

Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 8, 2026

[rnaQUAST](#)

RRID:SCR_016994

Type: Tool

Proper Citation

rnaQUAST (RRID:SCR_016994)

Resource Information

URL: <http://cab.spbu.ru/software/rnaquast/>

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Description: Software tool for evaluating RNA-Seq assembly quality and benchmarking transcriptome assemblers using reference genome and gene database. Capable to estimate gene database coverage by raw reads and de novo quality assessment using third party software.

Resource Type: data processing software, software application, software resource

Defining Citation: [PMID:27153654](#)

Keywords: evaluation, quality, RNA-Seq, assembly, data, transcriptome, assembler, reference, genome, gene, database, raw, read, , bio.tools

Funding: EMC Research and Development Department ;
St. Petersburg State University ;
Russia

Availability: Free, Available for download, Freely available

Resource Name: rnaQUAST

Resource ID: SCR_016994

Alternate IDs: biotools:rnaQUAST

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

License: GPL

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260905T133052+0000

Ratings and Alerts

No rating or validation information has been found for rnaQUAST.

No alerts have been found for rnaQUAST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Platova SE, et al. (2026) Transcriptomic analysis of three annelid species: looking for markers of positional information. BMC genomics, 27(1).

Juter??ek M, et al. (2024) Transcriptome-informed identification and characterization of Planococcus citri cis- and trans-isoprenyl diphosphate synthase genes. iScience, 27(4), 109441.

Bliznina A, et al. (2021) Telomere-to-telomere assembly of the genome of an individual Oikopleura dioica from Okinawa using Nanopore-based sequencing. BMC genomics, 22(1), 222.

Bushmanova E, et al. (2019) rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. GigaScience, 8(9).