Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 30, 2025

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.

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

Funding:

Availability: Acknowledgement requested, GNU General Public License, v3

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: 20250420T013954+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 17 mentions in open access literature.

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

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.

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

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.

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

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

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

, et al. (2017) Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 171(4), 950.

Kotini AG, et al. (2017) Stage-Specific Human Induced Pluripotent Stem Cells Map the Progression of Myeloid Transformation to Transplantable Leukemia. Cell stem cell, 20(3), 315.

Smith SD, et al. (2017) Lightning-fast genome variant detection with GROM. GigaScience, 6(10), 1.

Marchant TW, et al. (2017) Canine Brachycephaly Is Associated with a Retrotransposon-Mediated Missplicing of SMOC2. Current biology : CB, 27(11), 1573.

Chang CW, et al. (2015) Modeling Human Severe Combined Immunodeficiency and Correction by CRISPR/Cas9-Enhanced Gene Targeting. Cell reports, 12(10), 1668.