Resource Summary Report

Generated by NIF on May 4, 2025

RMAP

RRID:SCR_000695
Type: Tool

Proper Citation

RMAP (RRID:SCR_000695)

Resource Information

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

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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 limitaions 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

Funding:

Resource Name: RMAP

Resource ID: SCR_000695

Alternate IDs: OMICS_00681

Record Creation Time: 20220129T080203+0000

Record Last Update: 20250420T014002+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 NIF.

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.