Resource Summary Report

Generated by T1D on Jul 31, 2026

VarScan

RRID:SCR_006849
Type: Tool

Proper Citation

VarScan (RRID:SCR_006849)

Resource Information

URL: https://varscan.sourceforge.net/

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Description: Platform-independent, technology-independent software tool for identifying SNPs and indels in massively parallel sequencing of individual and pooled samples. Given data for a single sample, VarScan identifies and filters germline variants based on read counts, base quality, and allele frequency. Given data for a tumor-normal pair, VarScan also determines the somatic status of each variant (Germline, Somatic, or LOH) by comparing read counts between samples. (entry from Genetic Analysis Software).

Abbreviations: VarScan, VarScan 2

Synonyms: Varscan2, VarScan - variant detection in massively parallel sequencing data, Varscan

Resource Type: software resource, software application

Defining Citation: PMID:22300766, PMID:19542151, DOI:10.1101/gr.129684.111

Keywords: gene, genetic, genomic, java, illumina, solid, life/pgm, roche/454, next-generation sequencing, variant, mutation caller, exome, whole-genome, snp, copy number alteration, somatic mutation, subclonal mutation, mutation, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: VarScan

Resource ID: SCR_006849

Alternate IDs: , nlx_154687, biotools:varscan, OMICS_00094

Alternate URLs: http://varscan.sourceforge.net/, http://dkoboldt.github.io/varscan/, https://bio.tools/varscan, https://sources.debian.org/src/varscan/

Old URLs: http://genome.wustl.edu/software/varscan, http://tvap.genome.wustl.edu/tools/varscan/

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260731T042728+0000

Ratings and Alerts

No rating or validation information has been found for VarScan.

No alerts have been found for VarScan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1769 mentions in open access literature.

Listed below are recent publications. The full list is available at T1D .

Yang Q, et al. (2026) Molecular mechanism of resistance to lonafarnib conferred by mutations in the cysteine-rich region of respiratory syncytial virus fusion glycoprotein and discovery of a lonafarnib-derived antiviral PROTAC. Journal of virology, 100(1), e0148725.

Lee D, et al. (2025) Increased local DNA methylation disorder in AMLs with DNMT3A-destabilizing variants and its clinical implication. Nature communications, 16(1), 560.

Hu Q, et al. (2025) Circulating tumor DNA monitoring detects minimal residual disease and predicts outcomes in patients with esophageal adenocarcinoma or squamous cell carcinoma after esophagectomy. BJC reports, 3(1), 52.

Chauhan PS, et al. (2025) Genomic and Epigenomic Analysis of Plasma Cell-Free DNA Identifies Stemness Features Associated with Worse Survival in Lethal Prostate Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(1), 151.

Ye F, et al. (2025) Characteristics and filtering of low-frequency artificial short deletion variations based on nanopore sequencing. GigaScience, 14.

Xie D, et al. (2025) Deciphering genomic evolution of metastatic organotropism with 535 paired primary lung cancers and metastases. Cell reports, 44(10), 116449.

Peng T, et al. (2025) Individualized patient tumor organoids faithfully preserve human brain tumor ecosystems and predict patient response to therapy. Cell stem cell, 32(4), 652.

Umeda M, et al. (2025) Fusion oncoproteins and cooperating mutations define disease phenotypes in NUP98-rearranged leukemia. medRxiv : the preprint server for health sciences.

Liu M, et al. (2025) Sex disparities in the association between rare earth elements exposure and genetic mutation frequencies in lung cancer patients. Scientific reports, 15(1), 2185.

Zhang Y, et al. (2025) M6Allele: a toolkit for detection of allele-specific RNA N6-methyladenosine modifications. GigaScience, 14.

Smith JD, et al. (2025) Genomic Signatures of Poor Prognosis in Merkel Cell Carcinoma: A Single-Institution Prospective Study. Molecular cancer research : MCR.

Andersson N, et al. (2025) Tracing metastatic spread in pediatric solid tumors using copy number and targeted deep sequencing. The Journal of pathology.

Ishino T, et al. (2025) Immunopeptidomics combined with full-length transcriptomics uncovers diverse neoantigens. Cell reports, 45(1), 116781.

Sabatini PJB, et al. (2025) Multisite clinical cross-validation and variant interpretation of a next generation sequencing panel for lymphoid cancer prognostication. Journal of clinical pathology, 78(3), 187.

Wang G, et al. (2025) Comparative genomic analysis unveiling the mutational landscape associated with premalignant lesions and early-stage gastric cardia cancer. Medicine, 104(2), e40332.

Xiong Y-R, et al. (2025) Patterns of spontaneous and induced genomic alterations in Yarrowia lipolytica. Applied and environmental microbiology, 91(1), e0167824.

Huang Y, et al. (2025) RMVar 2.0: an updated database of functional variants in RNA modifications. Nucleic acids research, 53(D1), D275.

Zhang T, et al. (2025) Neoadjuvant fuzuloparib combined with abiraterone for localized high-risk prostate cancer (FAST-PC): A single-arm phase 2 study. Cell reports. Medicine, 6(3), 102018.

Zhao Y, et al. (2025) Pancreatic liposarcoma: A case report. Oncology letters, 29(6), 268.

Maruyama K, et al. (2025) Mechanisms of KRAS inhibitor resistance in KRAS-mutant colorectal cancer harboring Her2 amplification and aberrant KRAS localization. NPJ precision oncology, 9(1), 4.