

Resource Summary Report

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DELLY

RRID:SCR_004603

Type: Tool

Proper Citation

DELLY (RRID:SCR_004603)

Resource Information

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

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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: 20260905T132521+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 [Kravitz](#).

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.