Resource Summary Report

Generated by NIF on Apr 25, 2025

BreakSeq

RRID:SCR_001186
Type: Tool

Proper Citation

BreakSeq (RRID:SCR_001186)

Resource Information

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

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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

Funding:

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: 20250420T014022+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 NIF.

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