

Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

RMAP

RRID:SCR_000695

Type: Tool

Proper Citation

RMAP (RRID:SCR_000695)

Resource Information

URL: <http://rulai.cshl.edu/rmap/>

Proper Citation: RMAP (RRID:SCR_000695)

Description: Software for short-read mapping to accurately map reads from the next-generation sequencing technology. It can map reads with or without error probability information (quality scores) and supports paired-end reads or bisulfite-treated reads mapping. There is no limitations on read widths or number of mismatches. RMAP can now map more than 8 million reads in an hour at full sensitivity to 2 mismatches.

Abbreviations: RMAP

Resource Type: software resource

Defining Citation: [PMID:19736251](#)

Keywords: next-generation sequencing, solexa

Resource Name: RMAP

Resource ID: SCR_000695

Alternate IDs: OMICS_00681

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260808T185729+0000

Ratings and Alerts

No rating or validation information has been found for RMAP.

No alerts have been found for RMAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Wu Y, et al. (2016) A Genome-Wide Transcriptional Analysis of Yeast-Hyphal Transition in Candida tropicalis by RNA-Seq. PloS one, 11(11), e0166645.