

Resource Summary Report

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TagCleaner

RRID:SCR_011846

Type: Tool

Proper Citation

TagCleaner (RRID:SCR_011846)

Resource Information

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

Proper Citation: TagCleaner (RRID:SCR_011846)

Description: A software tool which can automatically detect and efficiently remove tag sequences from genomic and metagenomic datasets.

Resource Type: software resource, software application, web application, standalone software

Keywords: tag sequence, standalone software, web application, microbiome, genomic, metagenomic, datasets

Availability: Available for download

Resource Name: TagCleaner

Resource ID: SCR_011846

Alternate IDs: OMICS_01094

License: GNU General Public License

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260801T190421+0000

Ratings and Alerts

No rating or validation information has been found for TagCleaner.

No alerts have been found for TagCleaner.

Data and Source Information

Usage and Citation Metrics

We found 63 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Qiu Y, et al. (2025) High throughput construction of species characterized bacterial biobank for functional bacteria screening: demonstration with GABA-producing bacteria. *Frontiers in microbiology*, 16, 1545877.

Qi JQ, et al. (2025) Biochar amendment alters rare microbial taxa and enhances wheat growth in alkaline farmland: insights into soil microbiome dynamics. *Frontiers in microbiology*, 16, 1563712.

Kouraki A, et al. (2025) Physical Therapy for Knee Pain Relief Induces Changes in Gut Microbiome Composition: A Secondary Analysis of Data From a Randomized Controlled Trial. *Sports health*, 17(5), 1053.

van Veen FEE, et al. (2025) The Urinary Microbiome in Women Using Single-Use Versus Reusable Catheters for Intermittent Catheterization: An Exploratory Substudy of the COMPaRE Trial. *Neurourology and urodynamics*, 44(7), 1474.

Monari B, et al. (2025) The vaginal microbiota, symptoms, and local immune correlates in transmasculine individuals using sustained testosterone therapy. *bioRxiv : the preprint server for biology*.

Qu T, et al. (2025) Laser-assisted microbial culturomics. *Nature communications*, 16(1), 10614.

Rojas-Vargas J, et al. (2025) The neovaginal microbiota, symptoms, and local immune correlates in transfeminine individuals with penile inversion vaginoplasty. *Cell reports*, 44(12), 116546.

Demirkan A, et al. (2024) Linking the gut microbiome to host DNA methylation by a discovery and replication epigenome-wide association study. *BMC genomics*, 25(1), 1224.

Sato Y, et al. (2024) A systematic survey of environmental DNA in Palau's lakes and waterfalls reveals an increase in *Leptospira* levels after flooding. *One health (Amsterdam, Netherlands)*, 19, 100898.

Elsasser TH, et al. (2023) Short-term feeding of defatted bovine colostrum mitigates inflammation in the gut via changes in metabolites and microbiota in a chicken animal model. *Animal microbiome*, 5(1), 6.

Haddad LB, et al. (2023) Influence of Hormonal Contraceptive Use and HIV on Cervicovaginal Cytokines and Microbiota in Malawi. *mSphere*, 8(1), e0058522.

Mori T, et al. (2023) Construction of white-rot fungal-bacterial consortia with improved ligninolytic properties and stable bacterial community structure. *ISME communications*,

3(1), 61.

Ying H, et al. (2022) The Role of DNA Methylation in Genome Defense in Cnidaria and Other Invertebrates. *Molecular biology and evolution*, 39(2).

Ndungo E, et al. (2022) Dynamics of the Gut Microbiome in Shigella-Infected Children during the First Two Years of Life. *mSystems*, 7(5), e0044222.

Seymour M, et al. (2021) Environmental DNA provides higher resolution assessment of riverine biodiversity and ecosystem function via spatio-temporal nestedness and turnover partitioning. *Communications biology*, 4(1), 512.

Babszky G, et al. (2021) COVID-19 Infection Alters the Microbiome: Elite Athletes and Sedentary Patients Have Similar Bacterial Flora. *Genes*, 12(10).

Sanders MGH, et al. (2021) Composition of cutaneous bacterial microbiome in seborrheic dermatitis patients: A cross-sectional study. *PloS one*, 16(5), e0251136.

Dunlop AL, et al. (2021) Vaginal Microbiome Composition in Early Pregnancy and Risk of Spontaneous Preterm and Early Term Birth Among African American Women. *Frontiers in cellular and infection microbiology*, 11, 641005.

Hu C, et al. (2021) A population-based study on associations of stool microbiota with atopic diseases in school-age children. *The Journal of allergy and clinical immunology*, 148(2), 612.

Jašarević E, et al. (2021) The composition of human vaginal microbiota transferred at birth affects offspring health in a mouse model. *Nature communications*, 12(1), 6289.