

Resource Summary Report

Generated by [NIF](#) on Jul 31, 2026

GenomeTester4

RRID:SCR_024026

Type: Tool

Proper Citation

GenomeTester4 (RRID:SCR_024026)

Resource Information

URL: <https://github.com/bioinfo-ut/GenomeTester4>

Proper Citation: GenomeTester4 (RRID:SCR_024026)

Description: Software toolkit for performing set operations - union, intersection and complement on k-mer lists.

Synonyms: genometest

Resource Type: software toolkit, software resource

Defining Citation: [PMID:26640690](#)

Keywords: performing set operations on k-mer lists,

Availability: Free, Available for download, Freely available,

Resource Name: GenomeTester4

Resource ID: SCR_024026

Alternate IDs: OMICS_02363w

Alternate URLs: <https://sources.debian.org/src/genometest/>

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260729T044559+0000

Ratings and Alerts

No rating or validation information has been found for GenomeTester4.

No alerts have been found for GenomeTester4.

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 [NIF](#) .

Pajuste FD, et al. (2023) GeneToCN: an alignment-free method for gene copy number estimation directly from next-generation sequencing reads. Scientific reports, 13(1), 17765.

??rd T, et al. (2020) A human-specific VNTR in the TRIB3 promoter causes gene expression variation between individuals. PLoS genetics, 16(8), e1008981.

Krjutskov K, et al. (2008) Development of a single tube 640-plex genotyping method for detection of nucleic acid variations on microarrays. Nucleic acids research, 36(12), e75.

Andreson R, et al. (2008) Predicting failure rate of PCR in large genomes. Nucleic acids research, 36(11), e66.