Resource Summary Report

Generated by RRID on Aug 2, 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: 20260801T190247+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 RRID .

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.

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.

Kim SY, et al. (2025) Organoid drug profiling identifies methotrexate as a therapy for SCCOHT, a rare pediatric cancer. Science advances, 11(9), eadq1724.

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.

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.

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.

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

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

Wen S, et al. (2025) Association Analysis of the Circulating Proteome With Sarcopenia-Related Traits Reveals Potential Drug Targets for Sarcopenia. Journal of cachexia, sarcopenia and muscle, 16(1), e13720.

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

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).

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).

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.

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.

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.

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.

Van Swearingen AED, et al. (2025) Genomic and immune profiling of breast cancer brain metastases. Acta neuropathologica communications, 13(1), 99.