

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

MMseq2

RRID:SCR_026553

Type: Tool

Proper Citation

MMseq2 (RRID:SCR_026553)

Resource Information

URL: <https://github.com/soedinglab/mmseqs2>

Proper Citation: MMseq2 (RRID:SCR_026553)

Description: Software suite to search and cluster huge protein and nucleotide sequence sets. Sensitive protein sequence searching for analysis of massive data sets. Used for ultra fast and sensitive search and clustering.

Synonyms: Many-against-Many sequence searching

Resource Type: software toolkit, source code, software resource

Defining Citation: [PMID:29035372](#)

Keywords: search and cluster huge protein sets, search and cluster nucleotide sequence sets, protein sequence searching, analysis of massive data sets,

Funding: European Research Council's Horizon 2020 Framework Programme for Research and Innovation ;
German Federal Ministry for Education and Research

Availability: Free, Available for download, Freely available

Resource Name: MMseq2

Resource ID: SCR_026553

License: MIT license

Record Creation Time: 20250311T060327+0000

Record Last Update: 20260815T042918+0000

Ratings and Alerts

No rating or validation information has been found for MMseq2 .

No alerts have been found for MMseq2 .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Fujimura E, et al. (2026) A viral ORFeome library for systems-level genetic dissection of host-pathogen interactions. Cell.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. Current biology : CB, 36(6), 1481.

Lev?? M, et al. (2025) Metabolomics and metagenomics in mice reveal the role of the gut microbiota in tryptophan metabolism. iScience, 28(11), 113751.