

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 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:** 20260808T185739+0000

### Ratings and Alerts

No rating or validation information has been found for TALLYMER.

No alerts have been found for TALLYMER.

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## Data and Source Information

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

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## 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.