Resource Summary Report

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SAS/GENETICS

RRID:SCR_009343
Type: Tool

Proper Citation

SAS/GENETICS (RRID:SCR_009343)

Resource Information

URL: http://support.sas.com/documentation/onlinedoc/genetics/

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Description: Software application for summarizing marker properties (allele & genotype frequencies, tests for Hardy-Weinberg equilibrium, measures of marker informativeness), examining marker-marker relationships (tests and measures of linkage disequilibrium, and haplotype frequency estimation), and exploring marker-trait associations using case-control or family-based tests (entry from Genetic Analysis Software)

Abbreviations: SAS/GENETICS

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, ms-windows, unix, (hpux/aixr/solaris/..), mvs

Funding:

Resource Name: SAS/GENETICS

Resource ID: SCR_009343

Alternate IDs: nlx_154609

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063544+0000

Ratings and Alerts

No rating or validation information has been found for SAS/GENETICS.

No alerts have been found for SAS/GENETICS.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 119 mentions in open access literature.

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

Jan K, et al. (2024) The incidence of the thrombophilic SNPs rs6025, rs1799963, rs2066865, rs2289252, and rs8176719 in chronic thromboembolic pulmonary hypertension. Clinical and applied thrombosis/hemostasis : official journal of the International Academy of Clinical and Applied Thrombosis/Hemostasis, 30, 10760296241271369.

Mustafa I, et al. (2020) Genetic epidemiology of beta-thalassemia in the Maldives: 23 years of a beta-thalassemia screening program. Gene, 741, 144544.

Struck AK, et al. (2020) A structural UGDH variant associated with standard Munchkin cats. BMC genetics, 21(1), 67.

Totomoch-Serra A, et al. (2020) Data on a genome-wide association study of type 2 diabetes in a Maya population. Data in brief, 28, 104866.

Schachler K, et al. (2020) Tracing selection signatures in the pig genome gives evidence for selective pressures on a unique curly hair phenotype in Mangalitza. Scientific reports, 10(1), 22142.

Choi J, et al. (2019) Association Analysis of Interleukin-1?, Interleukin-6, and HMGB1 Variants with Postictal Serum Cytokine Levels in Children with Febrile Seizure and Generalized Epilepsy with Febrile Seizure Plus. Journal of clinical neurology (Seoul, Korea), 15(4), 555.

Ma YN, et al. (2019) Multiple Gene Polymorphisms Associated with Exfoliation Syndrome in the Uygur Population. Journal of ophthalmology, 2019, 9687823.

Domínguez-Cruz MG, et al. (2018) Pilot genome-wide association study identifying novel risk loci for type 2 diabetes in a Maya population. Gene, 677, 324.

Wang RY, et al. (2018) Impacts of GRIN3A, GRM6 and TPH2 genetic polymorphisms on quality of life in methadone maintenance therapy population. PloS one, 13(7), e0201408.

Thomer A, et al. (2018) An epistatic effect of KRT25 on SP6 is involved in curly coat in

horses. Scientific reports, 8(1), 6374.

Chen JY, et al. (2018) Interferon-?3/4 genetic variants and interferon-?3 serum levels are biomarkers of lupus nephritis and disease activity in Taiwanese. Arthritis research & therapy, 20(1), 193.

Mu F, et al. (2017) Structural Characterization and Association of Ovine Dickkopf-1 Gene with Wool Production and Quality Traits in Chinese Merino. Genes, 8(12).

Ma GW, et al. (2017) Polymorphisms of FST gene and their association with wool quality traits in Chinese Merino sheep. PloS one, 12(4), e0174868.

Gottschalk M, et al. (2016) Genome-wide association study for semen quality traits in German Warmblood stallions. Animal reproduction science, 171, 81.

Reinartz S, et al. (2016) Validation of Deleterious Mutations in Vorderwald Cattle. PloS one, 11(7), e0160013.

Ueda I, et al. (2016) Relationship between G1287A of the NET Gene Polymorphisms and Brain Volume in Major Depressive Disorder: A Voxel-Based MRI Study. PloS one, 11(3), e0150712.

Ku CL, et al. (2016) Anti-IFN-? autoantibodies are strongly associated with HLA-DR*15:02/16:02 and HLA-DQ*05:01/05:02 across Southeast Asia. The Journal of allergy and clinical immunology, 137(3), 945.

Metzger J, et al. (2016) Variant detection and runs of homozygosity in next generation sequencing data elucidate the genetic background of Lundehund syndrome. BMC genomics, 17, 535.

Schrimpf R, et al. (2016) Screening of whole genome sequences identified high-impact variants for stallion fertility. BMC genomics, 17, 288.

Liu YL, et al. (2016) Haplotypes of the D-Amino Acid Oxidase Gene Are Significantly Associated with Schizophrenia and Its Neurocognitive Deficits. PloS one, 11(3), e0150435.