

Resource Summary Report

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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](#)

Resource Name: MMSEQ

Resource ID: SCR_008184

Alternate IDs: OMICS_01280

Record Creation Time: 20220129T080246+0000

Record Last Update: 20260829T182309+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 66 mentions in open access literature.

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

Conry M, et al. (2026) Multiple myeloma risk linked to DNA damage response genes. *Journal of hematology & oncology*, 19(1), 10.

Tao M, et al. (2026) Metagenomic Analysis of Gut Microbiome Across Developmental Stage of Asian Corn Borer (*Ostrinia furnacalis*). *Insects*, 17(5).

Han ZR, et al. (2026) Chromosome-level genome assembly of *Neoseiulus longispinosus* (Phytoseiidae). *Scientific data*, 13(1).

Rapala JR, et al. (2026) Deep homology and design of proteasome chaperone proteins in *Candidozyma auris*. *Nature communications*, 17(1).

Lin A, et al. (2026) Chromosome-level genome assembly of the stonefly *Rhopalopsale triangulispina* Mo and Li, 2025 (Plecoptera: Leuctridae). *Scientific data*, 13(1).

Zhan Z, et al. (2026) Haplotype-resolved genome sequences of a springtail species, *Folsomia candida* (Collembola: Isotomidae). *Scientific data*, 13(1).

Florea M, et al. (2026) A pseudoenzyme enables indole biosynthesis in eudicot plants. *Nature chemical biology*, 22(1), 120.

Yang Y, et al. (2026) Chromosomal-level genome assembly of *Ichthyurus bourgeoisi* Gestro using PacBio HiFi and Hi-C sequencing. *Scientific data*, 13(1).

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. *Nature*, 643(8070), 252.

Abdollahi A, et al. (2025) The FGFR inhibitor pemigatinib overcomes cancer drug resistance to KRAS G12C inhibitors in mesenchymal lung cancer. *PloS one*, 20(8), e0327588.

Paul JK, et al. (2025) Exploration of Human Skin Phageome to Reveal Endolysins and Novel Antimicrobial Peptides for Therapeutic Applications. *MicrobiologyOpen*, 14(6), e70115.

Zhao Y, et al. (2025) Chromosome-level genome of the brown lacewing *Micromus angulatus* (Stephens, 1836) (Neuroptera: Hemerobiidae). *Scientific data*, 12(1), 394.

He HD, et al. (2025) A chromosome-level genome assembly of the flat mite *Brevipalpus obovatus*. *Scientific data*, 12(1), 1779.

Liang L, et al. (2025) A chromosome-level genome assembly of the dried fruit mite *Carpoglyphus lactis*. *Scientific data*, 12(1), 1753.

Jin Y, et al. (2025) Developing transcriptomic biomarkers for TAVO412 utilizing next generation sequencing analyses of preclinical tumor models. *Frontiers in immunology*, 16,

1505868.

Ortiz de Ora L, et al. (2025) Phollow reveals in situ phage transmission dynamics in the zebrafish gut microbiome at single-virion resolution. *Nature microbiology*, 10(5), 1067.

Wang C, et al. (2025) A chromosomal-level genome assembly of *Trichogramma chilonis* Ishii, 1941 (Hymenoptera: Trichogrammatidae). *Scientific data*, 12(1), 457.

Sullivan AE, et al. (2025) The Panoptes system uses decoy cyclic nucleotides to defend against phage. *Nature*, 647(8091), 988.

Muller H, et al. (2025) Diversification of the Staphylococcal Cassette Chromosome Through Distinct Mechanisms of Horizontal Transfer. *Genome biology and evolution*, 17(11).

Mo R, et al. (2025) Chromosome-level genome assembly of the stonefly *Indonemoura scalprata* (Plecoptera: Nemouridae). *Scientific data*, 13(1), 113.