

Resource Summary Report

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

Defining Citation: [PMID:25402007](#), [DOI: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: 20260912T195834+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 489 mentions in open access literature.

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

Guo X, et al. (2026) Reactive oxygen species in the rhizosphere orchestrate the recruitment of beneficial bacteria. The EMBO journal, 45(4), 1245.

Qiu Q, et al. (2026) Comparative Analysis of Microbial Community Structure and Function in the Gut of South China Tigers Under Different Dietary Treatments. Veterinary sciences, 13(3).

Ma L, et al. (2026) Ecological Reassembly of the Milk Microbiome and Its Associated Resistome During the Dry Period in Dairy Cows. Veterinary sciences, 13(6).

Xu F, et al. (2026) Comparative virome analysis of lake and domestic wastewater revealed the unexpected presence of swine acute diarrhea syndrome coronavirus and Ginkgo-associated viruses. Frontiers in microbiology, 17, 1831710.

Wei D, et al. (2026) The crayfish-rice coculture model contributes to regulating the soil fertility of rice fields and maintaining the stability of soil microbial community composition and function. Advanced biotechnology, 4(2).

El-Duah P, et al. (2026) Detection and complete genome characterisation of bat coronaviruses from Ghana. Archives of virology, 171(6).

Naitchede LHS, et al. (2026) Microbial community characterization in semi-hydroponic systems of Starbor kale (*Brassica oleracea* L.) grown under normal gravity and simulated microgravity. Current research in microbial sciences, 10, 100592.

Ali H, et al. (2026) Seasonal shifts in vegetation, soil properties, and microbial communities in Western Himalayan forests. Environmental microbiome, 21(1), 22.

Li C, et al. (2026) Altered rumen bacterial flora is associated with increased lipogenesis of adipose tissue in obese dairy cows before calving. Microbiome, 14(1), 66.

Huang Y, et al. (2026) The near-complete genome assembly of allotetraploid *Pennisetum purpureum* 'Purple' reveals the genetic and epigenetic landscape of centromeres. Horticulture research, 13(2), uhaf301.

Meng T, et al. (2026) Mechanistic insights into nitrogen fertilizer regulation of carbon-nitrogen cycling and greenhouse gas emissions: a metagenomics-based investigation. *Frontiers in microbiology*, 17, 1808047.

Zhang H, et al. (2026) Host intestinal microbiota adaptive changes following *Paranosema locustae* infection and mechanism of chronic pathogenesis. *Journal of insect science* (Online), 26(2).

Wu G, et al. (2026) Physiological and transcriptome analyses for revealing the mechanism of adventitious root formation in *Camellia luteoflora*. *BMC plant biology*, 26(1).

Douarre PE, et al. (2026) Genomic Features and Antimicrobial Susceptibility of *Listeria innocua* Isolated from Raw Drinking Milk in Poland. *Foods* (Basel, Switzerland), 15(6).

Huang F, et al. (2026) Transcriptome Analysis of Differentially Expressed Genes in Freshwater Pearl Mussel (*Sinohyriopsis cumingii*) with Four Different Shell Colors. *Animals : an open access journal from MDPI*, 16(3).

Zhang J, et al. (2026) Gut Microbiota-driven Tryptophan Metabolism Towards the Indole Pathway Mediates *Schisandra Chinensis* Polysaccharide's Alleviation of Ulcerative Colitis and Comorbid Depression via Aryl Hydrocarbon Receptor. *International journal of biological sciences*, 22(5), 2557.

Szablińska-Piernik J, et al. (2026) Giant chromosomes of a tiny plant-the complete telomere-to-telomere genome assembly of the simple thalloid liverwort *Apopellia endiviifolia* (Jungermanniopsida, Marchantiophyta). *GigaScience*, 15.

Wang X, et al. (2026) Multi-omics reveals microbial community characteristics and flavonoid biotransformation mechanisms during mung bean sour fermentation. *Current research in food science*, 12, 101342.

Guo J, et al. (2026) Metagenomics reveals gut microbial differences and ecological adaptation in plateau zokor (*Eospalax baileyi*) populations. *BMC microbiology*, 26(1).

Li H, et al. (2026) Dysbiosis and unsustainable delayed gut microbiota development as non-invasive biomarkers for predicting autism spectrum disorder in Chinese children. *Frontiers in microbiology*, 17, 1753665.