

Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

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

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: 20260912T195610+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

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Loureiro JR, et al. (2026) The insertion of an ATTTC repeat in an Alu element hyperactivates a neurodevelopmental enhancer in spinocerebellar ataxia type 37. *Cell reports*, 45(4), 117146.

Ishikawa N, et al. (2025) Allotetraploid Origin and Putative Ancient Introgression in *Plantago hakusanensis* (Plantaginaceae). *Ecology and evolution*, 15(3), e71144.

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.

Watt K, et al. (2025) Epigenetic alterations facilitate transcriptional and translational programs in hypoxia. *Nature cell biology*, 27(11), 1965.

Saito R, et al. (2025) Exploring the Genetic Basis of Wild Boar (*Sus scrofa*) and Its Connection to Classical Swine Fever Spread. *Transboundary and emerging diseases*, 2025, 9881511.

Conti A, et al. (2025) Senescence and inflammation are unintended adverse consequences of CRISPR-Cas9/AAV6-mediated gene editing in hematopoietic stem cells. *Cell reports. Medicine*, 6(6), 102157.

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.

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.

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

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.

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

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

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.

H??mmer 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.

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.