Resource Summary Report

Generated by NIF on Aug 31, 2026

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

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: 20260829T182200+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 3 mentions in open access literature.

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

Qin S, et al. (2025) SVseq discloses the genomic complexity of different prenatal, de novo, apparently balanced chromosome rearrangements detected by CMA and karyotype. Italian journal of pediatrics, 51(1), 155.

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.