Resource Summary Report

Generated by dkNET on Apr 30, 2025

Gzip

RRID:SCR 009291

Type: Tool

Proper Citation

Gzip (RRID:SCR_009291)

Resource Information

URL: http://www.gzip.org/

Proper Citation: Gzip (RRID:SCR_009291)

Description: A compression utility designed to be a replacement for compress.

Abbreviations: Gzip

Synonyms: GNU zip

Resource Type: software resource

Funding:

Resource Name: Gzip

Resource ID: SCR_009291

Alternate IDs: OMICS_00961

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250420T014451+0000

Ratings and Alerts

No rating or validation information has been found for Gzip.

No alerts have been found for Gzip.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Nijs J, et al. (2025) Is Word Order Responsive to Morphology? Disentangling Cause and Effect in Morphosyntactic Change in Five Western European Languages. Entropy (Basel, Switzerland), 27(1).

Hlayel M, et al. (2024) Enhancing unity-based AR with optimal lossless compression for digital twin assets. PloS one, 19(12), e0314691.

El-Shaikh A, et al. (2023) Content-based filter queries on DNA data storage systems. Scientific reports, 13(1), 7053.

B?inda K, et al. (2023) Efficient and Robust Search of Microbial Genomes via Phylogenetic Compression. bioRxiv: the preprint server for biology.

Bennett AM, et al. (2023) MIMIC-IV on FHIR: converting a decade of in-patient data into an exchangeable, interoperable format. Journal of the American Medical Informatics Association: JAMIA, 30(4), 718.

Borghesi A, et al. (2023) M100 ExaData: a data collection campaign on the CINECA's Marconi100 Tier-0 supercomputer. Scientific data, 10(1), 288.

Banday AR, et al. (2022) Genetic regulation of OAS1 nonsense-mediated decay underlies association with COVID-19 hospitalization in patients of European and African ancestries. Nature genetics, 54(8), 1103.

Umair M, et al. (2022) iRun: Horizontal and Vertical Shape of a Region-Based Graph Compression. Sensors (Basel, Switzerland), 22(24).

Zhu Q, et al. (2022) Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. mSystems, 7(2), e0016722.

Lyon MS, et al. (2021) The variant call format provides efficient and robust storage of GWAS summary statistics. Genome biology, 22(1), 32.

Chong LC, et al. (2021) An Alignment-Independent Approach for the Study of Viral Sequence Diversity at Any Given Rank of Taxonomy Lineage. Biology, 10(9).

Onabajo OO, et al. (2020) Interferons and viruses induce a novel primate-specific isoform dACE2 and not the SARS-CoV-2 receptor ACE2. bioRxiv: the preprint server for biology.

Pelz M, et al. (2020) The elaboration of exploratory play. Philosophical transactions of the Royal Society of London. Series B, Biological sciences, 375(1803), 20190503.

Samarfard S, et al. (2020) Viromes of Ten Alfalfa Plants in Australia Reveal Diverse Known Viruses and a Novel RNA Virus. Pathogens (Basel, Switzerland), 9(3).

Buchweitz LF, et al. (2020) Visualizing metabolic network dynamics through time-series metabolomic data. BMC bioinformatics, 21(1), 130.

Kredens KV, et al. (2020) Vertical lossless genomic data compression tools for assembled genomes: A systematic literature review. PloS one, 15(5), e0232942.

Tahir M, et al. (2020) A Fast and Scalable Workflow for SNPs Detection in Genome Sequences Using Hadoop Map-Reduce. Genes, 11(2).

Fagan-Solis KD, et al. (2020) A P53-Independent DNA Damage Response Suppresses Oncogenic Proliferation and Genome Instability. Cell reports, 30(5), 1385.

Shave S, et al. (2018) PuLSE: Quality control and quantification of peptide sequences explored by phage display libraries. PloS one, 13(2), e0193332.

Coltuc D, et al. (2018) On the Use of Normalized Compression Distances for Image Similarity Detection. Entropy (Basel, Switzerland), 20(2).