

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 2026

TALLYMER

RRID:SCR_001244

Type: Tool

Proper Citation

TALLYMER (RRID:SCR_001244)

Resource Information

URL: <http://www.zbh.uni-hamburg.de/?id=211>

Proper Citation: TALLYMER (RRID:SCR_001244)

Description: A collection of flexible and memory-efficient software programs for k-mer counting and indexing of large sequence sets. It is based on enhanced suffix arrays which gives a much larger flexibility concerning the choice of the k-mer size. It can process large data sizes of several billion bases.

Abbreviations: Tallymer

Resource Type: software resource

Defining Citation: [PMID:18976482](#)

Keywords: k-mer, counting, sequence, genome annotation, genome, annotation, bio.tools

Availability: Free, Freely available

Resource Name: TALLYMER

Resource ID: SCR_001244

Alternate IDs: biotools:tallymer, OMICS_02096

Alternate URLs: <https://bio.tools/tallymer>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195522+0000

Ratings and Alerts

No rating or validation information has been found for TALLYMER.

No alerts have been found for TALLYMER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Smith JP, et al. (2021) PEPPRO: quality control and processing of nascent RNA profiling data. *Genome biology*, 22(1), 155.

Monat C, et al. (2019) TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. *Genome biology*, 20(1), 284.

Bernard G, et al. (2019) Alignment-free inference of hierarchical and reticulate phylogenomic relationships. *Briefings in bioinformatics*, 20(2), 426.

Vandenbussche F, et al. (2016) A Tale of Tails: Dissecting the Enhancing Effect of Tailed Primers in Real-Time PCR. *PloS one*, 11(10), e0164463.

Wylie TN, et al. (2015) Development and Evaluation of an Enterovirus D68 Real-Time Reverse Transcriptase PCR Assay. *Journal of clinical microbiology*, 53(8), 2641.

Leung W, et al. (2015) Drosophila muller f elements maintain a distinct set of genomic properties over 40 million years of evolution. *G3 (Bethesda, Md.)*, 5(5), 719.

Dhillon B, et al. (2014) The landscape of transposable elements in the finished genome of the fungal wheat pathogen *Mycosphaerella graminicola*. *BMC genomics*, 15(1), 1132.