

Resource Summary Report

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HUMAnN

RRID:SCR_014620

Type: Tool

Proper Citation

HUMAnN (RRID:SCR_014620)

Resource Information

URL: <http://huttenhower.sph.harvard.edu/humann>

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Description: A pipeline which takes short DNA/RNA reads as inputs and produces gene and pathway summaries as outputs. The pipeline converts sequence reads into coverage and abundance tables summarizing the gene families and pathways in one or more microbial communities.

Synonyms: HMP Unified Metabolic Analysis Network (HUMAnN), HMP Unified Metabolic Analysis Network

Resource Type: software application, workflow software, software resource, data processing software

Keywords: microbiome, dna reads, rna reads, workflow software, pipeline

Resource Name: HUMAnN

Resource ID: SCR_014620

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260728T043441+0000

Ratings and Alerts

No rating or validation information has been found for HUMAnN.

No alerts have been found for HUMAnN.

Data and Source Information

Usage and Citation Metrics

We found 416 mentions in open access literature.

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

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.

Krueger ME, et al. (2025) Comparative analysis of Parkinson's and inflammatory bowel disease gut microbiomes reveals shared butyrate-producing bacteria depletion. *NPJ Parkinson's disease*, 11(1), 50.

Quraishi MN, et al. (2025) Open Label Vancomycin in Primary Sclerosing Cholangitis-Inflammatory Bowel Disease: Improved Colonic Disease Activity and Associations With Changes in Host-Microbiome-Metabolomic Signatures. *Journal of Crohn's & colitis*, 19(2).

Ismail HM, et al. (2025) Gut Microbial Changes Associated With Obesity in Youth With Type 1 Diabetes. *The Journal of clinical endocrinology and metabolism*, 110(2), 364.

Díez López C, et al. (2025) Unravelling the hidden side of laundry: malodour, microbiome and pathogenome. *BMC biology*, 23(1), 40.

Xiao L, et al. (2025) Elongation factor Tu promotes the onset of periodontitis through mediating bacteria adhesion. *NPJ biofilms and microbiomes*, 11(1), 47.

Zielińska K, et al. (2025) Healthy microbiome-moving towards functional interpretation. *GigaScience*, 14.

Barker HA, et al. (2025) Cannabinoid receptor deficiencies drive immune response dynamics in Salmonella infection. *bioRxiv : the preprint server for biology*.

Humińska-Lisowska K, et al. (2025) Gut microbiome and blood biomarkers reveal differential responses to aerobic and anaerobic exercise in collegiate men of diverse training backgrounds. *Scientific reports*, 15(1), 16061.

Kiu R, et al. (2025) Impact of early life antibiotic and probiotic treatment on gut microbiome and resistome of very-low-birth-weight preterm infants. *Nature communications*, 16(1), 7569.

Labisa-Morais F, et al. (2025) Bacterial transmission within social groups shapes the underexplored gut microbiome in the lemur *Indri indri*. *The ISME journal*, 19(1).

Naspolini NF, et al. (2025) Exclusive breastfeeding is associated with the gut microbiome maturation in infants according to delivery mode. *Gut microbes*, 17(1), 2493900.

Brown AA, et al. (2025) Associations of the gut microbiome and inflammatory markers with mental health symptoms: a cross-sectional study on Danish adolescents. *Scientific*

reports, 15(1), 10378.

Tian Y, et al. (2025) Multi-omics assessment of gut microbiota in circadian rhythm disorders: a cross-sectional clinical study. *Frontiers in cellular and infection microbiology*, 15, 1524987.

Lee S, et al. (2025) Enrichment of gut-derived metabolites in a Parkinson's disease subtype with REM sleep behavior disorder. *NPJ Parkinson's disease*, 11(1), 189.

Lyu L, et al. (2025) Glucocorticoid-induced changes of the gut microbiota and metabolic markers in healthy young men: Outcome of a randomized controlled trial. *Cell reports. Medicine*, 6(11), 102426.

Jeilu O, et al. (2025) Metagenomic profiling of airborne microbial communities from aircraft filters and face masks. *Microbiome*, 13(1), 249.

Trepka KR, et al. (2025) Shifts in the human gut microbiome during cancer chemotherapy are diet-dependent. *bioRxiv : the preprint server for biology*.

Park HA, et al. (2025) Metagenomic Analysis Identifies Sex-Related Gut Microbial Functions and Bacterial Taxa Associated With Skeletal Muscle Mass. *Journal of cachexia, sarcopenia and muscle*, 16(1), e13636.

Zhang L, et al. (2025) Induction of conidial traps in the nematode-trapping fungus *Drechlerella dactyloides* by soil microbes. *mSystems*, 10(3), e0129124.