

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

QUAST

RRID:SCR_001228

Type: Tool

Proper Citation

QUAST (RRID:SCR_001228)

Resource Information

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

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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: 20260829T182100+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 3293 mentions in open access literature.

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

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Tomé LMR, et al. (2026) Emergence of *Candida* (*Candidozyma*) *auris* in Minas Gerais, Brazil: Genomic Surveillance to Guide Rapid Public Health Responses. *Mycoses*, 69(2), e70146.

Pettersen KS, et al. (2026) Genomic insights into *Campylobacter jejuni* from Norwegian broilers: high genetic diversity and limited persistence on farms. *BMC microbiology*, 26(1).

Dauphin B, et al. (2026) Chromosome-scale Genome Assembly of the Most Abundant Ectomycorrhizal Fungus *Cenococcum Geophilum* Reveals Massive TE Expansion and RIP Defense Mechanism. *Genome biology and evolution*, 18(2).

Brynildsrud OB, et al. (2026) Evolutionary dynamics and virulence factor variability in invasive *Streptococcus pyogenes* in Norway, 2017-2023. *mSphere*, 11(3), e0077525.

Diep RE, et al. (2026) Natural maternal immunity protects neonates from *Escherichia coli* sepsis. *Nature*, 653(8114), 519.

Niyazi HA, et al. (2026) Pan-genome analysis and phylogenetic characterization of *Klebsiella pneumoniae* from global isolates. *Future microbiology*, 21(8), 701.

Jeong HY, et al. (2026) Hybrid Whole-Genome Sequencing for Genetic Stability Assessment of Infectious Laryngotracheitis Virus Vaccine Strains. *Vaccines*, 14(3).

Binion B, et al. (2026) The Urinary Tract commensal *Peptoniphilus* spp. Encodes a Novel 17 β -Hydroxysteroid Dehydrogenase. *bioRxiv : the preprint server for biology*.

Parween S, et al. (2026) Desert Plant Endophyte Genome Database: a curated repository of endophytic bacterial genomes across arid ecosystems. *Database : the journal of biological databases and curation*, 2026.

Magallanes Alba ME, et al. (2026) Genome assembly and annotation of the olive grass mouse *Abrothrix olivacea* reveal transcriptomic and cellular adaptations across contrasting biomes. *BMC genomics*, 27(1).

Escalante-Beltrán A, et al. (2026) Draft Genome Sequence of *Bacillus* sp. Strain 11B20, a Promising Plant-Growth Promoting Bacterium Associated with Maize (*Zea mays* L.) in the Yaqui Valley, Mexico. *Microorganisms*, 14(2).

Ibrahim MS, et al. (2026) AntiPan: a genome-informed in silico pipeline for advancing subunit vaccine discovery against *Staphylococcus aureus*. *Scientific reports*, 16(1), 5396.

Qian Y, et al. (2026) Metagenomic sequencing and binning reveal carbon cycling microorganisms and gene functions in park environments. *BMC microbiology*, 26(1).

Liu Y, et al. (2026) Phylogenomics reveals the evolution of floral traits associated with pollinators and pollinator-prey conflict within the carnivorous *Pinguicula* subgenus *Temnoceras*. *American journal of botany*, 113(2), e70156.

Singh N, et al. (2026) *Aeromonas* in South Asia: genomic insights into an environmental pathogen and reservoir of antimicrobial resistance. *Nature communications*, 17(1).

Pathomchai-Umporn C, et al. (2026) Genetic diversity, serotype, and antimicrobial profiles of *Riemerella anatipestifer* isolated from ducks and chickens in Thailand. *Poultry science*, 105(4), 106575.

Pickering AC, et al. (2026) Bacterial metabolic remodeling by convergent evolution unlocks nutrient availability after a host switch. *Science advances*, 12(6), eadw9419.

Sabry H, et al. (2026) Phage vB_AbaM_MU1 for biocontrol of carbapenem-resistant *Acinetobacter baumannii* (CRAB) isolated from wound infection. *Virology journal*, 23(1).

van Engelen E, et al. (2026) *Campylobacter bilis* caused spotty liver syndrome in laying hens in the Netherlands. *The veterinary quarterly*, 46(1), 2628724.