

Resource Summary Report

Generated by T1D on Sep 17, 2026

BFCounter

RRID:SCR_001248

Type: Tool

Proper Citation

BFCounter (RRID:SCR_001248)

Resource Information

URL: <https://github.com/pmelsted/BFCounter>

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Description: Software program for counting k-mers in DNA sequence data. It identifies all the k-mers that occur more than once in a DNA sequence data set using a Bloom filter, a probabilistic data structure that stores all the observed k-mers implicitly in memory with greatly reduced memory requirements.

Abbreviations: BFCounter

Synonyms: BF Counter: Memory efficient K-mer counting Software

Resource Type: software resource

Defining Citation: [PMID:21831268](#)

Keywords: c++, k-mer, dna sequence, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: BFCounter

Resource ID: SCR_001248

Alternate IDs: biotools:bfcounter, OMICS_02093

Alternate URLs: <https://bio.tools/bfcounter>

Old URLs: <http://pritch.bsd.uchicago.edu/bfcounter.html>,
<http://pritchardlab.stanford.edu/bfcounter.html>

License: GNU General Public License v3 or later

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195522+0000

Ratings and Alerts

No rating or validation information has been found for BFCOUNTER.

No alerts have been found for BFCOUNTER.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Leinonen M, et al. (2023) SAKE: Strobemer-assisted k-mer extraction. PloS one, 18(11), e0294415.

Pickett BD, et al. (2022) Genome assembly of the roundjaw bonefish (*Albula glossodonta*), a vulnerable circumtropical sportfish. GigaByte (Hong Kong, China), 2022, gigabyte44.

Nosi V, et al. (2021) MET Exon 14 Skipping: A Case Study for the Detection of Genetic Variants in Cancer Driver Genes by Deep Learning. International journal of molecular sciences, 22(8).

Manekar SC, et al. (2018) A benchmark study of k-mer counting methods for high-throughput sequencing. GigaScience, 7(12).

Wang M, et al. (2015) Subtractive assembly for comparative metagenomics, and its application to type 2 diabetes metagenomes. Genome biology, 16, 243.