Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 25, 2025

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/

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Description: Common repository for diverse human microbiome datsets 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 or information resource, storage service resource, database, service resource, data repository

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: 20250425T055428+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 221 mentions in open access literature.

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

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.

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

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

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

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

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 environmenthuman nexus. Applied microbiology and biotechnology, 107(2-3), 517.

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).

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

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

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.

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.

Chen HD, et al. (2021) Diversity Scaling of Human Digestive Tract (DT) Microbiomes: The Intra-DT and Inter-individual Patterns. Frontiers in genetics, 12, 724661.

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.

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

Zhou J, et al. (2021) VB12Path for Accurate Metagenomic Profiling of Microbially Driven Cobalamin Synthesis Pathways. mSystems, 6(3), e0049721.

Lin S, et al. (2021) Abundance of Lipopolysaccharide Heptosyltransferase I in Human Gut Microbiome and Its Association With Cardiovascular Disease and Liver Cirrhosis. Frontiers in microbiology, 12, 756976.