Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 15, 2025

KMC

RRID:SCR_001245
Type: Tool

Proper Citation

KMC (RRID:SCR_001245)

Resource Information

URL: http://sun.aei.polsl.pl/kmc/

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Description: Software utility for counting k-mers (sequences of consecutive k symbols) in a set of reads from genome sequencing projects. It scans the raw reads and produces a compact representation of all non-unique reads accompanied with number of their occurrences. The algorithm implemented makes use mostly of disk space rather than RAM, which allows to use KMC even on rather typical personal computers.

Abbreviations: KMC

Synonyms: KMC - K-mer Counter, K-mer Counter

Resource Type: software resource

Defining Citation: PMID:23679007, DOI:10.1093/bioinformatics/btv022

Keywords: c++, k-mer, genome sequencing, linux, windows, de bruijn graph

Funding:

Availability: GNU General Public License, v3

Resource Name: KMC

Resource ID: SCR_001245

Alternate IDs: OMICS_02095

Alternate URLs: https://sources.debian.org/src/kmc/

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250410T064657+0000

Ratings and Alerts

No rating or validation information has been found for KMC.

No alerts have been found for KMC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Weng YM, et al. (2024) Evolutionary genomics of three agricultural pest moths reveals rapid evolution of host adaptation and immune-related genes. GigaScience, 13.

Markee A, et al. (2024) De Novo Long-Read Genome Assembly and Annotation of the Luna Moth (Actias luna) Fully Resolves Repeat-Rich Silk Genes. Genome biology and evolution, 16(7).

Skojec C, et al. (2024) Long read genome assembly of Automeris io (Lepidoptera: Saturniidae) an emerging model for the evolution of deimatic displays. G3 (Bethesda, Md.), 14(3).

Godfrey RK, et al. (2023) A high-quality, long-read genome assembly of the whitelined sphinx moth (Lepidoptera: Sphingidae: Hyles lineata) shows highly conserved melanin synthesis pathway genes. G3 (Bethesda, Md.), 13(6).

Wang L, et al. (2022) The Capparis spinosa var. herbacea genome provides the first genomic instrument for a diversity and evolution study of the Capparaceae family. GigaScience, 11.

Huang Q, et al. (2022) Identification of sex chromosomes and primary sex ratio in the small hive beetle, a worldwide parasite of honey bees. GigaScience, 12.

Kawahara AY, et al. (2022) Long-read HiFi sequencing correctly assembles repetitive heavy fibroin silk genes in new moth and caddisfly genomes. GigaByte (Hong Kong, China), 2022,

gigabyte64.

Kim JH, et al. (2020) Dissecting seed pigmentation-associated genomic loci and genes by employing dual approaches of reference-based and k-mer-based GWAS with 438 Glycine accessions. PloS one, 15(12), e0243085.

Liang Q, et al. (2019) The genome assembly and annotation of yellowhorn (Xanthoceras sorbifolium Bunge). GigaScience, 8(6).