

Resource Summary Report

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Human Microbiome Project

RRID:SCR_012956

Type: Tool

Proper Citation

Human Microbiome Project (RRID:SCR_012956)

Resource Information

URL: <https://commonfund.nih.gov/hmp/>

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Description: NIH Project to generate resources to characterize the human microbiota and to analyze its role in human health and disease at several different sites on the human body, including nasal passages, oral cavities, skin, gastrointestinal tract, and urogenital tract using metagenomic and traditional approach to genomic DNA sequencing studies.HMP was supported by the Common Fund from 2007 to 2016.

Abbreviations: HMP, NIH HMP, HMP1

Synonyms: Human Microbiome Project, NIH HMP, HMP1, HMP, NIH Human Microbiome Project

Resource Type: portal, data or information resource, project portal

Keywords: generate, resource, human, body, microbiota, analyze, health, disease, metagenomic, DNA, sequencing, data

Funding: NIH

Resource Name: Human Microbiome Project

Resource ID: SCR_012956

Alternate IDs: nif-0000-25316

Alternate URLs: <https://www.hmpdacc.org/ihmp/>, <https://www.hmpdacc.org/hmp>

Old URLs: <http://nihroadmap.nih.gov/hmp/>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260801T190844+0000

Ratings and Alerts

No rating or validation information has been found for Human Microbiome Project.

No alerts have been found for Human Microbiome Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 385 mentions in open access literature.

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

Dinesh D, et al. (2026) Gut Microbial Variations Associated With Proton Pump Inhibitor Use in the Boston Puerto Rican Health Study. *Pharmacology research & perspectives*, 14(1), e70205.

Vu D, et al. (2026) Advancing Yeast Identification Using High-Throughput DNA Barcode Data From a Curated Culture Collection. *Molecular ecology resources*, 26(1), e70082.

Dowrick JM, et al. (2026) Integrated multi-omic and symptom clustering reveals lower-gastrointestinal disorders of gut-brain interaction heterogeneity. *Gut microbes*, 18(1), 2604871.

Ni M, et al. (2025) Epigenetic phase variation in the gut microbiome enhances bacterial adaptation. *bioRxiv : the preprint server for biology*.

Petrone BL, et al. (2025) A pilot study of metaproteomics and DNA metabarcoding as tools to assess dietary intake in humans. *Food & function*, 16(1), 282.

Alam Y, et al. (2025) Variation in human gut microbiota impacts tamoxifen pharmacokinetics. *mBio*, 16(1), e0167924.

Han W, et al. (2025) Exploring fecal microbiota signatures associated with immune response and antibiotic impact in NSCLC: insights from metagenomic and machine learning approaches. *Frontiers in cellular and infection microbiology*, 15, 1591076.

Gao Y, et al. (2025) The powerbend distribution provides a unified model for the species abundance distribution across animals, plants and microbes. *Nature communications*, 16(1), 4035.

Abdelkader A, et al. (2025) metaGEENOME: an integrated framework for differential abundance analysis of microbiome data in cross-sectional and longitudinal studies. *BMC bioinformatics*, 26(1), 189.

Wang M, et al. (2025) Periodontitis History Shapes the Early Peri-Implant Microbiome Formation: A Metagenomic Analysis. *Journal of clinical periodontology*, 52(7), 1011.

Comstock LE, et al. (2025) Lessons from the model gut Bacteroidales *Bacteroides fragilis* and *Bacteroides thetaiotaomicron* and future opportunities. *Journal of bacteriology*, 207(11), e0034625.

Rahman Hera M, et al. (2025) Estimating similarity and distance using FracMinHash. *Algorithms for molecular biology : AMB*, 20(1), 8.

Xiao L, et al. (2025) CLMT: graph contrastive learning model for microbe-drug associations prediction with transformer. *Frontiers in genetics*, 16, 1535279.

Cabral V, et al. (2025) *Klebsiella* ARO112 promotes microbiota recovery, pathobiont clearance and prevents inflammation in IBD mice. *Nature communications*, 16(1), 10911.

Molinsky RL, et al. (2025) Association Between Dietary Patterns and Subgingival Microbiota: Results From the Oral Infections, Glucose Intolerance, and Insulin Resistance Study (ORIGINS). *Journal of clinical periodontology*, 52(1), 2.

Akhi R, et al. (2025) Oral microbiome diversity associates with carotid intima media thickness in middle-aged male subjects. *Communications medicine*, 5(1), 66.

Kaplan JB, et al. (2025) Synergistic activity of dispersin B and benzoyl peroxide against *Cutibacterium acnes*/*Staphylococcus epidermidis* dual-species biofilms. *PloS one*, 20(3), e0320662.

Yan R, et al. (2025) Meta-analysis of gut microbiome reveals patterns of dysbiosis in colorectal cancer patients. *Journal of medical microbiology*, 74(7).

Strati P, et al. (2025) Frontline acalabrutinib, lenalidomide and rituximab for advanced stage follicular lymphoma with high tumor burden: phase II trial. *Nature communications*, 16(1), 7300.

Sato K, et al. (2025) Dietary fermentable polyols fuel gut inflammation through M1 macrophage polarization and gut microbiota. *iScience*, 28(7), 112934.