ, et al. (2017) Exome-wide association study of plasma lipids in >300,000 individuals. Nature genetics, 49(12), 1758.

Zanetti D, et al. (2016) Analysis of Genomic Regions Associated With Coronary Artery Disease Reveals Continent-Specific Single Nucleotide Polymorphisms in North African Populations. Journal of epidemiology, 26(5), 264.

Adam-Blondon AF, et al. (2016) Towards an open grapevine information system. Horticulture research, 3, 16056.

Abraham G, et al. (2016) Genomic prediction of coronary heart disease. European heart journal, 37(43), 3267.

Zhang H, et al. (2015) Novel Genes Affecting Blood Pressure Detected Via Gene-Based Association Analysis. G3 (Bethesda, Md.), 5(6), 1035.

Won HH, et al. (2015) Disproportionate Contributions of Select Genomic Compartments and Cell Types to Genetic Risk for Coronary Artery Disease. PLoS genetics, 11(10), e1005622.

Do R, et al. (2015) Exome sequencing identifies rare LDLR and APOA5 alleles conferring risk for myocardial infarction. Nature, 518(7537), 102.

Musameh MD, et al. (2015) Analysis of gene-gene interactions among common variants in candidate cardiovascular genes in coronary artery disease. PloS one, 10(2), e0117684.

Ruderfer DM, et al. (2014) Polygenic dissection of diagnosis and clinical dimensions of bipolar disorder and schizophrenia. Molecular psychiatry, 19(9), 1017.