Resource Summary Report

Generated by NIF on Aug 9, 2026

Breakway

RRID:SCR_001180
Type: Tool

Proper Citation

Breakway (RRID:SCR_001180)

Resource Information

URL: http://sourceforge.net/apps/mediawiki/breakway/index.php

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Description: A suite of software programs that take aligned genomic data and report structural variation breakpoints. Features include: * Takes in BAM formatted input, the current standard for genomic alignments. * Compatible with standard output from major alignment algorithms such as BFAST, BWA, MAQ, et cetera. * Capable of analyzing data from any major platform--Solexa, SOLiD, 454, et cetera. * Empirically identifies structural variation breakpoints. * Highly specific analysis generates very few false positives. * Includes a suite of downstream tools for annotating identified breakpoints and reducing false positives.

Abbreviations: Breakway

Synonyms: Breakway: Identify Structural Variations in Genomic Data

Resource Type: software resource

Defining Citation: PMID:20126413

Keywords: genome, structural variation, breakpoint

Availability: Free, Available for download, Freely available

Resource Name: Breakway

Resource ID: SCR_001180

Alternate IDs: OMICS_02176

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260808T185723+0000

Ratings and Alerts

No rating or validation information has been found for Breakway.

No alerts have been found for Breakway.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We have not found any literature mentions for this resource.