

# Resource Summary Report

Generated by [PRECISE-TBI](#) on Sep 7, 2026

## KMA

RRID:SCR\_024054

Type: Tool

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### Proper Citation

KMA (RRID:SCR\_024054)

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### Resource Information

**URL:** <https://bitbucket.org/genomicepidemiology/kma/src/master/>

**Proper Citation:** KMA (RRID:SCR\_024054)

**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:** alignment software, data processing software, image analysis software, software application, software resource

**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:** 20260905T133028+0000

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## Ratings and Alerts

No rating or validation information has been found for KMA.

No alerts have been found for KMA.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 1 mentions in open access literature.

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

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).