

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, software application, software resource, workflow 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: 20260821T194005+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 507 mentions in open access literature.

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

Moiseyenko A, et al. (2026) Faecalibacterium prausnitzii, depleted in the Parkinson's disease microbiome, improves motor deficits in α -synuclein overexpressing mice. NPJ Parkinson's disease, 12(1).

Lobel L, et al. (2026) Dietary sulfur amino acids enhance anti-tumor immunity in colon cancer via an NKT cell-XCL1-cDC1 circuit. Immunity, 59(6), 1708.

Sun J, et al. (2026) Gut microbiome convergence and functional adaptation underlie the evolution of predation in stink bugs (Heteroptera: Pentatomidae). Microbiome, 14(1), 56.

Nickols WA, et al. (2026) MaAsLin 3: refining and extending generalized multivariable linear models for meta-omic association discovery. Nature methods, 23(3), 554.

Wu J, et al. (2026) The interplay of sleep characteristics with health factors and gut microbiome. Nature communications, 17(1).

Wei H, et al. (2026) Population-Level Amplicon and Metagenomic Analyses Uncover Distinct Effects of Landscape-Level Pesticides on the Maternal Gut Microbiome. Environment & health (Washington, D.C.), 4(2), 246.

Burakova I, et al. (2026) The effect of short-term consumption of Bifidobacterium bifidum on the gut microbiome of obese individuals. Experimental biology and medicine (Maywood, N.J.), 251, 10894.

Yadav B, et al. (2026) Host-microbiome interplay supports heat stress resilience in zebu calves. Animal microbiome, 8(1).

Noecker C, et al. (2026) A widespread gut bacterial lineage distinguished by redox metabolism and phage defense. bioRxiv : the preprint server for biology.

Bargheet A, et al. (2026) Metabolic reprogramming of the infant gut by bifidobacteria-based probiotics drives exclusion of antibiotic-resistant pathobionts. Cell reports. Medicine, 7(5), 102752.

Fu J, et al. (2026) A global metagenomic atlas of aging identifies a microbiota phase transition associated with disease risk. NPJ biofilms and microbiomes, 12(1).

Zhang W, et al. (2026) Dynamic change patterns of the human gut microbiota-fluctuation, loss-acquisition, and turnover-and their underlying causes. ISME communications, 6(1), ycag046.

Aquino CI, et al. (2026) Decoding the microbial landscape of endometrial cancer: a case-control study. BMC microbiology, 26(1).

Krasaesin A, et al. (2026) Shotgun metagenomic profiling reveals ecological and functional alterations of the oral microbiome in craniosynostosis. *Journal of oral microbiology*, 18(1), 2687219.

Peugnet G, et al. (2026) Ghost-rocks' microbiota: metagenomic insights into their influence on the biogeochemistry of karstic cave and groundwater. *FEMS microbiology ecology*, 102(6).

Tabish RW, et al. (2026) Cecal metagenome and mucosal transcriptome of broilers after an enteric challenge and fed diets with different fiber types and concentrations¹. *Poultry science*, 105(9), 107151.

Tabish RW, et al. (2026) Jejunal histopathology, metagenome, and mucosal transcriptome of broilers after an enteric challenge and fed diets with different fiber types and concentrations. *Poultry science*, 105(9), 107215.

Wacker EM, et al. (2026) TOFU-MAaPO: fast, scalable and reproducible analysis of large metagenome sequence data from the Sequence Read Archive. *Nature communications*, 17(1).

Fernandes R, et al. (2026) Fecal microbiota transplantation plus immunotherapy in metastatic renal cell carcinoma: the phase 1 PERFORM trial. *Nature medicine*, 32(4), 1325.

Sui X, et al. (2026) Sex-biased associations between gut microbiota and hematologic toxicity of neoadjuvant chemoradiotherapy in locally advanced rectal cancer. *International journal of surgery (London, England)*, 112(4), 9740.