

Resource Summary Report

Generated by SPARC SAWG on Aug 1, 2026

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 outputted in addition to other common attributes, based on users demands.

Synonyms: kma

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

Defining Citation: [PMID:30157759](#)

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

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: 20260801T042915+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 [SPARC SAWG](#) .

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).