

Resource Summary Report

Generated by [dkNET](#) on Aug 30, 2026

pynast

RRID:SCR_024189

Type: Tool

Proper Citation

pynast (RRID:SCR_024189)

Resource Information

URL: <https://github.com/biocore/pynast>

Proper Citation: pynast (RRID:SCR_024189)

Description: Software tool for aligning sequences to template alignment.

Synonyms: Python Nearest Alignment Space Termination tool

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

Defining Citation: [PMID:19914921](#)

Keywords: aligning sequences to template alignment,

Availability: Free, Available for download, Freely available,

Resource Name: pynast

Resource ID: SCR_024189

Alternate IDs: OMICS_15419

Alternate URLs: <https://sources.debian.org/src/pynast/>

License: Modified BSD License

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260829T182833+0000

Ratings and Alerts

No rating or validation information has been found for pynast.

No alerts have been found for pynast.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

Meng Y, et al. (2026) The development of residential gut microbiota in mice at different phases in early life. *iScience*, 29(6), 115699.

Zhao B, et al. (2024) Microbial communities and metagenomes in methane-rich deep coastal sediments. *Scientific data*, 11(1), 1043.

Huang CG, et al. (2024) Exploring the Interplay of Gut Microbiota and Systemic Inflammation in Pediatric Obstructive Sleep Apnea Syndrome and Its Impact on Blood Pressure Status: A Cross-Sectional Study. *International journal of molecular sciences*, 25(24).

Cao J, et al. (2024) Graphene enhances artemisinin production in the traditional medicinal plant *Artemisia annua* via dynamic physiological processes and miRNA regulation. *Plant communications*, 5(3), 100742.

Liu Y, et al. (2024) The Diversity of Wolbachia and Other Bacterial Symbionts in *Spodoptera frugiperda*. *Insects*, 15(4).

Ma W, et al. (2024) Amelioration of inflammatory bowel disease by *Bifidobacterium animalis* subsp. *lactis* XLTG11 in combination with mesalazine. *Frontiers in microbiology*, 15, 1472776.

Wan S, et al. (2024) Gut microbiome changes in mouse, Mongolian gerbil, and hamster models following *Clostridioides difficile* challenge. *Frontiers in microbiology*, 15, 1368194.

Fan J, et al. (2024) Taxonomic composition and functional potentials of gastrointestinal microbiota in 12 wild-stranded cetaceans. *Frontiers in microbiology*, 15, 1394745.

Zhang H, et al. (2024) Fungal endophytes of *Taxus* species and regulatory effect of two strains on taxol synthesis. *BMC microbiology*, 24(1), 291.

Wang J, et al. (2023) The Periparturient Gut Microbiota's Modifications in Shaziling Sows concerning Bile Acids. *Metabolites*, 13(1).

Yi X, et al. (2023) Melatonin promotes gut anti-oxidative status in perinatal rat by remodeling the gut microbiome. *Redox biology*, 65, 102829.

Lu F, et al. (2023) Anthocyanin-rich blue potato meals protect against polychlorinated biphenyl-mediated disruption of short-chain fatty acid production and gut microbiota

profiles in a simulated human digestion model. *Frontiers in nutrition*, 10, 1130841.

Liu D, et al. (2023) Indoleacrylic acid produced by *Parabacteroides distasonis* alleviates type 2 diabetes via activation of AhR to repair intestinal barrier. *BMC biology*, 21(1), 90.

Mondal HK, et al. (2022) Alteration of gut microbiota composition and function of Indian major carp, rohu (*Labeo rohita*) infected with *Argulus siamensis*. *Microbial pathogenesis*, 164, 105420.

Yu HR, et al. (2022) Effects of Maternal Gut Microbiota-Targeted Therapy on the Programming of Nonalcoholic Fatty Liver Disease in Dams and Fetuses, Related to a Prenatal High-Fat Diet. *Nutrients*, 14(19).

Messer LF, et al. (2021) Temperate southern Australian coastal waters are characterised by surprisingly high rates of nitrogen fixation and diversity of diazotrophs. *PeerJ*, 9, e10809.

Hereira-Pacheco SE, et al. (2021) The root endophytic bacterial community of *Ricinus communis* L. resembles the seeds community more than the rhizosphere bacteria independent of soil water content. *Scientific reports*, 11(1), 2173.

Xiao Joe JT, et al. (2021) The Alteration of Intestinal Microbiota Profile and Immune Response in *Epinephelus coioides* during Pathogen Infection. *Life* (Basel, Switzerland), 11(2).

Afanador-Barajas LN, et al. (2021) Impact of a bacterial consortium on the soil bacterial community structure and maize (*Zea mays* L.) cultivation. *Scientific reports*, 11(1), 13092.

Yao Y, et al. (2021) Active Microbiome Structure and Functional Analyses of Freshwater Benthic Biofilm Samples Influenced by RNA Extraction Methods. *Frontiers in microbiology*, 12, 588025.