

Resource Summary Report

Generated by [RRID](#) on Aug 7, 2026

PRINSEQ

RRID:SCR_005454

Type: Tool

Proper Citation

PRINSEQ (RRID:SCR_005454)

Resource Information

URL: <http://edwards.sdsu.edu/cgi-bin/prinseq/prinseq.cgi>

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Description: A publicly available tool that is able to filter, reformat and trim your genomic and metagenomic sequence data and provide you summary statistics for your sequence data. The interactive web interface facilitates visualizations of the results and export functionality for subsequent data processing. The standalone lite version is written in Perl and does not require any non-core Perl modules. The lite version is primarily designed for data preprocessing and does not generate summary statistics in graphical form., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PRINSEQ

Synonyms: PReprocessing and INformation of SEquences, preprocessing and information of sequences

Resource Type: data analysis service, production service resource, analysis service resource, service resource

Defining Citation: [PMID:21278185](#)

Keywords: microbiome, data analysis, genomic sequence data, metagenomic sequence data, summary, perl, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PRINSEQ

Resource ID: SCR_005454

Alternate IDs: OMICS_01068, biotools:prinseq

Alternate URLs: <http://prinseq.sourceforge.net>, <https://bio.tools/prinseq>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260807T042624+0000

Ratings and Alerts

No rating or validation information has been found for PRINSEQ.

No alerts have been found for PRINSEQ.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1199 mentions in open access literature.

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

Caballero Gómez N, et al. (2026) Integrated Transcriptomics and Metabolomic Profiling Suggests That Thymol Adaptation Induces Multi-Layered Envelope and Metabolic Perturbations That Sensitize *Pseudomonas psychrophila* to Antibiotics. *International journal of molecular sciences*, 27(9).

Fan J, et al. (2025) Potential roles of cigarette smoking on gut microbiota profile among Chinese men. *BMC medicine*, 23(1), 25.

Abalde S, et al. (2025) A Phylogenomic Backbone for Acoelomorpha Inferred From Transcriptomic Data. *Systematic biology*, 74(1), 70.

Ishizaka A, et al. (2025) Dysbiosis of gut microbiota in COVID-19 is associated with intestinal DNA phage dynamics of lysogenic and lytic infection. *Microbiology spectrum*, 13(1), e0099824.

Fonseca A, et al. (2025) Large Filamentous Bacteria Isolated From Sulphidic Sediments Reveal Novel Species and Distinct Energy and Defence Mechanisms for Survival. *Environmental microbiology*, 27(3), e70083.

Vuori I, et al. (2025) Direct Evidence of Microbial Sunscreen Production by Scum-Forming Cyanobacteria in the Baltic Sea. *Environmental microbiology reports*, 17(1), e70056.

Cao Y, et al. (2025) Polyadenylation Complex CFII Recognizes Downstream Cis-element for Pre-mRNA Polyadenylation Through Interaction with an RNA-Binding Protein in *Arabidopsis*. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(41), e04562.

Zhao R, et al. (2025) Metagenomic next-generation sequencing assists in the diagnosis of visceral leishmaniasis in non-endemic areas of China. *Frontiers in cellular and infection microbiology*, 15, 1517046.

Raun N, et al. (2025) Trithorax regulates long-term memory in *Drosophila* through epigenetic maintenance of mushroom body metabolic state and translation capacity. *PLoS biology*, 23(1), e3003004.

Noell SE, et al. (2025) Antarctic Geothermal Soils Exhibit an Absence of Regional Habitat Generalist Microorganisms. *Environmental microbiology*, 27(1), e70032.

Horvath M, et al. (2025) Species- and strain-specific microbial modulation of interferon, innate immunity, and epithelial barrier in 2D air-liquid interface respiratory epithelial cultures. *BMC biology*, 23(1), 28.

Naim W, et al. (2025) Impact of disinfection methods used in the slaughterhouse environment on microbiome diversity throughout the meat production chain. *Current research in microbial sciences*, 8, 100336.

Florêncio GP, et al. (2025) Synergistic Effects of Probiotics and Lifestyle Interventions on Intestinal Microbiota Composition and Clinical Outcomes in Obese Adults. *Metabolites*, 15(2).

Yalvaç ES, et al. (2025) Composition of the vaginal microbiota in relation to cervical intraepithelial lesions. *Turkish journal of obstetrics and gynecology*, 22(3), 220.

Pardo-Esté C, et al. (2025) The ArcB kinase sensor participates in the phagocyte-mediated stress response in *Salmonella Typhimurium*. *Frontiers in microbiology*, 16, 1541797.

Harding KR, et al. (2025) Genome-wide identification of bacterial genes contributing to nucleus-forming jumbo phage infection. *Nucleic acids research*, 53(3).

Tiezzi F, et al. (2025) Multiple-trait genomic prediction for swine meat quality traits using gut microbiome features as a correlated trait. *Journal of animal breeding and genetics = Zeitschrift für Tierzucht und Zuchtungsbiologie*, 142(1), 102.

Fuhrmann L, et al. (2024) V-pipe 3.0: a sustainable pipeline for within-sample viral genetic diversity estimation. *GigaScience*, 13.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. *GigaScience*, 13.

Feng T, et al. (2024) MOBFinder: a tool for mobilization typing of plasmid metagenomic fragments based on a language model. *GigaScience*, 13.