

Resource Summary Report

Generated by T1D on Aug 2, 2026

QUASR

RRID:SCR_006820

Type: Tool

Proper Citation

QUASR (RRID:SCR_006820)

Resource Information

URL: <http://sourceforge.net/projects/quasr/>

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Description: A lightweight software pipeline written to process and analyse next-generation sequencing (NGS) data from Illumina, 454, and Ion Torrent platforms. Although originally written for viral data, it is generic enough to work on any NGS dataset. Functions include: duplicate removal, demultiplexing, primer-removal, quality-assurance (QA) graphing, quality control (QC), consensus-generation, minority-variant determination, minority-variant graphing.

Abbreviations: QUASR

Synonyms: QUASR - Cross-platform NGS processing and analysis pipeline in Python

Resource Type: software resource

Keywords: next generation sequencing, python3, java

Availability: GNU General Public License, v3

Resource Name: QUASR

Resource ID: SCR_006820

Alternate IDs: OMICS_01072

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260801T190318+0000

Ratings and Alerts

No rating or validation information has been found for QUASR.

No alerts have been found for QUASR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 213 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Chatsirisupachai K, et al. (2025) Mouse promoters are characterised by low occupancy and high turnover of RNA polymerase II. *Molecular systems biology*, 21(5), 447.

Silva JMF, et al. (2025) Taylor's Power Law rules the dynamics of allele frequencies during viral evolution in response to host changes. *Journal of the Royal Society, Interface*, 22(228), 20250146.

Kawamura YK, et al. (2025) Preventing CpG hypermethylation in oocytes safeguards mouse development. *Developmental cell*.

Fanourgakis G, et al. (2025) DNA methylation modulates nucleosome retention in sperm and H3K4 methylation deposition in early mouse embryos. *Nature communications*, 16(1), 465.

Gao J, et al. (2025) Structure of the TXNL1-bound proteasome. *Nature structural & molecular biology*, 32(12), 2398.

Zhao L, et al. (2025) Genetically distinct within-host subpopulations of hepatitis C virus persist after Direct-Acting Antiviral treatment failure. *PLoS pathogens*, 21(4), e1012959.

Petrov L, et al. (2025) Rewired type I IFN signaling is linked to age-dependent differences in COVID-19. *Cell reports. Medicine*, 6(8), 102285.

Matteo G, et al. (2025) High-throughput transcriptomics analysis of equipotent and human relevant mixtures of BPA alternatives reveal additive effects in vitro. *Archives of toxicology*, 99(9), 3707.

Lumley SF, et al. (2025) Whole genome sequencing of hepatitis B virus using tiled amplicon (HEPTILE) and probe based enrichment on Illumina and Nanopore platforms. *Scientific reports*, 15(1), 5795.

Kinney B, et al. (2025) FLYWCH transcription factors act in a LIN-42/Period autoregulatory loop during gonad migration in *C. elegans*. *bioRxiv : the preprint server for biology*.

Beal MA, et al. (2025) Impacts of Inorganic Arsenic Exposure on Genetic Stability of Human Mesenchymal Stromal Cells. *Journal of applied toxicology : JAT*, 45(8), 1555.

Gaidatzis D, et al. (2025) A scheduler for rhythmic gene expression. *Molecular systems biology*, 21(12), 1793.

Bocker MT, et al. (2025) The histone H3 lysine 36 demethylase KDM2A/FBXL11 controls Polycomb-mediated gene repression and germ cell development in male mice. *Nature communications*, 16(1), 6803.

Borden ES, et al. (2025) Towards a transcriptomic biomarker for the classification of melanocytic neoplasms. *PLoS genetics*, 21(10), e1011869.

Padmanarayana M, et al. (2025) Mutational scanning reveals substrate-assisted autoregulation of the WNT destruction complex. *bioRxiv : the preprint server for biology*.

Zoller JA, et al. (2024) DNA methylation clocks for clawed frogs reveal evolutionary conservation of epigenetic aging. *GeroScience*, 46(1), 945.

Gao Y, et al. (2024) The emergence of Sox and POU transcription factors predates the origins of animal stem cells. *Nature communications*, 15(1), 9868.

Hochstoeger T, et al. (2024) Distinct roles of LARP1 and 4EBP1/2 in regulating translation and stability of 5'TOP mRNAs. *Science advances*, 10(7), eadi7830.

Lee H, et al. (2024) Empirical Characterization of False Discovery Rates of Differentially Expressed Genes and Transcriptomic Benchmark Concentrations in Zebrafish Embryos. *Environmental science & technology*, 58(14), 6128.

Wang X, et al. (2024) House dust-derived mixtures of organophosphate esters alter the phenotype, function, transcriptome, and lipidome of KGN human ovarian granulosa cells. *Toxicological sciences : an official journal of the Society of Toxicology*, 200(1), 95.