Resource Summary Report

Generated by T1D on Jul 31, 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: data analysis service, data analysis software, service resource, software application, data processing software, production service resource, software resource, analysis service 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: 20260801T042604+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 T1D .

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.

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.

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.

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.

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.

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.

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.

Liu C, et al. (2025) Sodium azide mutagenesis induces a unique pattern of mutations. PLoS genetics, 21(6), e1011634.

Shilbayeh SAR, et al. (2025) Genetic polymorphisms as predictors of the response of hepatocellular carcinoma patients to doxorubicin chemotherapy: a genome-wide association study. Frontiers in pharmacology, 16, 1604473.

Sun Y, et al. (2025) A protein-based classifier for differentiating follicular thyroid adenoma and carcinoma. EMBO molecular medicine, 17(7), 1519.

Capon SJ, et al. (2025) A genetic modifier links integrin ??5 to the phenotypic variation in fibronectin 1a mutant zebrafish. PLoS genetics, 21(6), e1011747.

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

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).

Akatsuka H, et al. (2025) Molecular and genetic evidence for the role of AMBRA1 in suppressing S-phase entry and tumorigenesis. iScience, 28(8), 113054.

Zhang S, et al. (2025) Health risks and genetic architecture of objectively measured multidimensional sleep health. Nature communications, 16(1), 7026.

Chevallier L, et al. (2025) The RSPO2 gene is associated with bilateral anterior amelia in Chihuahuas. Mammalian genome : official journal of the International Mammalian Genome Society, 36(3), 746.

Williamson J, et al. (2025) Dramatic Responses to High-Dose Ipilimumab Plus Temozolomide After Progression on Standard- or Low-Dose Ipilimumab in Advanced Melanoma. Current oncology (Toronto, Ont.), 32(3).

Ma X, et al. (2025) Neanderthal adaptive introgression shaped LCT enhancer region diversity without linking to lactase persistence in East Asian populations. Proceedings of the National Academy of Sciences of the United States of America, 122(11), e2404393122.