

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 resource, software application

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 [ASWG](#) .

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

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.

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.

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

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.

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.

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.

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.

Vialle RA, et al. (2025) Structural variants linked to Alzheimer's disease and other common age-related clinical and neuropathologic traits. *Genome medicine*, 17(1), 20.