Resource Summary Report

Generated by dkNET on Sep 5, 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: software resource, source code

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: 20260904T000612+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 283 mentions in open access literature.

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

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.

Yang W, et al. (2026) Clinically actionable stratification of uncommon MET fusions: a precision oncology framework. Journal of translational medicine, 24(1).

Li Q, et al. (2026) Revealing the Potential Associations of Mutation-Related Genes with Lymph Node Metastasis in Gallbladder Cancer Through Transcriptome and Exome Sequencing. Biomedicines, 14(5).

Tirtei E, et al. (2026) Mapping Genomic Heterogeneity in Pediatric and Adolescent-Young Adult Sarcomas: Insights from the Italian SAR-GEN2016 and SAR-GEN_ITA Prospective Multicenter Trials. Cancer research communications, 6(4), 857.

Andersen L, et al. (2026) Cell-Free DNA-Derived Immune Cell Ratios Uncover Cancer-Associated Systemic Changes. Cancer research communications, 6(4), 811.

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.

Bhojnagarwala PS, et al. (2026) synDNA vaccine against TCR chains and neoantigens for T cell lymphoma therapy. Cancer immunology, immunotherapy : CII, 75(3), 80.

Bassiouni R, et al. (2026) Integrated Single-Cell Whole-Genome Sequencing and Spatial Transcriptomics Reveal Intratumoral Heterogeneity in Ovarian Cancer. Cancer research

communications, 6(5), 1020.

Shi Y, et al. (2026) Genomic, Clinical, and Spatial Predictors of Durable Response to BRAF/MEK Inhibition in BRAF-Mutant Melanoma. bioRxiv : the preprint server for biology.

Roush SM, et al. (2026) Mutational profiling of HIV+ diffuse large B-cell lymphoma reveals distinct mutational features with evidence of genomic instability. AIDS (London, England), 40(6), 719.

Adhikary U, et al. (2026) Cancer Susceptibility to Stapled Oncolytic Peptides Is Dictated by Membrane Cholesterol and Inflammatory Signaling. Cancer research, 86(11), 2810.

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.

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

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

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.

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.

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.

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.

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.