Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 16, 2025

KMA

RRID:SCR_024054
Type: Tool

Proper Citation

KMA (RRID:SCR_024054)

Resource Information

URL: https://bitbucket.org/genomicepidemiology/kma/src/master/

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Description: Software mapping method designed to map raw reads directly against redundant databases, in an ultra-fast manner using seed and extend.Used for aligning high quality reads against highly redundant databases, where unique matches often does not exist. Works for long low quality reads as well, such as those from Nanopore. Non-unique matches are resolved using the "ConClave" sorting scheme, and a consensus sequence are outputtet in addition to other common attributes, based on users demands.

Synonyms: kma

Resource Type: software resource, software application, alignment software, image analysis software, data processing software

Defining Citation: PMID:30157759

Keywords: aligning high quality reads against highly redundant databases, aligning high quality reads, highly redundant databases,

Funding:

Availability: Free, Available for download, Freely available,

Resource Name: KMA

Resource ID: SCR_024054

Alternate IDs: OMICS_31606

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

License: Apache License v2.0

Record Creation Time: 20230824T050211+0000

Record Last Update: 20250416T063952+0000

Ratings and Alerts

No rating or validation information has been found for KMA.

No alerts have been found for KMA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Solis MN, et al. (2024) Detecting Class 1 Integrons and Their Variable Regions in Escherichia coli Whole-Genome Sequences Reported from Andean Community Countries. Antibiotics (Basel, Switzerland), 13(5).