

Resource Summary Report

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SAMStat

RRID:SCR_005432

Type: Tool

Proper Citation

SAMStat (RRID:SCR_005432)

Resource Information

URL: <http://samstat.sourceforge.net/>

Proper Citation: SAMStat (RRID:SCR_005432)

Description: C software program for displaying sequence statistics for next generation sequencing. Works with large fasta, fastq and SAM/BAM files.

Abbreviations: SAMStat

Resource Type: software resource

Defining Citation: [PMID:21088025](#)

Keywords: sequence statistic, c, next generation sequencing, fasta file, fastq file, sam file, bam file, bio.tools

Availability: Acknowledgement requested

Resource Name: SAMStat

Resource ID: SCR_005432

Alternate IDs: biotools:samstat, OMICS_01073

Alternate URLs: <https://bio.tools/samstat>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260808T185839+0000

Ratings and Alerts

No rating or validation information has been found for SAMStat.

No alerts have been found for SAMStat.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Forbes CA, et al. (2026) A precision medicine approach to interpret a GATA4 genetic variant in a paediatric patient with congenital heart disease. *Human genomics*, 20(1), 29.

Newnes HV, et al. (2025) Interleukin-4 modulates type I interferon to augment antitumor immunity. *Science advances*, 11(20), eadt3618.

Larcombe AN, et al. (2025) Partial amelioration of a chronic cigarette-smoke-induced phenotype in mice by switching to electronic cigarettes. *Archives of toxicology*, 99(7), 3007.

Dujak C, et al. (2024) Genomic analysis of fruit size and shape traits in apple: unveiling candidate genes through GWAS analysis. *Horticulture research*, 11(2), uhad270.

Lê-Bury G, et al. (2023) HIV-1 active and latent infections induce disparate chromatin reorganization and transcriptional regulation of mRNAs and lncRNAs in SupT1 cells. *mBio*, 14(6), e0261923.

Lassmann T, et al. (2023) SAMStat 2: quality control for next generation sequencing data. *Bioinformatics (Oxford, England)*, 39(1).

Fear VS, et al. (2023) Gene editing and cardiac disease modelling for the interpretation of genetic variants of uncertain significance in congenital heart disease. *Stem cell research & therapy*, 14(1), 345.

Tsirigoti C, et al. (2022) Loss of SNAI1 induces cellular plasticity in invasive triple-negative breast cancer cells. *Cell death & disease*, 13(9), 832.

Durand R, et al. (2021) Crucial role of Salmonella genomic island 1 master activator in the parasitism of IncC plasmids. *Nucleic acids research*, 49(14), 7807.

de Jong E, et al. (2021) IRF7-Associated Immunophenotypes Have Dichotomous Responses to Virus/Allergen Coexposure and OM-85-Induced Reprogramming. *Frontiers in immunology*, 12, 699633.

Cardona K, et al. (2021) Inflammatory gene expression profiling in peripheral blood from patients with Alzheimer's disease reveals key pathways and hub genes with potential diagnostic utility: a preliminary study. *PeerJ*, 9, e12016.

González-Pech RA, et al. (2021) Comparison of 15 dinoflagellate genomes reveals extensive sequence and structural divergence in family Symbiodiniaceae and genus Symbiodinium. BMC biology, 19(1), 73.

Andradas C, et al. (2021) Assessment of Cannabidiol and Δ^9 -Tetrahydrocannabinol in Mouse Models of Medulloblastoma and Ependymoma. Cancers, 13(2).

Sobel J, et al. (2021) Scrt1, a transcriptional regulator of β -cell proliferation identified by differential chromatin accessibility during islet maturation. Scientific reports, 11(1), 8800.

Sobreiro MB, et al. (2021) RNA-Seq reveals different responses to drought in Neotropical trees from savannas and seasonally dry forests. BMC plant biology, 21(1), 463.

Roy M, et al. (2020) Viral infection impacts transposable element transcript amounts in Drosophila. Proceedings of the National Academy of Sciences of the United States of America, 117(22), 12249.

Piórkowska K, et al. (2020) Identification of candidate genes and regulatory factors related to growth rate through hypothalamus transcriptome analyses in broiler chickens. BMC genomics, 21(1), 509.

Zenteno JC, et al. (2020) Extensive genic and allelic heterogeneity underlying inherited retinal dystrophies in Mexican patients molecularly analyzed by next-generation sequencing. Molecular genetics & genomic medicine, 8(1).

García-Gómez BE, et al. (2020) Analysis of Metabolites and Gene Expression Changes Relative to Apricot (*Prunus armeniaca* L.) Fruit Quality During Development and Ripening. Frontiers in plant science, 11, 1269.

Ling KM, et al. (2020) Rhinovirus Infection Drives Complex Host Airway Molecular Responses in Children With Cystic Fibrosis. Frontiers in immunology, 11, 1327.