Resource Summary Report

Generated by Kravitz on Sep 10, 2026

VarScan

RRID:SCR_006849
Type: Tool

Proper Citation

VarScan (RRID:SCR_006849)

Resource Information

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

Proper Citation: VarScan (RRID:SCR_006849)

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 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

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: 20260905T133238+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 1983 mentions in open access literature.

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

Radulovich N, et al. (2026) Preclinical Combination Targeting VEGF and PI3K in a Rare, Aggressive Mixed Endometrial Carcinoma: An Applied Case Report. Cancer research communications, 6(4), 832.

Pregnall AM, et al. (2026) Metastatic progression of pheochromocytoma and paraganglioma occurs via parallel evolution. NPJ precision oncology, 10(1).

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.

Vemulamanda S, et al. (2026) Development of a Clinical Assay to Guide Patient Therapy in HPV-Associated Head and Neck Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(13), 2681.

Wang C, et al. (2026) A Deep Learning-Driven Framework Integrating Organoid-Based Functional Validation Identifies Universal Neoantigens from Recurrent Glioma Mutations. Cancer research, 86(12), 3074.

Ung M, et al. (2026) A multimodal atlas for immunotherapeutic targeting of AML surface heterogeneity. iScience, 29(4), 115337.

Gao Q, et al. (2026) ERBB2 I655V mutation correlates with efficacy of immunotherapy in gallbladder cancer. World journal of surgical oncology, 24(1).

N'Guessan A, et al. (2026) Parallel but distinct adaptive routes in the budding and fission yeasts after 10,000 generations of experimental evolution. Nature ecology & evolution,

10(4), 765.

Zhu M, et al. (2026) Integrative multi-omics analysis identified FUT9 and MS4A3 as novel immune-phenotype and prognosis biomarkers for colorectal cancer and analyze the role of FUT9 in oncoimmunology. Scientific reports, 16(1).

Zwyer M, et al. (2026) Human genetic ancestry, Mycobacterium tuberculosis diversity, and tuberculosis disease severity in Dar es Salaam, Tanzania. eLife, 14.

Hercent A, et al. (2026) Molecular alterations in high-grade neuroendocrine tumors of the small intestine. The Journal of pathology, 268(2), 215.

Zhao F, et al. (2026) Genetic landscape of Chinese colorectal cancer: insights into germline and somatic mutations. BMC cancer, 26(1).

Zhang R, et al. (2026) Genomic Instability and Adaptive Evolution Induced by RFA Insufficiency in Saccharomyces cerevisiae. Current issues in molecular biology, 48(2).

Teo HK, et al. (2026) Healthy donor T cell receptors expand functional neoantigen recognition beyond patient vaccination. Science advances, 12(16), eadz1156.

Ezquerra-Azn??rez JM, et al. (2026) New Chemical Scaffold with Antimicrobial Activity Identified in a Screening of Industrial Photoactive Compounds. Antibiotics (Basel, Switzerland), 15(3).

Krishnamachari K, et al. (2026) Improved tumor-only variant calling and mutation burden estimation with VarNet-T. Nature communications, 17(1).

Boldt J, et al. (2026) Phylogeny-Aware Metabologenomics Accurately Assigns Natural Products to Biosynthetic Gene Clusters. Microbial biotechnology, 19(1), e70298.

Li S, et al. (2026) Genomic landscape of paired primary and peritoneal metastatic lesions in gastric cancer highlights evolutionary dynamics and mutational drivers. Journal of advanced research, 81, 507.

Wei S, et al. (2026) A longitudinal, multi-omic atlas reveals the emergence of a spatially organized immunosuppressive ecosystem in resistant melanoma. Cell reports. Medicine, 7(4), 102716.

Aguilar D, et al. (2026) Beyond difficile: three novel toxin B-producing Clostridioides species from human patients with diarrhea. Emerging microbes & infections, 15(1), 2671473.