

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: 20260829T182220+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.

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.

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.

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.