

# Resource Summary Report

Generated by [nidm-terms](#) on Sep 21, 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 resource, software toolkit

**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:** 20260919T195617+0000

### Ratings and Alerts

No rating or validation information has been found for GenomeTester4.

No alerts have been found for GenomeTester4.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [nidm-terms](#) .

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.

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

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.