Resource Summary Report

Generated by dkNET on May 21, 2025

SVseq

RRID:SCR_004804
Type: Tool

Proper Citation

SVseq (RRID:SCR_004804)

Resource Information

URL: http://www.engr.uconn.edu/~jiz08001/svseq2.html

Proper Citation: SVseq (RRID:SCR_004804)

Description: Software for accurate and efficient calling of structural variations with low-coverage sequence data. Version 2 uses the BAM files of paired Illumina reads with soft-clip signature as input. It calls both deletions and insertions.

Abbreviations: SVseq

Synonyms: SVseq2, SVseq1

Resource Type: software resource

Defining Citation: PMID:22537045

Keywords: structural variant, deletion, insertion, breakpoint, bio.tools

Funding:

Resource Name: SVseq

Resource ID: SCR_004804

Alternate IDs: OMICS_00327, biotools:svseq

Alternate URLs: https://bio.tools/svseq

Record Creation Time: 20220129T080226+0000

Record Last Update: 20250519T203336+0000

Ratings and Alerts

No rating or validation information has been found for SVseq.

No alerts have been found for SVseq.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Pirooznia M, et al. (2015) Whole-genome CNV analysis: advances in computational approaches. Frontiers in genetics, 6, 138.

Thangam M, et al. (2015) CRCDA--Comprehensive resources for cancer NGS data analysis. Database : the journal of biological databases and curation, 2015.