

Resource Summary Report

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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: 20260905T132602+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 219 mentions in open access literature.

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

Liontis T, et al. (2026) Mutual regulation of spermatogenesis-specific Argonaute proteins and Insulin/IGF-1 signaling in aging control. EMBO reports, 27(6), 1437.

Matteo G, et al. (2026) Chemicals in plastics differentially affect the transcriptome of MCF-7 breast cancer cells. Archives of toxicology, 100(7), 3011.

Kobayashi W, et al. (2026) Protocol for integrative analysis of transcription factor-nucleosome interactions using SeEN-seq and cryo-EM structure determination. STAR protocols, 7(1), 104295.

Ambrosi C, et al. (2026) The H3K36me3 methyltransferase SETD2 contributes to PAF1C interactions with RNA Pol II and is required for neuronal differentiation. The EMBO journal, 45(10), 3430.

Katic I, et al. (2026) Large transgene arrays cause aberrant transcription and synthetic molting defects with myrf-1 mutation. bioRxiv : the preprint server for biology.

Addicks GC, et al. (2025) Identification of four mechanisms of toxicity for per- and polyfluoroalkyl substances through transcriptomic profiling in human liver spheroids exposed to 24 PFAS. Toxicological sciences : an official journal of the Society of Toxicology, 207(1), 161.

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.

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.

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