Resource Summary Report

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GENEVAR

RRID:SCR_009201
Type: Tool

Proper Citation

GENEVAR (RRID:SCR_009201)

Resource Information

URL: http://www.sanger.ac.uk/resources/software/genevar/

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Description: A database and Java tool designed to integrate multiple datasets, and provides analysis and visualization of associations between sequence variation and gene expression in eQTL studies. Genevar allows researchers to investigate eQTL (expression quantitative trait loci) associations within a gene locus of interest in real time. The database and application can be installed on a standard computer in database mode and, in addition, on a server to share discoveries among affiliations or the broader community over the internet via web services protocols. (entry from Genetic Analysis Software)

Abbreviations: GENEVAR

Synonyms: GENe Expression VARiation

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, java

Funding:

Resource Name: GENEVAR

Resource ID: SCR_009201

Alternate IDs: nlx_154342

Record Creation Time: 20220129T080251+0000

Record Last Update: 20250416T063539+0000

Ratings and Alerts

No rating or validation information has been found for GENEVAR.

No alerts have been found for GENEVAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Walker K, et al. (2022) The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. F1000Research, 11, 530.

Wang Y, et al. (2022) Identification of genetic variants of the IL-22 gene in association with an altered risk of COPD susceptibility. The clinical respiratory journal, 16(8), 537.

Mc Cartney AM, et al. (2021) An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. F1000Research, 10, 246.

Kim J, et al. (2020) Identification of Candidate Genes Associated with Susceptibility to Ovarian Clear Cell Adenocarcinoma Using cis-eQTL Analysis. Journal of clinical medicine, 9(4).

Fu X, et al. (2020) BDNF Gene's Role in Schizophrenia: From Risk Allele to Methylation Implications. Frontiers in psychiatry, 11, 564277.

Yu CC, et al. (2019) Genetic variants in the circadian rhythm pathway as indicators of prostate cancer progression. Cancer cell international, 19, 87.

Liu Y, et al. (2019) Changes E3 ubiquitin protein ligase 1 gene mRNA expression correlated with IgA1 glycosylation in patients with IgA nephropathy. Renal failure, 41(1), 370.

Li JX, et al. (2018) A functional SNP upstream of the ADRB2 gene is associated with COPD. International journal of chronic obstructive pulmonary disease, 13, 917.

Wolin A, et al. (2017) SNP Variants in Major Histocompatibility Complex Are Associated with Sarcoidosis Susceptibility-A Joint Analysis in Four European Populations. Frontiers in

immunology, 8, 422.

Li Y, et al. (2017) Hyposmia Is Associated with RBD for PD Patients with Variants of SNCA. Frontiers in aging neuroscience, 9, 303.

Bailey JN, et al. (2016) Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature genetics, 48(2), 189.

Zhang YB, et al. (2016) Genome-wide association study identifies multiple susceptibility loci for craniofacial microsomia. Nature communications, 7, 10605.

Finkel TH, et al. (2016) Variants in CXCR4 associate with juvenile idiopathic arthritis susceptibility. BMC medical genetics, 17, 24.

Mangino M, et al. (2016) Integrated multiomics approach identifies calcium and integrin-binding protein-2 as a novel gene for pulse wave velocity. Journal of hypertension, 34(1), 79.

Sellgren CM, et al. (2016) A genome-wide association study of kynurenic acid in cerebrospinal fluid: implications for psychosis and cognitive impairment in bipolar disorder. Molecular psychiatry, 21(10), 1342.

Li R, et al. (2016) MiRNA-Related Genetic Variations Associated with Radiotherapy-Induced Toxicities in Patients with Locally Advanced Non-Small Cell Lung Cancer. PloS one, 11(3), e0150467.

Campa D, et al. (2016) Functional single nucleotide polymorphisms within the cyclin-dependent kinase inhibitor 2A/2B region affect pancreatic cancer risk. Oncotarget, 7(35), 57011.

Zhu J, et al. (2016) Polymorphisms in the AKT1 and AKT2 genes and oesophageal squamous cell carcinoma risk in an Eastern Chinese population. Journal of cellular and molecular medicine, 20(4), 666.

Gong J, et al. (2016) Genome-Wide Interaction Analyses between Genetic Variants and Alcohol Consumption and Smoking for Risk of Colorectal Cancer. PLoS genetics, 12(10), e1006296.

Beaumont M, et al. (2016) Heritable components of the human fecal microbiome are associated with visceral fat. Genome biology, 17(1), 189.