

Resource Summary Report

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SVEngine

RRID:SCR_016235

Type: Tool

Proper Citation

SVEngine (RRID:SCR_016235)

Resource Information

URL: <https://bitbucket.org/charade/svengine>

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Description: Software for analysis and simulation of gene sequences and structural variants. This software works with FASTA, FASTQ, BAM, VAR, META, and NEWICK file formats.

Synonyms: SVEngine: Allele Specific and Haplotype Aware Structural Variants Simulator

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software, simulation software

Keywords: structural, alteration, clonality, NGS, simulator, gene, allele, haplotype, variant

Funding: NHGRI R01 HG006137;
CNSF 61370131

Availability: Free, Available to download

Resource Name: SVEngine

Resource ID: SCR_016235

License: BSD3

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260729T044412+0000

Ratings and Alerts

No rating or validation information has been found for SVEngine.

No alerts have been found for SVEngine.

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 [kravitz2](#) .

Gong T, et al. (2021) Detection of somatic structural variants from short-read next-generation sequencing data. Briefings in bioinformatics, 22(3).

Gong T, et al. (2020) Shiny-SoSV: A web-based performance calculator for somatic structural variant detection. PloS one, 15(8), e0238108.

Xia LC, et al. (2018) SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. GigaScience, 7(7).