

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, data processing software, sequence analysis software, software application, software resource

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: 20260821T194153+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 56 mentions in open access literature.

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

Pan W, et al. (2026) Analysis of chloroplast genomes and SSR classification and identification of *Agropyron* species and closely related species. *Scientific reports*, 16(1), 3579.

Kale SM, et al. (2026) Extensive variation between chromosomes of North American and European hop. *Nature communications*, 17(1).

Li Q, et al. (2026) The First Complete Mitochondrial Genome of *Corydalis impatiens* (Papaveraceae) and Its Phylogenetic Implications. *Current issues in molecular biology*, 48(3).

Liu S, et al. (2026) Complete chloroplast genome features and phylogenetic analysis of *Clematis cadmia*. *Scientific reports*, 16(1).

Song XF, et al. (2026) The complete mitochondrial genome of the *Perinereis linea* (Polychaeta: Nereididae) and Nereididae phylogenetic implications. *Mitochondrial DNA. Part B, Resources*, 11(5), 604.

Jiang J, et al. (2026) Phylogeny and Selection Pressure of Genus *Chimarrogale* in China Based on Mitochondrial Genomes. *Animals : an open access journal from MDPI*, 16(10).

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.

Zhang S, et al. (2025) Characterization of the Complete Mitochondrial Genome of *Angulyagra polyzonata* and Its Phylogenetic Status in Viviparidae. *Animals : an open access journal from MDPI*, 15(9).

Wei F, et al. (2025) Comparative analysis of complete chloroplast genomes of *Flemingia prostrata* and *Flemingia macrophylla*, two commonly used medicinal plants in southern China. *Frontiers in plant science*, 16, 1591427.

Zhu Z, et al. (2025) Sequencing, Assembly, and Comparative Evolutionary Analysis of the Chloroplast Genome of Kenaf (*Hibiscus cannabinus* L.). *Genes*, 16(12).

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.

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.

Zhao M, et al. (2024) Complete Chloroplast Genome Sequence Structure and Phylogenetic Analysis of Kohlrabi (*Brassica oleracea* var. *gongylodes* L.). *Genes*, 15(5).

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

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.

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.

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.

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