Resource Summary Report

Generated by NIF on Apr 27, 2025

TALLYMER

RRID:SCR_001244
Type: Tool

Proper Citation

TALLYMER (RRID:SCR_001244)

Resource Information

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

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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

Funding:

Availability: Free, Public

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: 20250420T014024+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 NIF.

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.