

# 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 toolkit, software resource

**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

**Record Last Update:** 20260803T040300+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.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 25 mentions in open access literature.

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

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.

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.

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.

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

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.

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

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

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

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

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

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).

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.

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.

Tulin S, et al. (2013) A quantitative reference transcriptome for *Nematostella vectensis* early embryonic development: a pipeline for de novo assembly in emerging model systems. EvoDevo, 4, 16.