

Resource Summary Report

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[quarTeT](#)

RRID:SCR_025258

Type: Tool

Proper Citation

quarTeT (RRID:SCR_025258)

Resource Information

URL: <http://www.atcgn.com:8080/quarTeT/home.html>

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Description: Web toolkit for studies of large scale T2T genomes. Collection of tools designed for T2T genome assembly and characterization, including reference guided genome assembly, ultra long sequence based gap filling, telomere identification, and de novo centromere prediction. Includes four modules: AssemblyMapper, GapFiller, TeloExplorer, and CentroMiner. Modules can be used alone or in combination with each other for T2T genome assembly and characterization.

Synonyms: quar Telomere-To-Telomere Toolkit

Resource Type: software resource, source code, web application

Defining Citation: [PMID:37560017](#)

Keywords: Telomere-To-Telomere genomes studies, guided genome assembly, ultra long sequence based gap filling, telomere identification, de novo centromere prediction, large scale T2T genomes, assemble and analyse multiple high quality genomes, highly repetitive regions in genomes,

Funding: National Natural Science Foundation of China

Availability: Free, Available for download, Freely available

Resource Name: quarTeT

Resource ID: SCR_025258

Alternate URLs: <https://github.com/aaranyue/quarTeT>

Record Creation Time: 20240412T053246+0000

Record Last Update: 20260804T043906+0000

Ratings and Alerts

No rating or validation information has been found for quarTeT.

No alerts have been found for quarTeT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 33 mentions in open access literature.

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

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 254 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Xing TF, et al. (2025) Extensive Recombination Suppression and Genetic Degeneration of a Young ZW Sex Chromosome System in Halfbeak Fish. *Molecular biology and evolution*, 42(7).

Qin H, et al. (2025) The complete genome assembly of *Astragalus membranaceus*: enabling more accurate genetic research. *GigaScience*, 14.

Yang W, et al. (2025) A haplotype-resolved chromosomal-level genome assembly of *Oxalis articulata*. *Scientific data*, 12(1), 856.

Yuan J, et al. (2025) A telomere-to-telomere genome assembly of koi carp (*Cyprinus carpio*) using long reads and Hi-C technology. *GigaScience*, 14.

Gao W, et al. (2025) Chromosome-scale and haplotype-resolved genome assembly of *Populus trichocarpa*. *Horticulture research*, 12(4), uhaf012.

Zhu M, et al. (2025) A chromosomal-level genome assembly of *Kibakoganea sinica*, Bouchard, 2005 (Coleoptera: Scarabaeidae). *Scientific data*, 12(1), 1012.

Wang XF, et al. (2025) A telomere-to-telomere genome assembly of *Camellia nitidissima*. *Scientific data*, 12(1), 815.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Chen S, et al. (2025) Analysis of a near telomere-to-telomere genome of *Phellodendron amurense* reveals insights into berberine biosynthesis. *Nature communications*, 16(1), 11437.

Qi Z, et al. (2025) Telomere-to-telomere genome assembly of *Electrophorus electricus* provides insights into the evolution of electric eels. *GigaScience*, 14.

Wang Y, et al. (2025) Telomere-to-telomere genome of common bean (*Phaseolus vulgaris* L., YP4). *GigaScience*, 14.

Northing PC, et al. (2025) Chromosome-scale reference genome of *Pectocarya recurvata*, the species with the smallest reported genome size in Boraginaceae. *Applications in plant sciences*, 13(3), e70008.

Zhong C, et al. (2025) Genome assembly and whole-genome resequencing study of Butuo Black sheep (*Ovis aries*). *Scientific data*, 12(1), 1725.

Ahmad B, et al. (2025) Mango pangenome reveals dramatic impacts of reference bias on population genomic analyses. *Horticulture research*, 12(9), uhaf166.

Wang C, et al. (2025) The telomere-to-telomere genome assembly of the *Triplophysa erythraea* (Nemacheilidae hypogean fishes). *Scientific data*, 12(1), 1978.

Jiang M, et al. (2025) The telomere-to-telomere gap-free reference genome and taxonomic reassessment of *Siniperca roulei*. *GigaScience*, 14.

Mu W, et al. (2025) The haplotype-resolved T2T genome for *Bauhinia* ?? *blakeana* sheds light on the genetic basis of flower heterosis. *GigaScience*, 14.

Bian C, et al. (2025) Telomere-to-telomere chromosome-scale genome assemblies of black and golden koi carp variants support construction of an ancient karyotype of Cypriniformes. *GigaScience*, 14.