

Resource Summary Report

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DeconSeq

RRID:SCR_007006

Type: Tool

Proper Citation

DeconSeq (RRID:SCR_007006)

Resource Information

URL: <http://deconseq.sourceforge.net/>

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Description: Software tool to automatically detect and efficiently remove sequence contaminations from genomic and metagenomic datasets. It is easily configurable and provides a user-friendly interface. The user can upload FASTA or FASTQ files and select the databases used for contamination screening, including seven human genomes, bacterial genomes, and viral genomes. The user can set the thresholds interactively and see the results directly using the functionality of the graphical interface. The results can be downloaded in joined or separated files in different formats. The coverage-identity plots provide additional information that can guide the selections of the thresholds using color coded points and connecting lines.

Synonyms: DECONtamination of SEQuence data, decontamination of sequence data

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Keywords: microbiome, sequence analysis, genomic, metagenomic, datasets, contamination, decontamination, FASEB list

Availability: Available for download

Resource Name: DeconSeq

Resource ID: SCR_007006

Alternate IDs: OMICS_01418

License: GNU General Public License v3

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260821T193759+0000

Ratings and Alerts

No rating or validation information has been found for DeconSeq.

No alerts have been found for DeconSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 213 mentions in open access literature.

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

Lindsay EC, et al. (2026) Gut microbial composition varies with host metabolic phenotype in juvenile Atlantic salmon. *The Journal of experimental biology*, 229(9).

Yang K, et al. (2026) Gut microbiome associations with acute malnutrition relapse in South Sudan. *Microbiology spectrum*, 14(6), e0358725.

Sassi FMC, et al. (2026) Cytogenomics of *Myloplus tiete* reveals conserved satellite DNAs since the Late Eocene in Serrasalminae (Teleostei, Characiformes). *Chromosome research : an international journal on the molecular, supramolecular and evolutionary aspects of chromosome biology*, 34(1).

Benedict EE, et al. (2026) Community-associated quinolone-resistant and extended-spectrum beta-lactamase-producing *Escherichia coli* isolates are similar to clinical infection isolates by sequence type and resistome. *mSystems*, 11(2), e0159125.

Rio-Aige K, et al. (2025) Maternal diet shapes infant microbiota and defensive capacity against infections in early life via differential human milk composition. *EBioMedicine*, 118, 105850.

Vignale FA, et al. (2025) Yerba mate (*Ilex paraguariensis*) genome provides new insights into convergent evolution of caffeine biosynthesis. *eLife*, 14.

Pozzobon LC, et al. (2025) Satellite DNA Mapping in Suliformes (Aves): Insights into the Evolution of the Multiple Sex Chromosome System in *Sula* spp. *Genes*, 16(6).

Chae JB, et al. (2025) Molecular characterization of ten viral pathogens causing calf diarrhea in Hanwoo (*Bos Taurus coreanae*) by next generation sequencing. *BMC veterinary research*, 21(1), 464.

Dietz-Ziegler S, et al. (2025) Extracellular Vesicles Derived From the Feces of Pregnant Women Modulate T Cells Toward a Pregnancy-Supportive Phenotype In Vitro. *European journal of immunology*, 55(9), e70056.

Vidal JAD, et al. (2025) Investigating the evolution of large meiotic rings of multiple X and Y sex chromosomes in two *Leptodactylus* frog species (Anura, Leptodactylidae). *Communications biology*, 8(1), 1636.

Roggen A, et al. (2025) The MIR157-SPL15 module regulates flowering and inflorescence development in *Arabidopsis thaliana* under short days and in *Arabis alpina*. *PLoS genetics*, 21(9), e1011799.

Oliveira AM, et al. (2025) Repetitive DNAs and differentiation of the ZZ/ZW sex chromosome system in the combtail fish *Belontia hasselti* (Perciformes: Osphronemidae). *BMC ecology and evolution*, 25(1), 25.

Vidal JAD, et al. (2025) Unraveling the role of satellite DNAs in the evolution of the giant XY sex chromosomes of the flea beetle *Omophoita octoguttata* (Coleoptera, Chrysomelidae). *BMC biology*, 23(1), 53.

Kruse CPS, et al. (2025) A multi-omic characterization of the physiological responses to salt stress in *Scenedesmus obliquus* UTEX393. *Communications biology*, 8(1), 1632.

Ishola OA, et al. (2024) Comparative Metagenomic Analysis of Bacteriophages and Prophages in Gnotobiotic Mouse Models. *Microorganisms*, 12(2).

Samarra A, et al. (2024) Unravelling the evolutionary dynamics of antibiotic resistance genes in the infant gut microbiota during the first four months of life. *Annals of clinical microbiology and antimicrobials*, 23(1), 72.

Samarra A, et al. (2024) The role of *Bifidobacterium* genus in modulating the neonate microbiota: implications for antibiotic resistance acquisition in early life. *Gut microbes*, 16(1), 2357176.

Choi J, et al. (2024) Gut microbiome correlates of recurrent urinary tract infection: a longitudinal, multi-center study. *EClinicalMedicine*, 71, 102490.

Souza GM, et al. (2024) Satellitome analysis on the pale-breasted thrush *Turdus leucomelas* (Passeriformes; Turdidae) uncovers the putative co-evolution of sex chromosomes and satellite DNAs. *Scientific reports*, 14(1), 20656.

Blake KS, et al. (2024) Gut microbiome and antibiotic resistance effects during travelers' diarrhea treatment and prevention. *mBio*, 15(1), e0279023.