

Resource Summary Report

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Vmatch

RRID:SCR_018968

Type: Tool

Proper Citation

Vmatch (RRID:SCR_018968)

Resource Information

URL: <http://www.vmatch.de/>

Proper Citation: Vmatch (RRID:SCR_018968)

Description: Software tool for efficiently solving large scale sequence matching tasks.

Resource Type: data analysis software, software application, software resource, sequence analysis software, data processing software

Keywords: Sequence analysis, large scale, sequence matching, sequence, matching, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: Vmatch

Resource ID: SCR_018968

Alternate IDs: OMICS_19963, biotools:vmatch

Alternate URLs: <https://bio.tools/vmatch>, <https://sources.debian.org/src/vmatch/>

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260801T190607+0000

Ratings and Alerts

No rating or validation information has been found for Vmatch.

No alerts have been found for Vmatch.

Data and Source Information

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Li D, et al. (2025) Assembly and comparative analysis of the first complete mitochondrial genome of *Camellia sinensis* var. *assamica* 'Hainan Dayezhong', endemic to Hainan Province, China. *BMC plant biology*, 25(1), 1304.

Zou T, et al. (2025) Chloroplast whole genome assembly and phylogenetic analysis of *Persicaria criopolitana* reveals its new taxonomic status. *Scientific reports*, 15(1), 19890.

Liu Z, et al. (2025) Genome architecture of the allotetraploid wild grass *Aegilops ventricosa* reveals its evolutionary history and contributions to wheat improvement. *Plant communications*, 6(1), 101131.

Hu J, et al. (2024) Comparative analysis of chloroplast genomes in ten holly (*Ilex*) species: insights into phylogenetics and genome evolution. *BMC ecology and evolution*, 24(1), 133.

Jayakodi M, et al. (2024) Structural variation in the pangenome of wild and domesticated barley. *Nature*, 636(8043), 654.

Liu Z, et al. (2024) Chromosome-level assembly of the synthetic hexaploid wheat-derived cultivar Chuanmai 104. *Scientific data*, 11(1), 670.

Zhan Q, et al. (2024) Comparative chloroplast genomics and phylogenetic analysis of *Oreomecon nudicaulis* (Papaveraceae). *BMC genomic data*, 25(1), 49.

Wang M, et al. (2024) ICEberg 3.0: functional categorization and analysis of the integrative and conjugative elements in bacteria. *Nucleic acids research*, 52(D1), D732.

Wiersma AT, et al. (2024) k-mer genome-wide association study for anthracnose and BCMV resistance in a *Phaseolus vulgaris* Andean Diversity Panel. *The plant genome*, 17(4), e20523.

Hu Q, et al. (2023) Complete chloroplast genome molecular structure, comparative and phylogenetic analyses of *Sphaeropteris lepifera* of Cyatheaceae family: a tree fern from China. *Scientific reports*, 13(1), 1356.

Kallies R, et al. (2023) Identification of Huge Phages from Wastewater Metagenomes. *Viruses*, 15(12).

Zhang H, et al. (2023) Complete Chloroplast Genomes and Phylogenetic Relationships of *Bougainvillea spectabilis* and *Bougainvillea glabra* (Nyctaginaceae). *International journal of molecular sciences*, 24(17).

Li LF, et al. (2022) Genome sequences of five *Sitopsis* species of *Aegilops* and the origin of polyploid wheat B subgenome. *Molecular plant*, 15(3), 488.

Riveros-Loaiza LM, et al. (2022) Uncovering anthocyanin diversity in potato landraces (*Solanum tuberosum* L. Phureja) using RNA-seq. *PloS one*, 17(9), e0273982.

Zangishei Z, et al. (2022) Parasitic plant small RNA analyses unveil parasite-specific signatures of microRNA retention, loss, and gain. *Plant physiology*, 190(2), 1242.

Mitrofanov A, et al. (2021) CRISPRidentify: identification of CRISPR arrays using machine learning approach. *Nucleic acids research*, 49(4), e20.

Xiong Q, et al. (2021) Chloroplast genomes of five *Oedogonium* species: genome structure, phylogenetic analysis and adaptive evolution. *BMC genomics*, 22(1), 707.

Xu Y, et al. (2021) Mobilization of the nonconjugative virulence plasmid from hypervirulent *Klebsiella pneumoniae*. *Genome medicine*, 13(1), 119.

Yoo MJ, et al. (2021) Complete Plastome of Three Korean Asarum (*Aristolochiaceae*): Confirmation Tripartite Structure within Korean Asarum and Comparative Analyses. *Plants (Basel, Switzerland)*, 10(10).

Alser M, et al. (2021) Technology dictates algorithms: recent developments in read alignment. *Genome biology*, 22(1), 249.