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.

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

Funding:

Availability: Acknowledgement requested, Public

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: 20250428T053156+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 1183 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

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.

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.

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.

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 Tierzuchtung 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.

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.

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

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

Wang H, et al. (2024) Recognition and Sequencing of Mutagenic DNA Adduct at Single-Base Resolution Through Unnatural Base Pair. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(40), e2404622.

Tsunematsu R, et al. (2024) Microbiological investigation of pregnancies following vaginal radical trachelectomy using 16S rRNA sequencing of FFPE placental specimens. FEBS open bio, 14(11), 1825.

Grodner B, et al. (2024) Spatial mapping of mobile genetic elements and their bacterial hosts in complex microbiomes. Nature microbiology, 9(9), 2262.

Xia X, et al. (2024) Impact of whole grain highland hull-less barley on the denaturing gradient gel electrophoresis profiles of gut microbial communities in rats fed high-fat diets. Microbiology spectrum, 12(6), e0408923.

Ismael NM, et al. (2024) Phage vB_Ec_ZCEC14 to treat antibiotic-resistant Escherichia coli isolated from urinary tract infections. Virology journal, 21(1), 44.

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.

Srigyan M, et al. (2024) Mitogenomic analysis of a late Pleistocene jaguar from North America. The Journal of heredity, 115(4), 424.

Shinde P, et al. (2024) A multi-omics systems vaccinology resource to develop and test computational models of immunity. Cell reports methods, 4(3), 100731.

Kink JA, et al. (2024) Large-scale bioreactor production of extracellular vesicles from mesenchymal stromal cells for treatment of acute radiation syndrome. Stem cell research &

therapy, 15(1), 72.