

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Telomerecat

RRID:SCR_027747

Type: Tool

Proper Citation

Telomerecat (RRID:SCR_027747)

Resource Information

URL: <https://github.com/cancerit/telomerecat>

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Description: Software R package for estimating average telomere length (TL) for paired end, whole genome sequencing (WGS) sample. Telomere computational analysis tool.

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:29358629](#)

Keywords: telomere, estimating average telomere length, paired end, whole genome sequencing sample,

Availability: Free, Available for download, Freely available

Resource Name: Telomerecat

Resource ID: SCR_027747

License: GNU GPL v3

Record Creation Time: 20251209T055453+0000

Record Last Update: 20260815T183310+0000

Ratings and Alerts

No rating or validation information has been found for Telomerecat .

No alerts have been found for Telomerecat .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Culliford R, et al. (2026) Contrasting Features of Papillary and Chromophobe Renal Cell Carcinoma Revealed by Whole-Genome Sequencing. Molecular cancer research : MCR, 24(5), 327.