VARSCAN

RRID:SCR_006849
Type: Tool

Proper Citation

VARSCAN (RRID:SCR_006849)

Resource Information

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

Description: A 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)

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Resource Type: Resource, software resource, software application

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

Resource ID: SCR_006849

Parent Organization: SourceForge, Washington University in St. Louis; Missouri; USA

References: PMID:22300766, PMID:19542151

Availability: Acknowledgement requested

Website Status: Last checked up
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 740 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch Infrastructure.


Abascal E, et al. (2020) Screening of inmates transferred to Spain reveals a Peruvian prison as a reservoir of persistent Mycobacterium tuberculosis MDR strains and mixed infections. Scientific reports, 10(1), 2704.

Makke G, et al. (2020) Whole-Genome-Sequence-Based Characterization of Extensively Drug-Resistant Acinetobacter baumannii Hospital Outbreak. mSphere, 5(1).


