Resource Summary Report

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GASSOC

RRID:SCR_013136
Type: Tool

Proper Citation

GASSOC (RRID:SCR_013136)

Resource Information

URL: http://mayoresearch.mayo.edu/mayo/research/schaid_lab/software.cfm

Proper Citation: GASSOC (RRID:SCR_013136)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on May 24,2023. Software application for statistical methods for disease and genetic marker associations using cases and their parents. These methods include an extension of the transmission/disequilibrium test (TDT) for multiple marker alleles, as well as additional general tests sensitive to associations that depend on dominant or recessive genetic mechanisms. (entry from Genetic Analysis Software)

Synonyms: Genetic ASSOCiation analysis software for cases and parent

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, unix, sunos, solaris

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GASSOC

Resource ID: SCR_013136

Alternate IDs: nlx_154077

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250411T055617+0000

Ratings and Alerts

No rating or validation information has been found for GASSOC.

No alerts have been found for GASSOC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Wakil SM, et al. (2014) A new susceptibility locus for myocardial infarction, hypertension, type 2 diabetes mellitus, and dyslipidemia on chromosome 12q24. Disease markers, 2014, 291419.

Zhang Z, et al. (2014) Functional genetic variants of TNFSF15 and their association with gastric adenocarcinoma: a case-control study. PloS one, 9(9), e108321.

Brighina L, et al. (2013) Analysis of vesicular monoamine transporter 2 polymorphisms in Parkinson's disease. Neurobiology of aging, 34(6), 1712.e9.

Al-Najai M, et al. (2013) Association of the angiotensinogen gene polymorphism with atherosclerosis and its risk traits in the Saudi population. BMC cardiovascular disorders, 13, 17.

Alshahid M, et al. (2013) New susceptibility locus for obesity and dyslipidaemia on chromosome 3q22.3. Human genomics, 7(1), 15.

Muiya N, et al. (2013) The 3'-UTR of the adiponectin Q gene harbours susceptibility loci for atherosclerosis and its metabolic risk traits. BMC medical genetics, 14, 127.

Hodži? A, et al. (2013) Genetic variation in circadian rhythm genes CLOCK and ARNTL as risk factor for male infertility. PloS one, 8(3), e59220.

Zhang X, et al. (2012) Association of single nucleotide polymorphisms in TCF2 with type 2 diabetes susceptibility in a Han Chinese population. PloS one, 7(12), e52938.

Razzaghi H, et al. (2012) Population-Based Resequencing of LIPG and ZNF202 Genes in Subjects with Extreme HDL Levels. Frontiers in genetics, 3, 89.

Beebe-Dimmer JL, et al. (2012) Genetic variation in glutathione S-transferase omega-1, arsenic methyltransferase and methylene-tetrahydrofolate reductase, arsenic exposure and

bladder cancer: a case-control study. Environmental health : a global access science source, 11, 43.

Guo X, et al. (2011) Mucin variable number tandem repeat polymorphisms and severity of cystic fibrosis lung disease: significant association with MUC5AC. PloS one, 6(10), e25452.

Del Greco M F, et al. (2011) Genome-wide association analysis and fine mapping of NT-proBNP level provide novel insight into the role of the MTHFR-CLCN6-NPPA-NPPB gene cluster. Human molecular genetics, 20(8), 1660.

Wang SS, et al. (2010) Common genetic variants and risk for HPV persistence and progression to cervical cancer. PloS one, 5(1), e8667.