

Resource Summary Report

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MashMap

RRID:SCR_022194

Type: Tool

Proper Citation

MashMap (RRID:SCR_022194)

Resource Information

URL: <https://github.com/marbl/MashMap>

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Description: Software tool as fast approximate aligner for long DNA sequences. Used for computing local alignment boundaries between long DNA sequences.

Resource Type: image analysis software, software resource, software application, data processing software, alignment software

Defining Citation: [PMID:30423094](#), [DOI:10.1007/978-3-319-56970-3_5](#)

Keywords: mapping genome assembly, long DNA sequences, long reads, reference genome, long DNA sequences aligner

Funding: NSF CCF1816027;
National Human Genome Research Institute ;
NIH

Availability: Free, Available for download, Freely available

Resource Name: MashMap

Resource ID: SCR_022194

License URLs: <https://github.com/marbl/MashMap/blob/master/LICENSE.txt>

Record Creation Time: 20220427T191217+0000

Record Last Update: 20260813T055241+0000

Ratings and Alerts

No rating or validation information has been found for MashMap.

No alerts have been found for MashMap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Bresnahan ST, et al. (2026) Long-read assembly reveals vast transcriptional complexity in the placenta associated with metabolic and endocrine function. *Nature communications*, 17(1).

Hallast P, et al. (2026) Population-scale Y chromosome assemblies reveal recurrent remodeling within constrained architectures. *bioRxiv : the preprint server for biology*.

Law STS, et al. (2026) The first chromosome-level cubozoan genome differentiates unique and common features in different cnidarian lineages. *BMC biology*, 24(1).

Ivancevic A, et al. (2026) Whole-genome sequences of the dwarf honey bee subgenus *Micrapis*: *Apis andreniformis* and *Apis florea*. *G3 (Bethesda, Md.)*, 16(3).

Francis BA, et al. (2025) Complete genome assemblies of two mouse subspecies reveal structural diversity of telomeres and centromeres. *Nature genetics*, 57(11), 2852.

Volpe E, et al. (2025) The reference genome of the human diploid cell line RPE-1. *Nature communications*, 16(1), 7751.

Chen Y, et al. (2025) Analysis of a Novel Human Protein, ORF3, Encoded by Spacer rDNA. *Journal of molecular evolution*, 93(5), 650.

Santoro DF, et al. (2025) Polyploidization-driven transcriptomic dynamics in *Medicago sativa* neotetraploids: mRNA, smRNA and allele-specific gene expression. *BMC plant biology*, 25(1), 108.

Formenti G, et al. (2025) The complete genome of a songbird. *bioRxiv : the preprint server for biology*.

Ilyukhin E, et al. (2025) ???Comprehensive genome analysis of two *Cytospora* (Cytosporaceae, Diaporthales) species associated with canker disease of spruce: *C.piceae* and *C.piceicola* sp. nov. *MycKeys*, 117, 89.

Makova KD, et al. (2024) The complete sequence and comparative analysis of ape sex chromosomes. *Nature*, 630(8016), 401.

Cavalet-Giorsa E, et al. (2024) Origin and evolution of the bread wheat D genome. *Nature*, 633(8031), 848.

Carroll RA, et al. (2024) A chromosome-scale fishing cat reference genome for the evaluation of potential germline risk variants. *Scientific reports*, 14(1), 8073.

Liu L, et al. (2024) Genome-wide survey of the bipartite structure and pathogenesis-related genes of *Neostagonosporella sichuanensis*, a causal agent of Fishscale bamboo rhombic-spot disease. *Frontiers in microbiology*, 15, 1456993.

Xu XW, et al. (2023) Assembly of the poorly differentiated *Verasper variegatus* W chromosome by different sequencing technologies. *Scientific data*, 10(1), 893.

Makova KD, et al. (2023) The Complete Sequence and Comparative Analysis of Ape Sex Chromosomes. *bioRxiv : the preprint server for biology*.

Kille B, et al. (2023) Minmers are a generalization of minimizers that enable unbiased local Jaccard estimation. *Bioinformatics (Oxford, England)*, 39(9).

Yang Y, et al. (2023) A near-complete assembly of asparagus bean provides insights into anthocyanin accumulation in pods. *Plant biotechnology journal*, 21(12), 2473.

Papa Y, et al. (2023) Genome assembly and isoform analysis of a highly heterozygous New Zealand fisheries species, the tarakihi (*Nemadactylus macropterus*). *G3 (Bethesda, Md.)*, 13(2).

Volpe E, et al. (2023) The complete diploid reference genome of RPE-1 identifies human phased epigenetic landscapes. *bioRxiv : the preprint server for biology*.