Resource Summary Report

Generated by dkNET on Aug 20, 2026

Pindel

RRID:SCR_000560
Type: Tool

Proper Citation

Pindel (RRID:SCR_000560)

Resource Information

URL: http://gmt.genome.wustl.edu/pindel/0.2.4/

Proper Citation: Pindel (RRID:SCR_000560)

Description: Software to detect breakpoints of large deletions, medium sized insertions, inversions, tandem duplications and other structural variants at single-based resolution from next-gen sequence data. It uses a pattern growth approach to identify the breakpoints of these variants from paired-end short reads., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Pindel

Resource Type: software resource

Defining Citation: PMID:19561018

Keywords: deletion, insertion, nucleotide, genome, read, inversion, tandem duplication, structural variant, next-generation sequencing, pattern growth, indel, breakpoint, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Pindel

Resource ID: SCR_000560

Alternate IDs: biotools:pindel, OMICS_00321

Alternate URLs: https://bio.tools/pindel

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260815T182146+0000

Ratings and Alerts

No rating or validation information has been found for Pindel.

No alerts have been found for Pindel.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Tang C, et al. (2026) Investigating the determinants of immunotherapy response in the primary tumour of clear cell renal cell carcinoma (RCC). BMJ oncology, 5(2), e001031.

Chen J, et al. (2026) A Genomically Tailored Multiagent Precision Medicine Clinical Trial for Adults with Recurrent Glioblastoma. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(9), 1652.

Chang HY, et al. (2026) Uniform Processing of Diverse Sequencing Data: A Cross-Population Comparison of Colon Cancer Genomic Landscapes from The Cancer Genome Atlas and a Chinese Cohort. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology, 35(5), 762.

Li YR, et al. (2025) Long-Term Latency of Highly Mutated Cells in Normal Mouse Skin Is Reversed by Exposure to Tumor Promoters and Chronic Tissue Damage. Cancer discovery, 15(6), 1115.

Lee LH, et al. (2025) Defining Non-small Cell Lung Cancer Tumor Microenvironment Changes at Primary and Acquired Immune Checkpoint Inhibitor Resistance Using Clinical and Real-World Data. Cancer research communications, 5(6), 1049.

Ghani H, et al. (2025) GPSai: A Clinically Validated AI Tool for Tissue of Origin Prediction during Routine Tumor Profiling. Cancer research communications, 5(9), 1477.

Wisniewski DJ, et al. (2025) Dual inhibition of EGFR and PI3Kinase signaling in EGFR amplified triple negative breast cancer cells induces apoptosis and reduces tumor growth. bioRxiv : the preprint server for biology.

Varadarajan K, et al. (2025) Efficacy of ATR Kinase Inhibitor Elimusertib Monotherapy or Combination in Tumors with DNA Damage Response Pathway and Other Genomic Alterations. Molecular cancer therapeutics, 24(9), 1402.

DiPeri TP, et al. (2024) Utilizing Patient-derived Xenografts to Model Precision Oncology for Biliary Tract Cancer. Clinical cancer research : an official journal of the American Association for Cancer Research.

Lheureux S, et al. (2023) Identifying Mechanisms of Resistance by Circulating Tumor DNA in EVOLVE, a Phase II Trial of Cediranib Plus Olaparib for Ovarian Cancer at Time of PARP Inhibitor Progression. Clinical cancer research : an official journal of the American Association for Cancer Research, 29(18), 3706.

Louw N, et al. (2023) Incorporating CNV analysis improves the yield of exome sequencing for rare monogenic disorders-an important consideration for resource-constrained settings. Frontiers in genetics, 14, 1277784.

Spitzer B, et al. (2022) Bone Marrow Surveillance of Pediatric Cancer Survivors Identifies Clones that Predict Therapy-Related Leukemia. Clinical cancer research : an official journal of the American Association for Cancer Research, 28(8), 1614.

Cao Q, et al. (2021) Dynamics of the Auditory Continuity Illusion. Frontiers in computational neuroscience, 15, 676637.

Kolora SRR, et al. (2019) Divergent evolution in the genomes of closely related lacertids, Lacerta viridis and L. bilineata, and implications for speciation. GigaScience, 8(2).

Lee B, et al. (2018) Clinical Relevance of Genomic Changes in Recurrent Pediatric Solid Tumors. Translational oncology, 11(6), 1390.

Maes T, et al. (2018) ORY-1001, a Potent and Selective Covalent KDM1A Inhibitor, for the Treatment of Acute Leukemia. Cancer cell, 33(3), 495.

Radovich M, et al. (2018) The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer cell, 33(2), 244.

Goryca K, et al. (2018) Exome scale map of genetic alterations promoting metastasis in colorectal cancer. BMC genetics, 19(1), 85.

Booth CAG, et al. (2018) Ezh2 and Runx1 Mutations Collaborate to Initiate Lympho-Myeloid Leukemia in Early Thymic Progenitors. Cancer cell, 33(2), 274.

Jing D, et al. (2018) Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. Cancer cell, 34(6), 906.