

Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

Tally

RRID:SCR_001239

Type: Tool

Proper Citation

Tally (RRID:SCR_001239)

Resource Information

URL: <http://www.ebi.ac.uk/~stijn/reaper/tally.html>

Proper Citation: Tally (RRID:SCR_001239)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 23,2022. Software program for deduplicating sequence fragments. It minimises memory usage by compressing sequences and using compact memory allocation techniques. A built-in parser allows a variety of input file formats and a simple specification language allows flexible output file formats. It can be made aware of paired-end reads, and it can handle degenerate sequence inserts intended to reveal amplification biases. Tally comes with reaper, a program for demultiplexing, trimming and filtering short read sequencing data.

Abbreviations: Tally

Synonyms: Tally - Deduplication of sequence fragments

Resource Type: software resource

Keywords: paired end read processing, deduplication, sequence fragment

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Tally

Resource ID: SCR_001239

Alternate IDs: OMICS_02100

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260815T182153+0000

Ratings and Alerts

No rating or validation information has been found for Tally.

No alerts have been found for Tally.

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 [dkNET](#) .

Mahmoud AA, et al. (2025) Influence of elevated temperature exposure on the residual compressive strength and radiation shielding efficiency of ordinary concrete incorporating granodiorite and ceramic powders. Scientific reports, 15(1), 3572.

Mukhamale SV, et al. (2024) Experimental, theoretical and numerical simulation-based investigations on the fabricated Cu₂ZnSn thin-film-based Schottky diodes with enhanced electron transport for solar cell. Scientific reports, 14(1), 15970.

Nishikawa KK, et al. (2024) Highly multiplexed design of an allosteric transcription factor to sense novel ligands. bioRxiv : the preprint server for biology.

Bosch-Capblanch X, et al. (2021) Researching, co-creating and testing innovations in paper-based health information systems (PHISICC) to support health workers' decision-making: protocol of a multi-country, transdisciplinary, mixed-methods research programme in three sub-Saharan countries. Health research policy and systems, 19(1), 112.

Lyra ML, et al. (2021) Initial Phylotranscriptomic Confirmation of Homoplastic Evolution of the Conspicuous Coloration and Bufoniform Morphology of Pumpkin-Toadlets in the Genus Brachycephalus. Toxins, 13(11).

Trahair T, et al. (2019) Crizotinib and Surgery for Long-Term Disease Control in Children and Adolescents With ALK-Positive Inflammatory Myofibroblastic Tumors. JCO precision oncology, 3.

Ravichandran S, et al. (2019) MicroRNA-guided regulation of heat stress response in wheat. BMC genomics, 20(1), 488.