

# Resource Summary Report

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## 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 toolkit, software resource

**Defining Citation:** [PMID:23314324](#)

**Keywords:** mac os x, linux, next-generation sequencing, illumina, solid, 454, ion torrent, pac bio, sequencing, dna resequcing, rna resequcing, 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 38 mentions in open access literature.

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

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

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).

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.

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.

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.

Jike W, et al. (2020) Phylogenomic proof of Recurrent Demipolyploidization and Evolutionary Stalling of the "Triploid Bridge" in *Arundo* (Poaceae). *International journal of molecular sciences*, 21(15).

Botton MR, et al. (2020) Phased Haplotype Resolution of the SLC6A4 Promoter Using Long-Read Single Molecule Real-Time (SMRT) Sequencing. *Genes*, 11(11).

Gallitto M, et al. (2020) Epigenetic preconditioning with decitabine sensitizes glioblastoma to temozolomide via induction of MLH1. *Journal of neuro-oncology*, 147(3), 557.

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