

Resource Summary Report

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khmer

RRID:SCR_001156

Type: Tool

Proper Citation

khmer (RRID:SCR_001156)

Resource Information

URL: <http://khmer.readthedocs.org/>

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Description: Software library and suite of command line tools for working with DNA sequence that takes a k-mer-centric approach to sequence analysis. It is primarily aimed at short-read sequencing data such as that produced by the Illumina platform.

Synonyms: khmer project, khmer - k-mer counting & filtering FTW, khmer - k-mer counting and filtering FTW, khmer: k-mer counting filtering and graph traversal FTW

Resource Type: software resource, software toolkit

Defining Citation: [PMID:26535114](#), [DOI:10.12688/f1000research.6924.1](#)

Keywords: dna sequence, short-read, sequencing, dna, illumina, sequence analysis, bio.tools

Funding: NHGRI R01HG007513

Availability: Free, Available for download, Freely available

Resource Name: khmer

Resource ID: SCR_001156

Alternate IDs: SciRes_000166, OMICS_02560, biotools:khmer

Alternate URLs: <https://github.com/dib-lab/khmer>, <https://bio.tools/khmer>, <https://sources.debian.org/src/khmer/>

Old URLs: <https://github.com/ged-lab/khmer>, <http://ged.msu.edu/papers/2012-diginorm/>

License: BSD License

Record Creation Time: 20220129T080205+0000

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Ratings and Alerts

No rating or validation information has been found for khmer.

No alerts have been found for khmer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Silva JM, et al. (2024) AltaiR: a C toolkit for alignment-free and temporal analysis of multi-FASTA data. GigaScience, 13.

Phillips AL, et al. (2022) The first long-read nuclear genome assembly of *Oryza australiensis*, a wild rice from northern Australia. Scientific reports, 12(1), 10823.

Johnson LK, et al. (2019) Re-assembly, quality evaluation, and annotation of 678 microbial eukaryotic reference transcriptomes. GigaScience, 8(4).

Mizzi JE, et al. (2017) Draft genome of tule elk *Cervus canadensis* nannodes. F1000Research, 6, 1691.

Crusoe MR, et al. (2015) The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research, 4, 900.

Hahn C, et al. (2014) Comparative genomics of flatworms (platyhelminthes) reveals shared genomic features of ecto- and endoparasitic neodermata. Genome biology and evolution, 6(5), 1105.

Busk PK, et al. (2014) Several genes encoding enzymes with the same activity are necessary for aerobic fungal degradation of cellulose in nature. PloS one, 9(12), e114138.

Beall CJ, et al. (2014) Single cell genomics of uncultured, health-associated *Tannerella* BU063 (Oral Taxon 286) and comparison to the closely related pathogen *Tannerella forsythia*. PloS one, 9(2), e89398.

Christenson MK, et al. (2014) De novo Assembly and Analysis of the Northern Leopard Frog *Rana pipiens* Transcriptome. Journal of genomics, 2, 141.

Zhang Q, et al. (2014) These are not the k-mers you are looking for: efficient online k-mer counting using a probabilistic data structure. *PloS one*, 9(7), e101271.

Abubucker S, et al. (2014) Identification and characterization of alternative splicing in parasitic nematode transcriptomes. *Parasites & vectors*, 7, 151.

Sharpton TJ, et al. (2014) An introduction to the analysis of shotgun metagenomic data. *Frontiers in plant science*, 5, 209.

Drezen E, et al. (2014) GATB: Genome Assembly & Analysis Tool Box. *Bioinformatics* (Oxford, England), 30(20), 2959.

Koutsovoulos G, et al. (2014) Palaeosymbiosis revealed by genomic fossils of *Wolbachia* in a strongyloidean nematode. *PLoS genetics*, 10(6), e1004397.

Schloss PD, et al. (2014) The dynamics of a family's gut microbiota reveal variations on a theme. *Microbiome*, 2, 25.

Neave MJ, et al. (2014) Whole-genome sequences of three symbiotic endozoicomonas strains. *Genome announcements*, 2(4).

Giorello FM, et al. (2014) Characterization of the kidney transcriptome of the South American olive mouse *Abrothrix olivacea*. *BMC genomics*, 15(1), 446.

Podar M, et al. (2013) Insights into archaeal evolution and symbiosis from the genomes of a nanoarchaeon and its inferred crenarchaeal host from Obsidian Pool, Yellowstone National Park. *Biology direct*, 8, 9.

Comandatore F, et al. (2013) Phylogenomics and analysis of shared genes suggest a single transition to mutualism in *Wolbachia* of nematodes. *Genome biology and evolution*, 5(9), 1668.

Segata N, et al. (2013) Computational meta'omics for microbial community studies. *Molecular systems biology*, 9, 666.