

Resource Summary Report

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BREAKDANCER

RRID:SCR_001799

Type: Tool

Proper Citation

BREAKDANCER (RRID:SCR_001799)

Resource Information

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

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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 [ASWG](#) .

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.

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

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

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).

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

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.

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.

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).

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.

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).

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).

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

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.

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.

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