

Resource Summary Report

Generated by [NIF](#) on Aug 21, 2026

[rapmap](#)

RRID:SCR_024204

Type: Tool

Proper Citation

rapmap (RRID:SCR_024204)

Resource Information

URL: <https://github.com/COMBINE-lab/RapMap>

Proper Citation: rapmap (RRID:SCR_024204)

Description: Software tool for mapping RNA-seq reads to transcriptomes. Used for rapid sensitive and accurate read mapping via quasi-mapping

Synonyms: RapMap

Resource Type: software library, software resource, software toolkit

Defining Citation: [PMID:27307617](#)

Keywords: mapping RNA-seq reads to transcriptomes, mapping RNA-seq reads,

Availability: Free, Available for download, Freely available,

Resource Name: rapmap

Resource ID: SCR_024204

Alternate IDs: OMICS_10349

Alternate URLs: <https://sources.debian.org/src/rapmap/>

License: GPL-3.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260821T194250+0000

Ratings and Alerts

No rating or validation information has been found for rapmap.

No alerts have been found for rapmap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Wang H, et al. (2025) Unveiling Novel Viral Diversity, Biogeography, and Host Networks in Wildlife Through High-Throughput Sequencing Data Mining. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(46), e11920.

Zahid M, et al. (2023) Cardiomyocyte-Targeting Peptide to Deliver Amiodarone. *Pharmaceutics*, 15(8).

Zahid M, et al. (2023) Cardiomyocyte Targeting Peptide to Deliver Amiodarone. *bioRxiv* : the preprint server for biology.

Doherty LM, et al. (2022) Integrating multi-omics data reveals function and therapeutic potential of deubiquitinating enzymes. *eLife*, 11.

Yeo AT, et al. (2022) Single-cell RNA sequencing reveals evolution of immune landscape during glioblastoma progression. *Nature immunology*, 23(6), 971.

Nguyen DT, et al. (2021) Circall: fast and accurate methodology for discovery of circular RNAs from paired-end RNA-sequencing data. *BMC bioinformatics*, 22(1), 495.

Grassi L, et al. (2021) Cell type-specific novel long non-coding RNA and circular RNA in the BLUEPRINT hematopoietic transcriptomes atlas. *Haematologica*, 106(10), 2613.

Tattikota SG, et al. (2020) A single-cell survey of Drosophila blood. *eLife*, 9.

Ha CWY, et al. (2020) Translocation of Viable Gut Microbiota to Mesenteric Adipose Drives Formation of Creeping Fat in Humans. *Cell*, 183(3), 666.