

Resource Summary Report

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KAT

RRID:SCR_016741

Type: Tool

Proper Citation

KAT (RRID:SCR_016741)

Resource Information

URL: <https://github.com/TGAC/KAT>

Proper Citation: KAT (RRID:SCR_016741)

Description: Software that generates, analyses and compares k-mer spectra produced from sequence files. Used to quality control NGS datasets and genome assemblies.

Abbreviations: KAT

Synonyms: K-mer Analysis Toolkit

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [DOI:10.1093/bioinformatics/btw663](https://doi.org/10.1093/bioinformatics/btw663)

Keywords: generate, analyse, compare, k-mer, spectra, sequence, file, quality, control, NGS, dataset, genome, assembly, bio.tools

Funding: BBSRC

Availability: Free, Available for download, Freely available

Resource Name: KAT

Resource ID: SCR_016741

Alternate IDs: biotools:kat

Alternate URLs: <http://www.earlham.ac.uk/kat-tools>, <https://bio.tools/kat>

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260905T132813+0000

Ratings and Alerts

No rating or validation information has been found for KAT.

No alerts have been found for KAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 21 mentions in open access literature.

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

Chen X, et al. (2025) Comparative genomic analysis of *Artemisia argyi* reveals asymmetric expansion of terpene synthases and conservation of artemisinin biosynthesis. *The Plant journal : for cell and molecular biology*, 124(5), e70548.

Xin H, et al. (2025) Jan and mini-Jan, a model system for potato functional genomics. *Plant biotechnology journal*, 23(4), 1243.

Etherington G, et al. (2025) Reconstruction of the X and Y haplotypes in the genetically improved Abbassa Nile tilapia genome assembly. *Scientific reports*, 15(1), 16057.

Hu Y, et al. (2025) Highly contiguous genome of the medicinal plant *Sarcandra glabra* (Thunb.) Nakai. *Scientific data*, 12(1), 1508.

Garsmeur O, et al. (2025) The genomic footprints of wild *Saccharum* species trace domestication, diversification, and modern breeding of sugarcane. *Cell*, 188(25), 7252.

Pajares IG, et al. (2024) Draft genome sequence of *Rhodotorula* sp. BUB8, an oleaginous yeast isolated from Mt. Makiling Forest Reserve, Laguna, Philippines. *Microbiology resource announcements*, 13(10), e0037724.

Xin H, et al. (2024) Jan and mini-Jan, a model system for potato functional genomics. *bioRxiv : the preprint server for biology*.

Patel S, et al. (2023) Genome assembly of the hybrid grapevine *Vitis* 'Chambourcin'. *GigaByte (Hong Kong, China)*, 2023, gigabyte84.

Kim J, et al. (2022) A beginner's guide to assembling a draft genome and analyzing structural variants with long-read sequencing technologies. *STAR protocols*, 3(3), 101506.

Boyes D, et al. (2022) The genome sequence of the small elephant hawk moth, *Deilephila porcellus* (Linnaeus, 1758). *Wellcome open research*, 7, 80.

Dinh HX, et al. (2022) The barley leaf rust resistance gene *Rph3* encodes a predicted membrane protein and is induced upon infection by avirulent pathotypes of *Puccinia hordei*. *Nature communications*, 13(1), 2386.

Çilingir FG, et al. (2022) Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. *GigaScience*, 11.

Theelen B, et al. (2022) Multiple Hybridization Events Punctuate the Evolutionary Trajectory of *Malassezia furfur*. *mBio*, 13(2), e0385321.

Machado AM, et al. (2022) A genome assembly of the Atlantic chub mackerel (*Scomber colias*): a valuable teleost fishing resource. *GigaByte* (Hong Kong, China), 2022, gigabyte40.

Palmieri D, et al. (2021) Complete genome sequence of the biocontrol yeast *Papiliotrema terrestris* strain LS28. *G3* (Bethesda, Md.), 11(12).

Sheffer MM, et al. (2021) Chromosome-level reference genome of the European wasp spider *Argiope bruennichi*: a resource for studies on range expansion and evolutionary adaptation. *GigaScience*, 10(1).

He C, et al. (2020) Factorial estimating assembly base errors using k-mer abundance difference (KAD) between short reads and genome assembled sequences. *NAR genomics and bioinformatics*, 2(3), lqaa075.

Murigneux V, et al. (2020) Comparison of long-read methods for sequencing and assembly of a plant genome. *GigaScience*, 9(12).

Paajanen P, et al. (2019) A critical comparison of technologies for a plant genome sequencing project. *GigaScience*, 8(3).

Lonardi S, et al. (2019) The genome of cowpea (*Vigna unguiculata* [L.] Walp.). *The Plant journal : for cell and molecular biology*, 98(5), 767.