

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

BREAKDANCER

RRID:SCR_001799

Type: Tool

Proper Citation

BREAKDANCER (RRID:SCR_001799)

Resource Information

URL: <http://gmt.genome.wustl.edu/packages/breakdancer/>

Proper Citation: BREAKDANCER (RRID:SCR_001799)

Description: A Perl/C++ software package that provides genome-wide detection of structural variants from next generation paired-end sequencing reads. BreakDancerMax predicts five types of structural variants: insertions, deletions, inversions, inter- and intra-chromosomal translocations from next-generation short paired-end sequencing reads using read pairs that are mapped with unexpected separation distances or orientation. (entry from Genetic Analysis Software)

Abbreviations: BreakDancer

Resource Type: software application, software resource

Defining Citation: [PMID:19668202](#)

Keywords: gene, genetic, genomic, perl, c++, next generation sequencing, structural variant, insertion, deletion, inversion, inter-chromosomal translocation, intra-chromosomal translocation, chromosomal translocation, indel, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: BREAKDANCER

Resource ID: SCR_001799

Alternate IDs: biotools:breakdancer, nlx_154253, OMICS_00307

Alternate URLs: <https://bio.tools/breakdancer>

License: GNU General Public License, v3

Record Creation Time: 20220129T080209+0000

Ratings and Alerts

No rating or validation information has been found for BREAKDANCER.

No alerts have been found for BREAKDANCER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 370 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Garcia GL, et al. (2025) Aged and BRCA-Mutated Stromal Cells Drive Epithelial Cell Transformation. *Cancer discovery*, 15(6), 1203.

Cong P, et al. (2025) Molecular characterization of Echinocandin resistance and the CHS3-mediated adaptive response in *Candida glabrata* bloodstream infections in Eastern China. *BMC microbiology*, 25(1), 490.

Zhang Q, et al. (2025) LINC01235 Promotes Clonal Evolution through DNA Replication Licensing-Induced Chromosomal Instability in Breast Cancer. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(14), e2413527.

Xiao H, et al. (2025) Uncovering minimal pathways in melanoma initiation. *Nature communications*, 16(1), 5369.

Dandasena D, et al. (2025) Genomic characterization of host gene alterations in *Theileria annulata*-transformed leukocytes. *Communications biology*, 8(1), 1622.

Chen Y, et al. (2025) Comprehensive characterization of PD-L1 expression and immunotherapy-related genomic biomarkers in early- versus advanced-stage non-small cell lung cancer. *BMC pulmonary medicine*, 25(1), 219.

Ma W, et al. (2025) Whole-genome and whole-exome sequencing of Mayer-Rokitansky-Küster-Hauser syndrome-discordant monozygotic twins. *Journal of assisted reproduction and genetics*, 42(5), 1577.

Zhao M, et al. (2025) RNA sequencing and genome-wide association analysis reveal key genes responsible for different feather colors in Youjiang goose. *Poultry science*, 104(8), 105305.

Hameed HMA, et al. (2025) The Identification of Novel Mutations in ATP-Dependent Protease ClpC1 Assists in the Molecular Diagnosis of Obscured Pyrazinamide-Resistant Tuberculosis Clinical Isolates. *Microorganisms*, 13(6).

Zhao S, et al. (2025) Benchmarking strategies for CNV calling from whole genome bisulfite data in humans. *Computational and structural biotechnology journal*, 27, 912.

Jin L, et al. (2025) The evolving landscape of genetic biomarkers for immunotherapy in primary and metastatic breast cancer. *Frontiers in oncology*, 15, 1522262.

Su SC, et al. (2025) Multimodal profiling of oral squamous cell carcinoma identifies genomic alterations and expression programs associated with betel quid chewing. *Neoplasia (New York, N.Y.)*, 68, 101218.

Wei ZG, et al. (2025) Neoadjuvant tislelizumab with afatinib for locally advanced head and neck squamous cell carcinoma (neoCHANCE-1): a phase 2 clinical trial. *Nature communications*, 16(1), 8918.

Zech M, et al. (2025) Combined genomics and proteomics unveils elusive variants and vast aetiologic heterogeneity in dystonia. *Brain : a journal of neurology*, 148(8), 2827.

Wang F, et al. (2025) ARTP mutagenesis for genome-wide identification of genes important for biofilm regulation in spoilage bacterium *Pseudomonas fluorescens* PF08. *Applied and environmental microbiology*, 91(6), e0021825.

Mok KC, et al. (2025) Laboratory evolution of *E. coli* with a natural vitamin B12 analog reveals roles for cobamide uptake and adenosylation in methionine synthase-dependent growth. *Journal of bacteriology*, 207(2), e0028424.

Du R, et al. (2025) Comparative study of tools for copy number variation detection using next-generation sequencing data. *Scientific reports*, 15(1), 22145.

Liu K, et al. (2025) Analysis of genetic differences underlying chilling stress tolerance using whole genome Re-Sequencing in walnut (*Juglans regia* L.). *BMC genomics*, 26(1), 934.

García-Berro A, et al. (2025) A north-south hemispheric migratory divide in the butterfly *Vanessa cardui*. *Nature communications*, 16(1), 11341.

Chen Z, et al. (2025) Conditional lethality and suppressor analysis of plasmid-based temperature-sensitive *fabZ* expression in *Pseudomonas aeruginosa*. *The Journal of biological chemistry*, 301(6), 108553.