

Resource Summary Report

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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: software application, commercial organization, 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.svapproject.org/>, <https://bio.tools/sequencevariantanalyzer>

Record Creation Time: 20220129T080211+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 16 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

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.

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

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

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.