

Resource Summary Report

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HMP Data Analysis and Coordination Center

RRID:SCR_004919

Type: Tool

Proper Citation

HMP Data Analysis and Coordination Center (RRID:SCR_004919)

Resource Information

URL: <http://www.hmpdacc.org/>

Proper Citation: HMP Data Analysis and Coordination Center (RRID:SCR_004919)

Description: Common repository for diverse human microbiome datasets and minimum reporting standards for Common Fund Human Microbiome Project.

Abbreviations: HMP DACC

Synonyms: Data Analysis and Coordination Center for the Human Microbiome Project, HMPDACC, Human Microbiome Project Data Analysis and Coordination Center

Resource Type: data repository, data or information resource, database, storage service resource, service resource

Keywords: Repository, diverse, human, microbiome, minimum, reporting, standard, common, fund, microbiome, project, dataset, FASEB list

Funding: NIH

Resource Name: HMP Data Analysis and Coordination Center

Resource ID: SCR_004919

Alternate IDs: nlx_88368

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260804T043245+0000

Ratings and Alerts

No rating or validation information has been found for HMP Data Analysis and Coordination Center.

No alerts have been found for HMP Data Analysis and Coordination Center.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 224 mentions in open access literature.

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

Pržulj N, et al. (2025) Simplicity within biological complexity. Bioinformatics advances, 5(1), vbae164.

Safarchi A, et al. (2025) Understanding dysbiosis and resilience in the human gut microbiome: biomarkers, interventions, and challenges. Frontiers in microbiology, 16, 1559521.

Yang SY, et al. (2025) Advancing Gut Microbiome Research: The Shift from Metagenomics to Multi-Omics and Future Perspectives. Journal of microbiology and biotechnology, 35, e2412001.

Suárez J, et al. (2024) Scrutinizing microbiome determinism: why deterministic hypotheses about the microbiome are conceptually ungrounded. History and philosophy of the life sciences, 46(1), 12.

McFall-Ngai M, et al. (2024) Symbiosis takes a front and center role in biology. PLoS biology, 22(4), e3002571.

Wu EH, et al. (2024) [Microbial metaproteomics--From sample processing to data acquisition and analysis]. Se pu = Chinese journal of chromatography, 42(7), 658.

Guan Y, et al. (2024) Genomic and Metagenomic Insights into the Distribution of Nicotine-degrading Enzymes in Human Microbiota. Current genomics, 25(3), 226.

Ma ZS, et al. (2024) Revisiting microgenderome: detecting and cataloguing sexually unique and enriched species in human microbiomes. BMC biology, 22(1), 284.

Zhu Q, et al. (2023) Advances in psoriasis and gut microorganisms with co-metabolites. Frontiers in microbiology, 14, 1192543.

Song Z, et al. (2023) Taxonomic identification of bile salt hydrolase-encoding lactobacilli: Modulation of the enterohepatic bile acid profile. iMeta, 2(3), e128.

Fernandez-Cantos MV, et al. (2023) Bioinformatic mining for RiPP biosynthetic gene clusters in Bacteroidales reveals possible new subfamily architectures and novel natural

products. *Frontiers in microbiology*, 14, 1219272.

Leão I, et al. (2023) Pseudomonadota in the oral cavity: a glimpse into the environment-human nexus. *Applied microbiology and biotechnology*, 107(2-3), 517.

Simon LM, et al. (2023) Microbial fingerprints reveal interaction between museum objects, curators, and visitors. *iScience*, 26(9), 107578.

Hsu TY, et al. (2023) Profiling novel lateral gene transfer events in the human microbiome. *bioRxiv : the preprint server for biology*.

Qin F, et al. (2023) 2 Hydroxybutyric Acid-Producing Bacteria in Gut Microbiome and *Fusobacterium nucleatum* Regulates 2 Hydroxybutyric Acid Level In Vivo. *Metabolites*, 13(3).

Zhang W, et al. (2022) The Spatial Features and Temporal Changes in the Gut Microbiota of a Healthy Chinese Population. *Microbiology spectrum*, 10(6), e0131022.

Gao P, et al. (2022) Precision environmental health monitoring by longitudinal exposome and multi-omics profiling. *Genome research*, 32(6), 1199.

Münch PC, et al. (2021) Identification of Natural CRISPR Systems and Targets in the Human Microbiome. *Cell host & microbe*, 29(1), 94.

Olekhnovich EI, et al. (2021) Separation of Donor and Recipient Microbial Diversity Allows Determination of Taxonomic and Functional Features of Gut Microbiota Restructuring following Fecal Transplantation. *mSystems*, 6(4), e0081121.

Dong Z, et al. (2021) Gut Microbiome: A Potential Indicator for Differential Diagnosis of Major Depressive Disorder and General Anxiety Disorder. *Frontiers in psychiatry*, 12, 651536.