## **Resource Summary Report**

Generated by dkNET on May 5, 2025

# **MFCompress**

RRID:SCR\_009301 Type: Tool

#### **Proper Citation**

MFCompress (RRID:SCR\_009301)

#### **Resource Information**

URL: http://bioinformatics.ua.pt/software/mfcompress/

Proper Citation: MFCompress (RRID:SCR\_009301)

Description: A compression tool for FASTA and multi-FASTA files.

Abbreviations: MFCompress

Resource Type: software resource

Defining Citation: PMID:24132931

Funding:

Resource Name: MFCompress

Resource ID: SCR\_009301

Alternate IDs: OMICS\_00963

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250420T014451+0000

#### **Ratings and Alerts**

No rating or validation information has been found for MFCompress.

No alerts have been found for MFCompress.

### Data and Source Information

Source: <u>SciCrunch Registry</u>

#### **Usage and Citation Metrics**

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

Al Yami S, et al. (2019) LFastqC: A lossless non-reference-based FASTQ compressor. PloS one, 14(11), e0224806.

Kim M, et al. (2016) MetaCRAM: an integrated pipeline for metagenomic taxonomy identification and compression. BMC bioinformatics, 17, 94.

Pinho AJ, et al. (2014) MFCompress: a compression tool for FASTA and multi-FASTA data. Bioinformatics (Oxford, England), 30(1), 117.