Resource Summary Report

Generated by RRID on Aug 12, 2026

VarDict

RRID:SCR_023658
Type: Tool

Proper Citation

VarDict (RRID:SCR_023658)

Resource Information

URL: https://github.com/AstraZeneca-NGS/VarDictJava

Proper Citation: VarDict (RRID:SCR_023658)

Description: Software tool as variant caller for both single and paired sample variant calling from BAM files. Implements amplicon bias aware variant calling from targeted sequencing experiments, rescue of long indels by realigning bwa soft clipped reads.Novel and versatile variant caller for next generation sequencing in cancer research.

Resource Type: software application, software resource

Defining Citation: PMID:27060149

Keywords: variant caller, BAM files, amplicon bias aware variant calling, sequencing experiments, next generation sequencing, long indels,

Funding: AstraZeneca

Availability: Free, Available for download, Freely available

Resource Name: VarDict

Resource ID: SCR_023658

License: MIT License

Record Creation Time: 20230606T050222+0000

Record Last Update: 20260810T040839+0000

Ratings and Alerts

No rating or validation information has been found for VarDict.

No alerts have been found for VarDict.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Boyle J, et al. (2026) Characterization of the Immunogenomic Landscape of Ovarian Cancer Uncovers a Distinct Subset of Endometroid Tumors Associated with High CST2 Expression and a Favorable Prognosis. Cancer research communications, 6(1), 224.

Shen B, et al. (2026) Double-dose firmonertinib as first-line treatment in patients with locally advanced or metastatic non-small-cell lung cancer harboring EGFR L858R mutation: a prospective, multicenter, phase II study (FIRM). Nature communications, 17(1), 1840.

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

Ramsheh MY, et al. (2026) Development of a LiDia-SEQ??? platform compatible breast cancer panel and testing with metastatic breast cancer patient samples: A rapid, sample-to-result, fully integrated next-generation sequencing (NGS)-based platform, LiDia-SEQ, for use at the point-of-need. The journal of liquid biopsy, 12, 100474.

Ni J, et al. (2026) Tislelizumab and Hypofractionated Radiotherapy plus Nab-Paclitaxel/Gemcitabine as Conversion Therapy for BRPC/LAPC: A Phase II Trial with Dynamic Biomarker Monitoring. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(3), 516.

Qu S, et al. (2026) Redefining Treatment Paradigms for Glioma in Adolescents and Young Adults: Population-Based Evidence for Molecular Classification. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(7), 1349.

Ye S, et al. (2025) MUTE-Seq: An Ultrasensitive Method for Detecting Low-Frequency Mutations in cfDNA With Engineered Advanced-Fidelity FnCas9. Advanced materials (Deerfield Beach, Fla.), 37(47), e05208.

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.

Yang W, et al. (2025) Deficiencies in germline DNA repair are associated with early-onset gastrointestinal cancers and inform precision prevention strategies. Journal of translational medicine, 24(1), 220.

Fei K, et al. (2025) Tumor-Informed ctDNA in Guiding First-Line Immunochemotherapy in Advanced Non-Small Cell Lung Cancers. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(48), e06565.

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.

Calvet F, et al. (2025) Sex and smoking bias in the selection of somatic mutations in human bladder. Nature, 647(8089), 436.

Axelsson TA, et al. (2025) Diagnostic and prognostic genomic aberrations in upper tract urothelial carcinoma can be identified in focal barbotage samples. BJU international, 135(5), 792.

Kapadia CD, et al. (2025) Clonal dynamics and somatic evolution of haematopoiesis in mouse. Nature, 641(8063), 681.

George SL, et al. (2025) Stratified Medicine Pediatrics: Cell-Free DNA and Serial Tumor Sequencing Identifies Subtype-Specific Cancer Evolution and Epigenetic States. Cancer discovery, 15(4), 717.

Heo S, et al. (2025) Analytical validation of a hybrid-approach combining tumor-informed and tumor-agnostic bespoke ctDNA panel assay for the sensitive detection of minimal residual disease. PloS one, 20(11), e0334282.

Salgkamis D, et al. (2024) Systematic review and feasibility study on pre-analytical factors and genomic analyses on archival formalin-fixed paraffin-embedded breast cancer tissue. Scientific reports, 14(1), 18275.

Kapadia CD, et al. (2024) Clonal dynamics and somatic evolution of haematopoiesis in mouse. bioRxiv : the preprint server for biology.

Jakobsen NA, et al. (2024) Selective advantage of mutant stem cells in human clonal hematopoiesis is associated with attenuated response to inflammation and aging. Cell stem cell, 31(8), 1127.

D'Angelo SP, et al. (2024) Biomarker Analyses Investigating Disease Biology and Associations with Outcomes in the JAVELIN Merkel 200 Trial of Avelumab in Metastatic Merkel Cell Carcinoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 30(19), 4352.