Resource Summary Report

Generated by NIF on Apr 19, 2025

VARSCAN

RRID:SCR_006849
Type: Tool

Proper Citation

VARSCAN (RRID:SCR_006849)

Resource Information

URL: http://tvap.genome.wustl.edu/tools/varscan/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 7,2024. 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

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

Resource Type: software application, software resource

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

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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

Record Creation Time: 20220129T080238+0000

Record Last Update: 20250419T055059+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 1739 mentions in open access literature.

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

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.

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.

Kamilari E, et al. (2025) Bacillus safensis APC 4099 has broad-spectrum antimicrobial

activity against both bacteria and fungi and produces several antimicrobial peptides, including the novel circular bacteriocin safencin E. Applied and environmental microbiology, 91(1), e0194224.

Lucek K, et al. (2025) Genomic implications of the repeated shift to self-fertilization across a species' geographic distribution. The Journal of heredity, 116(1), 43.

Walsh R, et al. (2025) A Rare Noncoding Enhancer Variant in SCN5A Contributes to the High Prevalence of Brugada Syndrome in Thailand. Circulation, 151(1), 31.

Mendeville MS, et al. (2025) Integrating genetic subtypes with PET scan monitoring to predict outcome in diffuse large B-cell lymphoma. Nature communications, 16(1), 109.

Fathi Kazerooni A, et al. (2025) Multiparametric MRI along with machine learning predicts prognosis and treatment response in pediatric low-grade glioma. Nature communications, 16(1), 340.

Lu WT, et al. (2025) TRACERx analysis identifies a role for FAT1 in regulating chromosomal instability and whole-genome doubling via Hippo signalling. Nature cell biology, 27(1), 154.

Martins Rodrigues F, et al. (2025) Germline predisposition in multiple myeloma. iScience, 28(1), 111620.

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.

Hao W, et al. (2025) Advances in predicting breast cancer driver mutations: Tools for precision oncology (Review). International journal of molecular medicine, 55(1).

Subramanian DN, et al. (2025) Assessment of candidate high-grade serous ovarian carcinoma predisposition genes through integrated germline and tumour sequencing. NPJ genomic medicine, 10(1), 1.

Leko V, et al. (2025) Utilization of primary tumor samples for cancer neoantigen discovery. Journal for immunotherapy of cancer, 13(1).

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.

Liu M, et al. (2024) Unveiling the metal mutation nexus: Exploring the genomic impacts of heavy metal exposure in lung adenocarcinoma and colorectal cancer. Journal of hazardous materials, 461, 132590.

Gardi N, et al. (2024) Natural History of Germline BRCA1 Mutated and BRCA Wild-type Triple-negative Breast Cancer. Cancer research communications, 4(2), 404.

Kebede AM, et al. (2024) Comprehensive genomic characterization of hematologic malignancies at a pediatric tertiary care center. Frontiers in oncology, 14, 1498409.

Liu H, et al. (2024) Integrative molecular and spatial analysis reveals evolutionary dynamics

and tumor-immune interplay of in situ and invasive acral melanoma. Cancer cell, 42(6), 1067.