

Resource Summary Report

Generated by T1D on Aug 1, 2026

DIAMOND

RRID:SCR_016071

Type: Tool

Proper Citation

DIAMOND (RRID:SCR_016071)

Resource Information

URL: <https://github.com/bbuchfink/diamond>

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Description: Software that performs sequence alignment for protein and translated DNA searches and functions. Used for high performance analysis of big sequence data, protein-protein search, and DNA-protein search.

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

Defining Citation: [PMID:25402007](https://pubmed.ncbi.nlm.nih.gov/25402007/), [DOI:10.1038/nmeth.3176](https://doi.org/10.1038/nmeth.3176)

Keywords: sequence, aligner, high, performance, analysis, big, data, protein, DNA, bio.tools

Availability: Free, Available for download

Resource Name: DIAMOND

Resource ID: SCR_016071

Alternate IDs: OMICS_08011, biotools:diamond

Alternate URLs: <https://bio.tools/diamond>, <https://sources.debian.org/src/diamond-aligner/>

License: AGPL-3.0

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260801T042755+0000

Ratings and Alerts

No rating or validation information has been found for DIAMOND.

No alerts have been found for DIAMOND.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 386 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Kong Y, et al. (2026) Prebiotics as adjunctive treatment ameliorates DSS-induced colitis and gut microbiota. *Microbiology spectrum*, 14(1), e0150225.

Wangwiwatsin A, et al. (2025) The genome sequence of the liver fluke *Opisthorchis viverrini* (Poirier, 1886) Stiles & Hassall, 1896. *Wellcome open research*, 10, 1.

Chen XX, et al. (2025) Microbial dysbiosis with tryptophan metabolites alteration in lower respiratory tract is associated with clinical responses to anti-PD-1 immunotherapy in advanced non-small cell lung cancer. *Cancer immunology, immunotherapy : CII*, 74(4), 140.

Sivell D, et al. (2025) The genome sequence of the click beetle, *Ampedus sanguinolentus sanguinolentus* (Schrank, 1776). *Wellcome open research*, 10, 96.

Geiser MF, et al. (2025) The genome sequence of a flea beetle, *Neocrepidodera transversa* (Marsham, 1802). *Wellcome open research*, 10, 62.

Sivell D, et al. (2025) The genome sequence of a carabid beetle, *Carabus problematicus* Herbst, 1786. *Wellcome open research*, 10, 59.

Shi M, et al. (2025) Salt stress alters the selectivity of mature pecan for the rhizosphere community and its associated functional traits. *Frontiers in plant science*, 16, 1473473.

Ma R, et al. (2025) The bacterial diversity and potential pathogenic risks of giant panda-infesting ticks. *Microbiology spectrum*, 13(7), e0219724.

You Y, et al. (2025) Ecological effects of water and fertilizer addition on poplar-planting soil. *mSystems*, 10(7), e0050125.

Márquez R, et al. (2025) A draft genome assembly for the dart-poison frog *Phylllobates terribilis*. *GigaByte* (Hong Kong, China), 2025, gigabyte157.

Wei M, et al. (2025) Elevated phenylacetylglutamine caused by gut dysbiosis associated with type 2 diabetes increases neutrophil extracellular traps formation and exacerbates brain infarction. *Clinical science* (London, England : 1979), 139(12), 717.

Yao XQ, et al. (2025) Gut microbiota contribute to cold adaptation in mammals-primates and ungulates. *iScience*, 28(4), 112245.

Crowley LM, et al. (2025) The genome sequence of a snail-killing fly, *Dichetophora obliterata* (Fabricius, 1805). *Wellcome open research*, 10, 176.

Boyes D, et al. (2025) The genome sequence of the Warty Knot-Horn moth, *Acrobasis repandana* Fabricius, 1798. *Wellcome open research*, 10, 50.

Yang R, et al. (2025) *Lactobacillus rhamnosus* GR-1 prevents autism-like behaviors by reshaping the maternal and offspring microbiome. *NPJ biofilms and microbiomes*, 11(1), 187.

Shittu OE, et al. (2025) Deciphering the influence of fertilization systems on the *Allium ampeloprasum* rhizosphere microbial diversity and community structure through a shotgun metagenomics profiling approach. *Environmental microbiome*, 20(1), 126.

Khan F, et al. (2025) Functional Division of Insect Blood Cells by Single-Cell RNA-Sequencing and Cell-Type-Specific FISH Markers. *Cells*, 14(23).

Shi M, et al. (2025) Multi-omics mechanical analysis of gut microbiota, carboxylic acids, and cardiac gene expression interaction triggering diabetic cardiomyopathy. *mSystems*, 10(1), e0145024.

Falk S, et al. (2025) The genome sequence of the Coppice Mining Bee, *Andrena helvola* (Linnaeus, 1758). *Wellcome open research*, 10, 102.

Willink B, et al. (2025) The genome sequence of the Tropical Bluetail Damselfly, *Ischnura senegalensis* (Rambur, 1842). *Wellcome open research*, 10, 104.