

Resource Summary Report

Generated by [nidm-terms](#) on Jul 29, 2026

PRINSEQ

RRID:SCR_024178

Type: Tool

Proper Citation

PRINSEQ (RRID:SCR_024178)

Resource Information

URL: <https://prinseq.sourceforge.net/>

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Description: Software Perl application for quality control and data preprocessing of genomic and metagenomic datasets. Used to filter, reformat, or trim genomic and metagenomic sequence data. Generates summary statistics of sequences in graphical and tabular format.

Synonyms: prinseq-lite

Resource Type: software resource, software toolkit, software library

Defining Citation: [PMID:21278185](#)

Keywords: data quality control, data preprocessing, genomic and metagenomic datasets,

Availability: Free, Available for download, Freely available,

Resource Name: PRINSEQ

Resource ID: SCR_024178

Alternate URLs: <https://sources.debian.org/src/prinseq-lite/>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260729T044603+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 72 mentions in open access literature.

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

Laiho JE, et al. (2025) Detection of enterovirus RNA in pancreas and lymphoid tissues of organ donors with type 1 diabetes. *Diabetologia*, 68(6), 1211.

Peng T, et al. (2025) Dynamics of endophytic fungi composition in paris polyphylla var. chinensis (franch.) hara seeds during storage and growth, and responses of seedlings to phytohormones. *Frontiers in microbiology*, 16, 1540651.

Hidaka K, et al. (2025) Identifying gene expression predictive of response to neoadjuvant endocrine therapy in early breast cancer. *Breast cancer research and treatment*, 211(3), 717.

Dong W, et al. (2025) Synergistic Effects of Paenibacillus polymyxa NBmelon-1 Inoculation and Grafting Restructure of Rhizosphere Microbiome and Enhanced Disease Resistance in Melon Self-Rootstocks. *Microorganisms*, 13(6).

Jiang F, et al. (2025) The RNA splicing factor PRPF8 is required for left-right organiser cilia function and determination of cardiac left-right asymmetry via regulation of Arl13b splicing. *bioRxiv : the preprint server for biology*.

Vieira FC, et al. (2025) Amicoumacins produced by the native citrus microbiome isolate *Bacillus safensis* inhibit the Huanglongbing-associated bacterial pathogen "*Candidatus Liberibacter asiaticus*". *Applied and environmental microbiology*, 91(8), e0086925.

Wang Z, et al. (2025) METTL3 facilitates the translation of CircSIK2 during chicken myogenesis in an m6A dependent manner. *PLoS genetics*, 21(10), e1011934.

Castelo-Branco R, et al. (2025) Phosphorylation of peptides by a kinase domain in cyanobactin pathways. *Nature communications*, 16(1), 10279.

Varg JE, et al. (2025) Interplay between antipredator behavior, parasitism, and gut microbiome in wild stickleback populations. *NPJ biofilms and microbiomes*, 11(1), 138.

Frezarim GB, et al. (2025) Multi-omics integration identifies molecular markers and biological pathways for carcass and meat quality traits in Nellore cattle. *Scientific reports*, 15(1), 10467.

IJdema F, et al. (2025) Metagenome-based identification of functional traits of the black soldier fly gut microbiome associated with larval performance. *BMC microbiology*, 25(1), 612.

Soto-López JD, et al. (2025) Taxonomic and functional profiling of bat guano microbiota from hiking trail-associated tunnels: a potential risk for human health? *Environmental microbiome*, 20(1), 123.

Shinde P, et al. (2025) Putting computational models of immunity to the test-An invited challenge to predict B.pertussis vaccination responses. *PLoS computational biology*, 21(3), e1012927.

Duan Y, et al. (2025) The impact of green spaces, urban settings, seasonal changes, and pollutants on dissemination of antimicrobial genes in air. *Scientific reports*, 15(1), 20818.

Kaufmann H, et al. (2025) Genomic Repertoire of Twenty-Two Novel Vibrionaceae Species Isolated from Marine Sediments. *Microbial ecology*, 88(1), 36.

Josephs-Spaulding J, et al. (2025) Metatranscriptomics-based metabolic modeling of patient-specific urinary microbiome during infection. *NPJ biofilms and microbiomes*, 11(1), 183.

Ji Q, et al. (2025) Relaxation of selective constraint on the sweet-taste receptor gene TAS1R2 in loriform primates. *Scientific reports*, 15(1), 38091.

Baud A, et al. (2025) Unveiling Host Interactions and Evolutionary Constraints of a Novel Bacteriophage Infecting *Xanthomonas hortorum* pv. *vitians*. *Environmental microbiology reports*, 17(6), e70171.

Aggarwal D, et al. (2025) Large-scale characterisation of the nasal microbiome redefines *Staphylococcus aureus* colonisation status. *Nature communications*, 16(1), 10415.

Toxqui-Rodríguez S, et al. (2025) Interactions between gilthead seabream intestinal transcriptome and microbiota upon *Enteromyxum leei* infection: a multi-omic approach. *Animal microbiome*, 7(1), 22.