Resource Summary Report

Generated by NIF on Aug 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: production service resource, software resource, data analysis service, software application, analysis service resource, data analysis software, service resource, data processing software

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: 20260808T185832+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 NIF .

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.

Nørgaard M, et al. (2025) Deep targeted sequencing of circulating tumor DNA to inform treatment in patients with metastatic castration-resistant prostate cancer. Journal of experimental & clinical cancer research : CR, 44(1), 120.

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.

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.

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.

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

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.

Jing X, et al. (2025) Protein-truncating variants in UQCRC1 are associated with Parkinson's disease: evidence from half-million people. NPJ Parkinson's disease, 11(1), 120.

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

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.

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).

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

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.

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).

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.