Resource Summary Report

Generated by kravitz2 on Jul 30, 2026

Strelka2

RRID:SCR_005109
Type: Tool

Proper Citation

Strelka2 (RRID:SCR_005109)

Resource Information

URL: https://github.com/Illumina/strelka/

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Description: Software for somatic single nucleotide variant (SNV) and small indel detection from sequencing data of matched tumor-normal samples. Strelka2 germline and somatic small variant caller.

Synonyms: Strelka

Resource Type: source code, software resource

Defining Citation: PMID:22581179, PMID:30013048

Keywords: single nucleotide variant, indel, somatic snv, next-generation sequencing, bio.tools

Related Condition: Cancer, Tumor, Normal

Availability: Free, Available for download, Freely available

Resource Name: Strelka2

Resource ID: SCR_005109

Alternate IDs: biotools:strelka

Alternate URLs: https://bio.tools/strelka, https://sources.debian.org/src/strelka/

Old URLs: http://bioinformatics.oxfordjournals.org/content/early/2012/05/10/bioinformatics.bts271.full.pdf

License: GNU GPL v3

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260729T044113+0000

Ratings and Alerts

No rating or validation information has been found for Strelka2.

No alerts have been found for Strelka2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 261 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

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.

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

Rebello RJ, et al. (2025) Whole genome sequencing improves tissue-of-origin diagnosis and treatment options for cancer of unknown primary. Nature communications, 16(1), 4422.

Lu S, et al. (2025) Safety and feasibility of anlotinib in children with high risk, recurrent or refractory sarcomas: an open-label, single-centre, single-arm, phase Ia/Ib trial. EClinicalMedicine, 84, 103258.

Fiorica PN, et al. (2025) Germline Pathogenic DROSHA Variants Are Linked to Pineoblastoma and Wilms Tumor Predisposition. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(8), 1491.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. Cancer discovery, 15(8), 1630.

Ishikawa R, et al. (2025) Immunohistochemical and molecular evolutionary features of jejunoileal adenocarcinoma unveiled through comparative analysis with colorectal adenocarcinoma. Neoplasia (New York, N.Y.), 66, 101180.

Lilljebjörn H, et al. (2025) The AML cellular state space unveils NPM1 immune evasion subtypes with distinct clinical outcomes. Nature communications, 16(1), 10592.

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.

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

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. Cancer discovery, 15(6), 1203.

Ku AT, et al. (2025) Radiogenomic Profiling of Prostate Tumors prior to External Beam Radiotherapy Converges on a Transcriptomic Signature of TGF-? Activity Driving Tumor Recurrence. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(24), 5211.

Sun J, et al. (2025) TP53 gene mutation in lymphoepithelioma?like carcinoma of the breast with thyroid cancer: A case report. Oncology letters, 29(5), 247.

Kratz JD, et al. (2025) Subclonal response heterogeneity to define cancer organoid therapeutic sensitivity. Scientific reports, 15(1), 12072.

Roush SM, et al. (2025) Shared genomic features of HIV+ diffuse large B-cell lymphoma in two African cohorts. Scientific reports, 15(1), 24599.

Lüönd F, et al. (2025) DLBCL Cells Emerge after CD19 CAR T Cells with Cross-Antigen Resistance and a Gene Signature Predictive of Clinical CAR T-cell Response. Blood cancer discovery, 6(6), 580.

He S, et al. (2025) Comprehensive assessment of computational methods for cancer immunoediting. Cell reports methods, 5(3), 101006.

Bergsma P, et al. (2025) Integration of Whole-Genome Sequencing Analysis with Unique Patient-Derived Models Reveals Clinically Relevant Drug Targets in TFCP2 Fusion-Defined Rhabdomyosarcoma. Molecular cancer therapeutics, 24(12), 1989.

Stanciu A, et al. (2025) Personalized ctDNA detection and genomic profiling in the NeoRHEA Study. NPJ breast cancer, 11(1), 137.

Lawson-Michod KA, et al. (2025) Homologous recombination deficiency in ovarian high-grade serous carcinoma by self-reported race. medRxiv : the preprint server for health sciences.