

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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 390 mentions in open access literature.

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

Si YW, et al. (2026) Evolution of rhizobial siderophore utilization via accessory xeno-siderophore receptors and flexible intake machinery for self-produced siderophores. The ISME journal, 20(1).

Tasnawijitwong N, et al. (2026) Characterization of adaptive evolution strains for the development of triclosan resistance in *Agrobacterium tumefaciens* C58. Applied and environmental microbiology, 92(1), e0123225.

Zhang J, et al. (2026) Genomic resequencing provides new insights into ecological diversification of four *Saccharina Japonica* varieties. BMC genomics, 27(1).

Liu L, et al. (2026) Exploring Speckle Change Genes of *Rhynchophorus ferrugineus* (Coleoptera: Curculionidae) Based on Genome-Wide Association Studies (GWASs). Biology, 15(7).

Tang Y, et al. (2026) Genomic variation analysis and discovery of stable heterozygous loci in Loquat (*Eriobotrya Japonica* Lindl.). BMC plant biology, 26(1).

Ma Q, et al. (2026) The pan-genome provides insights into evolutionary dynamics and fatty acid metabolism in Aceraceae family. Genome biology, 27(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.

Bohner F, et al. (2026) Micafungin microevolution in *Candida auris* reveals resistance development without in vivo fitness compromise. Virulence, 17(1), 2664993.

Kubo S, et al. (2026) Characterization of fucoxanthin-deficient strains in the haptophyte *Tisochrysis lutea* induced by heavy-ion beam irradiation. Plant & cell physiology, 67(3), 265.

Dan Z, et al. (2026) Additive and Partially Dominant Effects from Genomic Variation Contribute to Rice Heterosis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(20), e23376.

Wang J, et al. (2026) Whole-Genome Resequencing of *Cucurbita maxima* and *Cucurbita moschata* Provides Insights into Genomic Variants Associated with Morphology and Quality Traits. *International journal of molecular sciences*, 27(11).

Chai Y, et al. (2026) A Comprehensive Adenoid Cystic Carcinoma-Derived Organoid Platform for Disease Modeling and Drug Screening Captures Interpatient Heterogeneity. *Cells*, 15(4).

Houtman AH, et al. (2026) Genomic fusion breakpoints for DNA-based measurable residual disease monitoring in pediatric acute lymphoblastic leukemia. *Leukemia*, 40(6), 1261.

Fu M, et al. (2026) Dual-single-guide RNA strategy improves CRISPR-mediated homology-directed repair in *Aspergillus*. *Nucleic acids research*, 54(4).

Kerkeni N, et al. (2026) First Detection of 1p36 Deletion by Whole-Exome Sequencing in a Tunisian Patient. *Birth defects research*, 118(1), e70017.

Marangoni S, et al. (2026) GeNePi: a graphics processing unit enhanced next-generation bioinformatics pipeline for whole-genome sequencing analysis. *Briefings in bioinformatics*, 27(1).

Wang YH, et al. (2026) Association of homologous recombination repair gene mutation with clinical prognosis in histological subtypes of epithelial ovarian cancer patients. *Journal of gynecologic oncology*, 37(3), e35.

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

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

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.