

# Resource Summary Report

Generated by [T1D](#) on Aug 1, 2026

## Gzip

RRID:SCR\_009291

Type: Tool

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### Proper Citation

Gzip (RRID:SCR\_009291)

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### 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

**Resource Name:** Gzip

**Resource ID:** SCR\_009291

**Alternate IDs:** OMICS\_00961

**Record Creation Time:** 20220129T080252+0000

**Record Last Update:** 20260725T190653+0000

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### Ratings and Alerts

No rating or validation information has been found for Gzip.

No alerts have been found for Gzip.

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### Data and Source Information

**Source:** [SciCrunch Registry](#)

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### Usage and Citation Metrics

We found 30 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

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).

Hackenberg M, et al. (2025) Infusing structural assumptions into dimensionality reduction for single-cell RNA sequencing data to identify small gene sets. *Communications biology*, 8(1), 414.

Nordin MNB, et al. (2025) A Comparative Analysis of Machine-Learning Algorithms for Automated International Classification of Diseases (ICD)-10 Coding in Malaysian Death Records. *Cureus*, 17(1), e77342.

Li C, et al. (2025) A Novel QR Code-Based Solution for Secure Electronic Health Record Transfer in Venous Thromboembolism Home Rehabilitation Management: Algorithm Development and Validation. *JMIR rehabilitation and assistive technologies*, 12, e69230.

Madsen CD, et al. (2025) The topological properties of the protein universe. *Nature communications*, 16(1), 7503.

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

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

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

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

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.

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.

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

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

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).

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.

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*.

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.