Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

DELLY

RRID:SCR_004603
Type: Tool

Proper Citation

DELLY (RRID:SCR_004603)

Resource Information

URL: https://tobiasrausch.com/delly/

Proper Citation: DELLY (RRID:SCR_004603)

Description: Integrated structural variant prediction software that can detect deletions, tandem duplications, inversions and translocations at single-nucleotide resolution in short-read massively parallel sequencing data. It uses paired-ends and split-reads to sensitively and accurately delineate genomic rearrangements throughout genome.

Abbreviations: DELLY

Synonyms: DELLY, Structural variant discovery by integrated paired-end and split-read analysis

Resource Type: software resource

Defining Citation: PMID:22962449, DOI:10.1093/bioinformatics/bts378

Keywords: structural variant, genomic rearrangement, deletion, tandem duplication, inversion, translocation, bio.tools

Resource Name: DELLY

Resource ID: SCR_004603

Alternate IDs: OMICS_00313, biotools:delly2

Alternate URLs: https://bio.tools/delly2, https://github.com/dellytools/delly/, https://sources.debian.org/src/delly/

License: BSD 3-Clause

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260903T234723+0000

Ratings and Alerts

No rating or validation information has been found for DELLY.

No alerts have been found for DELLY.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 639 mentions in open access literature.

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

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.

Valentín López JC, et al. (2026) Evolution of AR and Non-AR Alterations in ctDNA of Patients with Metastatic Prostate Cancer Treated in the Phase III Alliance A031201 Trial. Clinical cancer research : an official journal of the American Association for Cancer Research, 32(12), 2413.

Kamimae-Lanning AN, et al. (2026) Metabolite-induced DNA damage drives stochastic stem cell loss and clonal hematopoiesis. Cell stem cell, 33(4), 642.

Han SY, et al. (2026) Hearing loss phenotypes in Alport syndrome: experience in a tertiary referral center. Kidney research and clinical practice, 45(3), 357.

Everall A, et al. (2026) Comprehensive repertoire of the chromosomal alteration and mutational signatures across 16 cancer types. Nature genetics, 58(3), 570.

McClelland P, et al. (2026) A multi-ancestry genetic reference for the Quebec population. Nature communications, 17(1), 1319.

Sui Y, et al. (2026) Using the linear references from the pangenome to discover missing autism variants. Nature communications, 17(1), 1681.

Chen Q, et al. (2026) Full spatio-temporal analyses of migration and colonization in evolution-dense 3D mapping of cancer metastases provides new insights. Molecular biology and evolution, 43(2).

Modlin SJ, et al. (2026) Updated Erdman reveals tandem repeat copy number is phase-variable and impacts M. tuberculosis adaptation across evolutionary timescales. mSystems, 11(1), e0102625.

Dong Y, et al. (2026) Structural variation drives enhancer hijacking via 3D genome disruption in ccRCC. NPJ digital medicine, 9(1), 85.

Schifano A, et al. (2026) Mutational biases and selection in mitochondrial genomes: insights from a comparative analysis of natural and laboratory populations of Caenorhabditis elegans. G3 (Bethesda, Md.), 16(3).

Zhang H, et al. (2026) The clinical application value of dynamic monitoring of HPV ctDNA in concurrent chemoradiotherapy for locally advanced cervical cancer. NPJ precision oncology, 10(1).

Tergemina E, et al. (2026) Convergent evolution increases boron transport through SNPs and tandem duplications at BOR1 and BOR2 in Arabidopsis thaliana. Proceedings of the National Academy of Sciences of the United States of America, 123(13), e2525676123.

de Diego Fuertes M, et al. (2026) Targeted and whole-genome sequencing for drug resistance and genetic relatedness inference of rifampicin-resistant Mycobacterium tuberculosis: an in-depth comparison. ERJ open research, 12(1).

Zhang J, et al. (2026) Cancer genome standards for long-read sequencing using cancer cell line mixtures. GigaScience, 15.

Corazzi L, et al. (2026) Recurrent DNA break clusters drive replication-stress-induced copy number variants and genome diversification. Nature communications, 17(1).

de Araujo AT, et al. (2026) KitBase Expanded: An Integrated Genomic and Phenotypic Resource for 3,268 Fast-Neutron-Irradiated Rice Mutants. Database : the journal of biological databases and curation, 2026.

Liu Z, et al. (2026) Fuscan: a robust DNA fusion caller for targeted sequencing data in cancer diagnostics. Bioinformatics advances, 6(1), vbag152.

Kim Y, et al. (2026) High-resolution Chromosomal Microarray with Diagnostic Potential for Detecting Exon-level Copy Number Variations Using Targeted and Non-targeted Approaches. Annals of laboratory medicine, 46(2), 190.

Quarello P, et al. (2026) DNA Methylation Episignature as a Novel Diagnostic Tool for Diamond-Blackfan Anemia Syndrome. American journal of hematology, 101(2), 228.