# Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 11, 2025

## MMSEQ

RRID:SCR_008184
Type: Tool

### Proper Citation

MMSEQ (RRID:SCR_008184)

### Resource Information

**URL:** https://github.com/eturro/mmseq#mmseq-transcript-and-gene-level-expression-analysis-using-multi-mapping-rna-seq-reads

**Proper Citation:** MMSEQ (RRID:SCR_008184)

**Description:** Software package that contains a collection of statistical tools for analysing RNA-seq expression data.

**Abbreviations:** MMSEQ

**Resource Type:** software resource

**Defining Citation:** PMID:24281695

**Funding:**

**Resource Name:** MMSEQ

**Resource ID:** SCR_008184

**Alternate IDs:** OMICS_01280

**Record Creation Time:** 20220129T080246+0000

**Record Last Update:** 20250410T065711+0000

### Ratings and Alerts

No rating or validation information has been found for MMSEQ.

No alerts have been found for MMSEQ.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 45 mentions in open access literature.

**Listed below are recent publications.** The full list is available at FDI Lab - SciCrunch.org.


Jo J, et al. (2024) The first Chromosomal-level genome assembly of Sageretia thea using Nanopore long reads and Pore-C technology. Scientific data, 11(1), 959.

Jousheghani ZZ, et al. (2024) Oarfish: Enhanced probabilistic modeling leads to improved accuracy in long read transcriptome quantification. bioRxiv : the preprint server for biology.

Dos Santos JC, et al. (2024) Leishmania braziliensis enhances monocyte responses to promote anti-tumor activity. Cell reports, 43(3), 113932.

Pang B, et al. (2024) A chromosome-level genome assembly of Prosopocoilus inquinatus Westwood, 1848 (Coleoptera: Lucanidae). Scientific data, 11(1), 808.

Campbell A, et al. (2024) The RNA helicase HrpA rescues collided ribosomes in E. coli. bioRxiv : the preprint server for biology.

Bekkering S, et al. (2024) Increased innate immune responses in adolescents with obesity and its relation to subclinical cardiovascular measures: An exploratory study. iScience, 27(5), 109762.

Zhang Y, et al. (2024) Insights into the mechanisms of serplulimab: a distinctive anti-PD-1 monoclonal antibody, in combination with a TIGIT or LAG3 inhibitor in preclinical tumor immunotherapy studies. mAbs, 16(1), 2419838.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. Cell, 187(24), 6943.

Modi R, et al. (2023) Stapled Peptides as Direct Inhibitors of Nrf2-sMAF Transcription Factors. Journal of medicinal chemistry, 66(9), 6184.

Torosyan H, et al. (2023) Structural insights into regulation of the PEAK3 pseudokinase scaffold by 14-3-3. Nature communications, 14(1), 3543.

Schrijver DP, et al. (2023) Resolving sepsis-induced immunoparalysis via trained immunity by targeting interleukin-4 to myeloid cells. Nature biomedical engineering, 7(9), 1097.

van Puffelen JH, et al. (2023) Intravesical BCG in patients with non-muscle invasive bladder cancer induces trained immunity and decreases respiratory infections. Journal for immunotherapy of cancer, 11(1).

Hernández IM, et al. (2023) Predicting protein stability changes upon mutation using a simple orientational potential. Bioinformatics (Oxford, England), 39(1).

Jeong YS, et al. (2023) Clinically conserved genomic subtypes of gastric adenocarcinoma. Molecular cancer, 22(1), 147.

Viehweger A, et al. (2023) Nanopore-based enrichment of antimicrobial resistance genes - a case-based study. GigaByte (Hong Kong, China), 2023, gigabyte75.

Wang C, et al. (2022) Abnormal global alternative RNA splicing in COVID-19 patients. PLoS genetics, 18(4), e1010137.

Wen J, et al. (2022) Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS genetics, 18(1), e1009984.

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.

Groh LA, et al. (2021) oxLDL-Induced Trained Immunity Is Dependent on Mitochondrial Metabolic Reprogramming. Immunometabolism, 3(3), e210025.

Kaur G, et al. (2021) Bacterial death and TRADD-N domains help define novel apoptosis and immunity mechanisms shared by prokaryotes and metazoans. eLife, 10.