

Resource Summary Report

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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, service resource, analysis 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: 20260806T054417+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 1192 mentions in open access literature.

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

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.

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.

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.

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.

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.

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.

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.

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.

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.

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 fur Tierzucht und Zuchtungsbiologie*, 142(1), 102.

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

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.

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.

Aoki H, et al. (2024) CD8+ T cell memory induced by successive SARS-CoV-2 mRNA vaccinations is characterized by shifts in clonal dominance. *Cell reports*, 43(3), 113887.

Conde-Pérez K, et al. (2024) *Parvimonas micra* can translocate from the subgingival sulcus of the human oral cavity to colorectal adenocarcinoma. *Molecular oncology*, 18(5), 1143.