Resource Summary Report

Generated by dkNET on Sep 9, 2026

VARIANT

RRID:SCR_005194
Type: Tool

Proper Citation

VARIANT (RRID:SCR_005194)

Resource Information

URL: http://variant.bioinfo.cipf.es/

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Description: Analysis tool that can report the functional properties of any variant in all the human, mouse or rat genes (and soon new model organisms will be added) and the corresponding neighborhoods. Also other non-coding extra-genic regions, such as miRNAs are included in the analysis. It not only reports the obvious functional effects in the coding regions but also analyzes noncoding SNVs situated both within the gene and in the neighborhood that could affect different regulatory motifs, splicing signals, and other structural elements. These include: Jaspar regulatory motifs, miRNA targets, splice sites, exonic splicing silencers, calculations of selective pressures on the particular polymorphic positions, etc. Software analysis pipelines used in the analysis of NGS data are highly modular, heterogeneous, and rapidly evolving. VARIANT can easily be incorporated into a NGS resequencing pipeline either as a CLI or invoked a webservice. It inputs data directly from the most widely used programs for SNV detection., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: VARIANT

Synonyms: Variant effect, VARIant ANalysis Tool

Resource Type: analysis service resource, data analysis service, data analysis software, data processing software, production service resource, service resource, software application, software resource

Defining Citation: PMID:22693211

Keywords: functional property, variant, gene, non-coding region, mirna, function, single nucleotide variant, next generation sequencing, command line

Funding: Spanish Ministry of Science and Innovation BIO2011-27069

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: VARIANT

Resource ID: SCR_005194

Alternate IDs: OMICS_00193

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260905T132531+0000

Ratings and Alerts

No rating or validation information has been found for VARIANT.

No alerts have been found for VARIANT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1366 mentions in open access literature.

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

Lim SH, et al. (2025) Determinants of Response to Sequential Pembrolizumab with Trastuzumab plus Platinum/5-FU in HER2-Positive Gastric Cancer: A Phase II Chemoimmunotherapy Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(8), 1476.

Belonogova NM, et al. (2025) A multi-trait approach identified 7 novel genes for back pain. Pain reports, 10(1), e1218.

Delles C, et al. (2025) Response of Blood Pressure to Renal Denervation Is Not Associated With Genetic Variants. Hypertension (Dallas, Tex. : 1979), 82(1), 118.

Cao J, et al. (2025) Integrating rare pathogenic variant prioritization with gene-based association analysis to identify novel genes and relevant multimodal traits for Alzheimer's disease. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(2), e14444.

Gao J, et al. (2025) RMRP variants inhibit the cell cycle checkpoints pathway in cartilage???hair hypoplasia. Molecular medicine reports, 31(3).

Li R, et al. (2025) Whole genome sequence-based association analysis of African American individuals with bipolar disorder and schizophrenia. medRxiv : the preprint server for health sciences.

Ali A, et al. (2025) Genetic variants associated with age-related episodic memory decline implicate distinct memory pathologies. Alzheimer's & dementia : the journal of the Alzheimer's Association, 21(1), e14379.

Sonowal H, et al. (2025) Preclinical Development of Tuspetinib for the Treatment of Acute Myeloid Leukemia. Cancer research communications, 5(1), 74.

Xi Z, et al. (2025) Clonal hematopoiesis of indeterminate potential is a risk factor of gastric cancer: A Prospective Cohort in UK Biobank study. Translational oncology, 52, 102242.

Roback EY, et al. (2025) Population Genomics of Premature Termination Codons in Cavefish With Substantial Trait Loss. Molecular biology and evolution, 42(2).

Sousa-Squiavinato ACM, et al. (2025) Modelling Acral Melanoma in Admixed Brazilians Uncovers Genomic Drivers and Targetable Pathways. medRxiv : the preprint server for health sciences.

Shi Y, et al. (2025) Genetic Commonalities Between Metabolic Syndrome and Rheumatic Diseases Through Disease Interactome Modules. Journal of cellular and molecular medicine, 29(1), e70329.

Turk A, et al. (2025) Increased burden of rare variants in GWAS associated genes in familial multiple sclerosis. Scientific reports, 15(1), 21200.

Sharapov S, et al. (2025) A genome-wide association study in 10,000 individuals links plasma N-glycome to liver disease and anti-inflammatory proteins. Nature communications, 16(1), 5525.

Zhang M, et al. (2025) EZH2 loss promotes gastric squamous cell carcinoma. Nature communications, 16(1), 6032.

Lepage M, et al. (2025) Prevalence of Constitutional Pathogenic Variant in a Cohort of 348 Patients With Multiple Primary Cancer Addressed in Oncogenetic Consultation. Molecular genetics & genomic medicine, 13(3), e70086.

Trastulli G, et al. (2025) Sample Tracking Tool: A Comprehensive Approach Based on OpenArray Technology and R Scripting for Genomic Sample Monitoring. Diagnostics (Basel, Switzerland), 15(2).

Wang RJ, et al. (2025) Unprecedented female mutation bias in the aye-aye, a highly unusual lemur from Madagascar. PLoS biology, 23(2), e3003015.

Kayaalp B, et al. (2025) Inherited burden for disease predisposition in diverse populations. Research square.

Foguet C, et al. (2025) Metabolic reaction fluxes as amplifiers and buffers of risk alleles for coronary artery disease. Molecular systems biology, 21(6), 676.