Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

TagDust

RRID:SCR_004175
Type: Tool

Proper Citation

TagDust (RRID:SCR_004175)

Resource Information

URL: http://genome.gsc.riken.jp/osc/english/dataresource/

Proper Citation: TagDust (RRID:SCR_004175)

Description: A program to eliminate artifactual reads from next-generation sequencing data sets.

Abbreviations: TagDust

Resource Type: software resource

Defining Citation: PMID:19737799

Keywords: unix/linux, bio.tools, bio.tools

Funding:

Resource Name: TagDust

Resource ID: SCR_004175

Alternate IDs: biotools:tagdust, OMICS_01095, biotools:nexalign

Alternate URLs: https://bio.tools/tagdust, https://bio.tools/nexalign

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250410T065129+0000

Ratings and Alerts

No rating or validation information has been found for TagDust.

No alerts have been found for TagDust.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 50 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zhang Y, et al. (2025) Super-silencer perturbation by EZH2 and REST inhibition leads to large loss of chromatin interactions and reduction in cancer growth. Nature structural & molecular biology, 32(1), 137.

Pidon H, et al. (2024) High-resolution mapping of Ryd4Hb, a major resistance gene to Barley yellow dwarf virus from Hordeum bulbosum. TAG. Theoretical and applied genetics. Theoretische und angewandte Genetik, 137(3), 60.

Della Volpe L, et al. (2024) A p38 MAPK-ROS axis fuels proliferation stress and DNA damage during CRISPR-Cas9 gene editing in hematopoietic stem and progenitor cells. Cell reports. Medicine, 5(11), 101823.

Fiumara M, et al. (2023) Genotoxic effects of base and prime editing in human hematopoietic stem cells. Nature biotechnology.

Menden K, et al. (2023) A multi-omics dataset for the analysis of frontotemporal dementia genetic subtypes. Scientific data, 10(1), 849.

Xia B, et al. (2023) Pooled genome-wide CRISPR activation screening for rapamycin resistance genes in Drosophila cells. eLife, 12.

Tamaki I, et al. (2023) Phylogenetic, population structure, and population demographic analyses reveal that Vicia sepium in Japan is native and not introduced. Scientific reports, 13(1), 20746.

Laubscher F, et al. (2022) Genomic Diversity of Torque Teno Virus in Blood Samples from Febrile Paediatric Outpatients in Tanzania: A Descriptive Cohort Study. Viruses, 14(8).

Lee HJ, et al. (2022) Epigenomic analysis reveals prevalent contribution of transposable elements to cis-regulatory elements, tissue-specific expression, and alternative promoters in zebrafish. Genome research, 32(7), 1424.

Wilbanks EG, et al. (2022) Metagenomic methylation patterns resolve bacterial genomes of unusual size and structural complexity. The ISME journal, 16(8), 1921.

de Hoon M, et al. (2022) Deep sequencing of short capped RNAs reveals novel families of noncoding RNAs. Genome research, 32(9), 1727.

Cai Y, et al. (2021) H3K27me3-rich genomic regions can function as silencers to repress gene expression via chromatin interactions. Nature communications, 12(1), 719.

Marx HE, et al. (2021) Pilot RNA-seq data from 24 species of vascular plants at Harvard Forest. Applications in plant sciences, 9(2), e11409.

Cho MS, et al. (2021) Genome-Wide Single Nucleotide Polymorphism Analysis Elucidates the Evolution of Prunus takesimensis in Ulleung Island: The Genetic Consequences of Anagenetic Speciation. Frontiers in plant science, 12, 706195.

Hümmer S, et al. (2021) Cross talk between the upstream exon-intron junction and Prp2 facilitates splicing of non-consensus introns. Cell reports, 37(4), 109893.

Cordey S, et al. (2021) Blood virosphere in febrile Tanzanian children. Emerging microbes & infections, 10(1), 982.

Slaughter MJ, et al. (2021) HDAC inhibition results in widespread alteration of the histone acetylation landscape and BRD4 targeting to gene bodies. Cell reports, 34(3), 108638.

Marx HE, et al. (2020) TagSeq for gene expression in non-model plants: A pilot study at the Santa Rita Experimental Range NEON core site. Applications in plant sciences, 8(11), e11398.

Keele GR, et al. (2020) Integrative QTL analysis of gene expression and chromatin accessibility identifies multi-tissue patterns of genetic regulation. PLoS genetics, 16(1), e1008537.

Takano A, et al. (2020) A Narrow Endemic or a Species Showing Disjunct Distribution? Studies on Meehania montis-koyae Ohwi (Lamiaceae). Plants (Basel, Switzerland), 9(9).