

Resource Summary Report

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QUAST

RRID:SCR_001228

Type: Tool

Proper Citation

QUAST (RRID:SCR_001228)

Resource Information

URL: <http://bioinf.spbau.ru/quast>

Proper Citation: QUAST (RRID:SCR_001228)

Description: Quality assessment software tool for evaluating and comparing genome assemblies. It works both with and without a given reference genome. It produces many reports, summary tables and plots.

Abbreviations: QUAST

Synonyms: QUAST: Quality Assessment Tool for Genome Assemblies

Resource Type: software resource

Defining Citation: [PMID:23422339](#)

Keywords: genome assembly, genomics, bio.tools

Resource Name: QUAST

Resource ID: SCR_001228

Alternate IDs: biotools:quast, OMICS_02115

Alternate URLs: <https://bio.tools/quast>, <https://sources.debian.org/src/quast/>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260801T190125+0000

Ratings and Alerts

No rating or validation information has been found for QUAST.

No alerts have been found for QUASt.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2863 mentions in open access literature.

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

Kirkland C, et al. (2026) Chromosome-Level Genomics and Historical Museum Collections Reveal New Insights Into the Population Structure and Chromosome Evolution of Waterbuck. *Molecular ecology*, 35(1), e70218.

Barel M, et al. (2026) Colistin and Biofilm-Related Genes of Positive *Escherichia coli* O157:H7 in Cattle (*Bos taurus*) Carcasses Antibiotic Resistance Profiles, Biofilm and Molecular Characterisation of Isolates. *Veterinary medicine and science*, 12(1), e70730.

Kimbrel JA, et al. (2026) High-quality *Acinetobacter* genomes recovered from combat wounds via metagenomic sequencing resemble cultured isolate genomes. *Microbiology spectrum*, 14(1), e0187625.

Huang C, et al. (2026) The High-Altitude Adaptation Characteristics of Microbiota-Host Cross-Talk in Yak Gastrointestinal Track. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e14862.

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anselli*). *G3 (Bethesda, Md.)*, 16(1).

Wang X-Y, et al. (2026) Genomic epidemiology and plasmid characterization of antimicrobial resistance and virulence in cattle *Escherichia coli* from China. *Microbiology spectrum*, 14(1), e0325625.

Carlson BJ, et al. (2026) A reference genome assembly for the pink volcano barnacle, *Tetraclita rubescens*, Nilsson-Cantell, 1931. *The Journal of heredity*, 117(1), 173.

Visser M, et al. (2026) *Neisseria gonorrhoeae* Sequence Types During an Increase of Gonorrhea Among Young Women in 2022 and 2023 in the Netherlands. *Open forum infectious diseases*, 13(1), ofaf767.

Wang B, et al. (2026) The expansion of culturable opportunistic pathogens and antibiotic resistance in mouse gut following antibiotic exposure. *Microbiology spectrum*, 14(1), e0110425.

Lawson LP, et al. (2026) Whole-genome sequence of the African Common Reed Frog (*Hyperolius viridiflavus viridiflavus*) from Ethiopia. *G3 (Bethesda, Md.)*, 16(1).

Alemán S, et al. (2026) Unraveling Cytomegalovirus Drug Resistance in Transplant Patients by Targeting Deep Sequencing. *Journal of medical virology*, 98(1), e70768.

Sari E, et al. (2026) Gene duplication, horizontal gene transfer, and trait trade-offs drive evolution of postfire resource acquisition in pyrophilous fungi. *Proceedings of the National Academy of Sciences of the United States of America*, 123(1), e2519152123.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Nebenführ M, et al. (2025) Chromosome-level genome assembly of the lemon sole, *Microstomus kitt* (Pleuronectiformes: Pleuronectidae). *GigaByte (Hong Kong, China)*, 2025, gigabyte156.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. *GigaByte (Hong Kong, China)*, 2025, gigabyte150.

Liang H, et al. (2025) Efficiently constructing complete genomes with CycloneSEQ to fill gaps in bacterial draft assemblies. *GigaByte (Hong Kong, China)*, 2025, gigabyte154.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte (Hong Kong, China)*, 2025, gigabyte157.

Winter S, et al. (2025) Chromosome-Level genome assembly and transcriptome analysis of the ural owl, *Strix uralensis* Pallas, 1771. *The Journal of heredity*.

Yen EC, et al. (2025) Chromosome-level genome assembly and methylome profile yield insights for the conservation of endangered loggerhead sea turtles. *GigaScience*, 14.