Resource Summary Report

Generated by kravitz2 on Sep 4, 2026

SVA

RRID:SCR_002155
Type: Tool

Proper Citation

SVA (RRID:SCR_002155)

Resource Information

URL: http://www.omicsexpress.com/sva.php

Proper Citation: SVA (RRID:SCR_002155)

Description: Software package to annotate, visualize, and analyze the genetic variants identified through next-generation sequencing studies, including whole-genome sequencing (WGS) and exome sequencing studies. SVA aims to provide the research community with a user-friendly and efficient tool to analyze large amount of genetic variants, and to facilitate the identification of the genetic causes of human diseases and related traits.

Abbreviations: SVA

Synonyms: Sequence Variant Analyzer, SVA: Sequence Variant Analyzer

Resource Type: commercial organization, software application, software resource

Defining Citation: PMID:21624899

Keywords: gene, genetic, genomic, annotate, visualize, genetic variant, next-generation sequencing, whole-genome sequencing, exome, sequencing, genome, disease, trait, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SVA

Resource ID: SCR_002155

Alternate IDs: nlx_154666, OMICS_00190, biotools:sequencevariantanalyzer

Alternate URLs: http://www.svaproject.org/, https://bio.tools/sequencevariantanalyzer

Record Creation Time: 20220129T080211+0000

Record Last Update: 20260904T000400+0000

Ratings and Alerts

No rating or validation information has been found for SVA.

No alerts have been found for SVA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Katko A, et al. (2026) Gene regulatory network determinants of rapid recall in human memory CD4+ T cells. Cell reports, 45(4), 117103.

Jin N, et al. (2025) Epigenetic Modulation, Intratumoral Microbiome, and Immunity in Early-Onset Colorectal Cancer. Cancer research communications, 5(11), 1985.

Elias R, et al. (2025) Clear-Cell Renal Cell Carcinoma Molecular Subtypes Differ by African and European Genetic Similarity. Cancer research communications, 5(5), 743.

Sudalagunta PR, et al. (2024) The Functional Transcriptomic Landscape Informs Therapeutic Strategies in Multiple Myeloma. Cancer research.

April-Monn SL, et al. (2024) Patient derived tumoroids of high grade neuroendocrine neoplasms for more personalized therapies. NPJ precision oncology, 8(1), 59.

Gaare JJ, et al. (2023) Nicotinamide riboside supplementation is not associated with altered methylation homeostasis in Parkinson's disease. iScience, 26(3), 106278.

Das M, et al. (2021) Interdependence of neural network dysfunction and microglial alterations in Alzheimer's disease-related models. iScience, 24(11), 103245.

Chen MS, et al. (2020) De novo genome assembly and Hi-C analysis reveal an association between chromatin architecture alterations and sex differentiation in the woody plant Jatropha curcas. GigaScience, 9(2).

Jacob F, et al. (2020) A Patient-Derived Glioblastoma Organoid Model and Biobank Recapitulates Inter- and Intra-tumoral Heterogeneity. Cell, 180(1), 188.

Ren Q, et al. (2019) Shear stress and oxygen availability drive differential changes in opossum kidney proximal tubule cell metabolism and endocytosis. Traffic (Copenhagen, Denmark), 20(6), 448.

Panopoulos AD, et al. (2017) Aberrant DNA Methylation in Human iPSCs Associates with MYC-Binding Motifs in a Clone-Specific Manner Independent of Genetics. Cell stem cell, 20(4), 505.

He M, et al. (2015) SeqHBase: a big data toolset for family based sequencing data analysis. Journal of medical genetics, 52(4), 282.

Vasli N, et al. (2012) Next generation sequencing for molecular diagnosis of neuromuscular diseases. Acta neuropathologica, 124(2), 273.

Torri F, et al. (2012) Next generation sequence analysis and computational genomics using graphical pipeline workflows. Genes, 3(3), 545.

Lyon GJ, et al. (2012) Identifying disease mutations in genomic medicine settings: current challenges and how to accelerate progress. Genome medicine, 4(7), 58.

Sobreira NL, et al. (2010) Whole-genome sequencing of a single proband together with linkage analysis identifies a Mendelian disease gene. PLoS genetics, 6(6), e1000991.

Pelak K, et al. (2010) The characterization of twenty sequenced human genomes. PLoS genetics, 6(9), e1001111.