

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 2026

NGSUtils

RRID:SCR_001236

Type: Tool

Proper Citation

NGSUtils (RRID:SCR_001236)

Resource Information

URL: <http://ngsutils.org/>

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Description: A suite of software tools for analyzing and manipulating next-generation sequencing datasets, such as FASTQ, BED and BAM format files. These tools provide a stable and modular platform for data management and analysis.

Abbreviations: NGSUtils

Synonyms: NGSUtils - Tools for next-generation sequencing analysis

Resource Type: software resource, software toolkit

Defining Citation: [PMID:23314324](#)

Keywords: mac os x, linux, next-generation sequencing, illumina, solid, 454, ion torrent, pac bio, sequencing, dna resequencing, rna resequencing, chip-seq, clip-seq, targeted resequencing, agilent exome capture, pcr targeting, dna, rna, mapping pipeline, python, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: NGSUtils

Resource ID: SCR_001236

Alternate IDs: biotools:ngsutils, OMICS_02104

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

License: BSD License

Record Creation Time: 20220129T080206+0000

Ratings and Alerts

No rating or validation information has been found for NGSUtils.

No alerts have been found for NGSUtils.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

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

López-Fuentes E, et al. (2026) Epigenetic and Transcriptional Programs Define Osteosarcoma Subtypes and Establish Targetable Vulnerabilities. *Cancer discovery*, 16(2), 296.

Gracilla DE, et al. (2026) FET Fusion Oncoproteins Disrupt Physiologic DNA Repair and Create a Targetable Opportunity for ATR Inhibitor Therapy. *Cancer research*, 86(11), 2660.

Singh S, et al. (2025) High Glucose-induced transcriptomic changes in human trabecular meshwork cells. *Molecular biology reports*, 52(1), 427.

Stanley KB, et al. (2025) Combined genome and transcriptome analysis identifies molecular signatures of aortic disease in patients with Marfan syndrome. *Journal of molecular and cellular cardiology plus*, 13, 100467.

Temme N, et al. (2025) Host-induced gene silencing of the amino acid biosynthesis gene acetolactate synthase of *Phytophthora infestans* caused strong enhanced late blight resistance of potato in the field. *Plant biotechnology journal*, 23(8), 3054.

Núñez-Martínez HN, et al. (2025) The lncRNA DUBR is regulated by CTCF and coordinates chromatin landscape and gene expression in hematopoietic cells. *Nucleic acids research*, 53(4).

Singh S, et al. (2024) High Glucose-Induced Transcriptomic Changes in Human Trabecular Meshwork Cells. *Research square*.

Geng K, et al. (2024) Intrinsic deletion at 10q23.31, including the PTEN gene locus, is aggravated upon CRISPR-Cas9-mediated genome engineering in HAP1 cells mimicking cancer profiles. *Life science alliance*, 7(2).

Stejskalova K, et al. (2024) Twelve toll-like receptor (TLR) genes in the family Equidae - comparative genomics, selection and evolution. *Veterinary research communications*,

48(2), 725.

Sommerauer C, et al. (2024) Estrogen receptor activation remodels TEAD1 gene expression to alleviate hepatic steatosis. *Molecular systems biology*, 20(4), 374.

Twesigomwe D, et al. (2023) Characterization of CYP2D6 Pharmacogenetic Variation in Sub-Saharan African Populations. *Clinical pharmacology and therapeutics*, 113(3), 643.

Doimo M, et al. (2023) Enhanced mitochondrial G-quadruplex formation impedes replication fork progression leading to mtDNA loss in human cells. *Nucleic acids research*, 51(14), 7392.

Geng K, et al. (2022) Target-enriched nanopore sequencing and de novo assembly reveals co-occurrences of complex on-target genomic rearrangements induced by CRISPR-Cas9 in human cells. *Genome research*, 32(10), 1876.

Maruki T, et al. (2022) Evolutionary Genomics of a Subdivided Species. *Molecular biology and evolution*, 39(8).

Futas J, et al. (2021) A Deadly Cargo: Gene Repertoire of Cytotoxic Effector Proteins in the Camelidae. *Genes*, 12(2).

Chauhan P, et al. (2021) Genome assembly, sex-biased gene expression and dosage compensation in the damselfly *Ischnura elegans*. *Genomics*, 113(4), 1828.

Shah AT, et al. (2021) A Comprehensive Circulating Tumor DNA Assay for Detection of Translocation and Copy-Number Changes in Pediatric Sarcomas. *Molecular cancer therapeutics*, 20(10), 2016.

Afzal M, et al. (2020) Legume genomics and transcriptomics: From classic breeding to modern technologies. *Saudi journal of biological sciences*, 27(1), 543.

Coppola C, et al. (2020) Investigation of the Impact from IL-2, IL-7, and IL-15 on the Growth and Signaling of Activated CD4⁺ T Cells. *International journal of molecular sciences*, 21(21).

Victorino JF, et al. (2020) RNA Polymerase II CTD phosphatase Rtr1 fine-tunes transcription termination. *PLoS genetics*, 16(3), e1008317.