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

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

Funding:

Resource Name: HUMAnN

Resource ID: SCR_014620

Record Creation Time: 20220129T080321+0000

Record Last Update: 20250401T061124+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

Source: SciCrunch Registry

Usage and Citation Metrics

We found 315 mentions in open access literature.

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

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.

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.

Fackelmann G, et al. (2025) Gut microbiome signatures of vegan, vegetarian and omnivore diets and associated health outcomes across 21,561 individuals. Nature microbiology, 10(1), 41.

Fahur Bottino G, et al. (2025) Early life microbial succession in the gut follows common patterns in humans across the globe. Nature communications, 16(1), 660.

Ghazi AR, et al. (2025) Quantifying Metagenomic Strain Associations from Microbiomes with Anpan. bioRxiv : the preprint server for biology.

Banerjee G, et al. (2025) Deep sequencing-derived Metagenome Assembled Genomes from the gut microbiome of liver transplant patients. Scientific data, 12(1), 39.

Portlock T, et al. (2025) Interconnected pathways link faecal microbiota plasma lipids and brain activity to childhood malnutrition related cognition. Nature communications, 16(1), 473.

Bhosle A, et al. (2025) Response of the gut microbiome and metabolome to dietary fiber in healthy dogs. mSystems, 10(1), e0045224.

Sun L, et al. (2025) Shallow-water mussels (Mytilus galloprovincialis) adapt to deep-sea environment through transcriptomic and metagenomic insights. Communications biology, 8(1), 46.

Nychas E, et al. (2025) Discovery of robust and highly specific microbiome signatures of non-alcoholic fatty liver disease. Microbiome, 13(1), 10.

Roos M, et al. (2025) Optimizing mouse metatranscriptome profiling by selective removal of redundant nucleic acid sequences. bioRxiv : the preprint server for biology.

Wu X, et al. (2025) A legume-enriched diet improves metabolic health in prediabetes mediated through gut microbiome: a randomized controlled trial. Nature communications, 16(1), 942.

Liu L, et al. (2025) Associations of alcohol intake with gut microbiome: a prospective study in a predominantly low-income Black/African American population. The American journal of clinical nutrition, 121(1), 134.

Glitza IC, et al. (2024) Randomized Placebo-Controlled, Biomarker-Stratified Phase Ib Microbiome Modulation in Melanoma: Impact of Antibiotic Preconditioning on Microbiome and Immunity. Cancer discovery, 14(7), 1161.

Yang L, et al. (2024) Taxonomic and functional assembly cues enrich the endophytic tobacco microbiota across epiphytic compartments. mSphere, 9(1), e0060723.

Manzoor M, et al. (2024) Shotgun metagenomic analysis of the oral microbiome in gingivitis: a nested case-control study. Journal of oral microbiology, 16(1), 2330867.

Lee I, et al. (2024) Proton pump inhibitors increase the risk of carbapenem-resistant Enterobacteriaceae colonization by facilitating the transfer of antibiotic resistance genes among bacteria in the gut microbiome. Gut microbes, 16(1), 2341635.

Tagliamonte S, et al. (2024) Relationships between diet and gut microbiome in an Italian and Dutch cohort: does the dietary protein to fiber ratio play a role? European journal of nutrition, 63(3), 741.

Ladakis DC, et al. (2024) Bile acid metabolites predict multiple sclerosis progression and supplementation is safe in progressive disease. medRxiv : the preprint server for health sciences.

Murovec B, et al. (2024) MetaBakery: a Singularity implementation of bioBakery tools as a skeleton application for efficient HPC deconvolution of microbiome metagenomic sequencing data to machine learning ready information. Frontiers in microbiology, 15, 1426465.