

Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 2026

BreakSeq

RRID:SCR_001186

Type: Tool

Proper Citation

BreakSeq (RRID:SCR_001186)

Resource Information

URL: <http://sv.gersteinlab.org/breakseq/>

Proper Citation: BreakSeq (RRID:SCR_001186)

Description: Software for scanning reads from short-read sequenced genomes against a human breakpoint library to accurately identify structural variants (SVs). The library of breakpoints at nucleotide resolution were assembled from collating and standardizing ~2,000 published structural variants (SVs). For each breakpoint, its ancestral state (through comparison to primate genomes) was inferred and its mechanism of formation (e.g., nonallelic homologous recombination, NAHR).

Abbreviations: BreakSeq

Synonyms: Breakpoint Library and BreakSeq

Resource Type: software resource

Defining Citation: [PMID:20037582](#)

Keywords: structural variant, breakpoint, nucleotide, fasta, gff, bowtie, genomic variation, junction mapping, insertion sequence, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BreakSeq

Resource ID: SCR_001186

Alternate IDs: biotools:breakseq, OMICS_02168

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260919T194936+0000

Ratings and Alerts

No rating or validation information has been found for BreakSeq.

No alerts have been found for BreakSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Rausch T, et al. (2012) Genome sequencing of pediatric medulloblastoma links catastrophic DNA rearrangements with TP53 mutations. Cell, 148(1-2), 59.