Resource Summary Report

Generated by dkNET on May 18, 2025

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

Defining Citation: DOI: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: 20250517T060306+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 13 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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.

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.

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).

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

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.

Johnson RN, et al. (2018) Adaptation and conservation insights from the koala genome. Nature genetics, 50(8), 1102.