

Resource Summary Report

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HUMAnN2

RRID:SCR_016280

Type: Tool

Proper Citation

HUMAnN2 (RRID:SCR_016280)

Resource Information

URL: <https://huttenhower.sph.harvard.edu/humann2>

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Description: Software for profiling the presence/absence and abundance of microbial pathways in a community from metagenomic or metatranscriptomic sequencing data Used for millions of short DNA/RNA reads. This process, referred to as functional profiling, aims to describe the metabolic potential of a microbial community and its members.

Abbreviations: HUMAnN2

Synonyms: The HMP Unified Metabolic Analysis Network 2

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Keywords: microbe, matagenome, metatranscription, sequence, short, read, dna, rna, metabolism

Availability: Free, Available for download, Tutorial available, Acknowledgement requested

Resource Name: HUMAnN2

Resource ID: SCR_016280

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260829T182537+0000

Ratings and Alerts

No rating or validation information has been found for HUMAnN2 .

No alerts have been found for HUMAnN2 .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 82 mentions in open access literature.

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

Libera KD, et al. (2026) Metabolic modeling and functional genomics reveal taxa and host gene interactions in colorectal cancer. bioRxiv : the preprint server for biology.

Zheng W, et al. (2026) Mutation elevation and functional alterations in Escherichia coli are pertinent to the onset of gestational diabetes mellitus. Cell reports, 45(4), 117143.

Werner L, et al. (2026) Antibiotic disruption of the gut microbiome triggers IBD-like proteolytic activity. Cell reports, 45(6), 117478.

Hog L, et al. (2025) ARFID Initiative Sweden (ARIES): study protocol for a large-scale genetic and registry-linked cohort study on avoidant/restrictive food intake disorder. BMJ open, 15(4), e095559.

Wang M, et al. (2025) Fecal Microbiome and Metabolomic Profiles of Mixed-Fed Infants Are More Similar to Formula-Fed than Breastfed Infants. Microorganisms, 13(1).

Ni D, et al. (2024) Breastfeeding is associated with enhanced intestinal gluconeogenesis in infants. BMC medicine, 22(1), 106.

Del Chierico F, et al. (2024) Solute Transporter OCTN1/Slc22a4 Affects Disease Severity and Response to Infliximab in Experimental Colitis: Role of Gut Microbiota and Immune Modulation. Inflammatory bowel diseases, 30(12), 2259.

Griffiths JA, et al. (2024) Peripheral neuronal activation shapes the microbiome and alters gut physiology. Cell reports, 43(4), 113953.

Cheng S, et al. (2024) Multi-omics of the gut microbial ecosystem in patients with microsatellite-instability-high gastrointestinal cancer resistant to immunotherapy. Cell reports. Medicine, 5(1), 101355.

Ma H, et al. (2024) B. thetaiotaomicron-derived acetic acid modulate immune microenvironment and tumor growth in hepatocellular carcinoma. Gut microbes, 16(1), 2297846.

Leon-Gomez P, et al. (2024) Human papillomavirus, vaginal microbiota and metagenomics: the interplay between development and progression of cervical cancer. Frontiers in microbiology, 15, 1515258.

Yu J, et al. (2024) Dietary supplementation with *Lactiplantibacillus plantarum* P-8 improves the growth performance and gut microbiota of weaned piglets. *Microbiology spectrum*, 12(2), e0234522.

Shen Y, et al. (2024) Early microbial intervention reshapes phenotypes of newborn *Bos taurus* through metabolic regulations. *GigaScience*, 13.

Zhu L, et al. (2024) Gut microbiota facilitate chronic spontaneous urticaria. *Nature communications*, 15(1), 112.

Freeman CN, et al. (2024) Temporal metagenomic characterization of microbial community structure and nitrogen modification genes within an activated sludge bioreactor system. *Microbiology spectrum*, 12(1), e0283223.

Wang S, et al. (2023) Grazing exclusion alters soil methane flux and methanotrophic and methanogenic communities in alpine meadows on the Qinghai-Tibet Plateau. *Frontiers in microbiology*, 14, 1293720.

Seelbinder B, et al. (2023) *Candida* expansion in the gut of lung cancer patients associates with an ecological signature that supports growth under dysbiotic conditions. *Nature communications*, 14(1), 2673.

Sukumar S, et al. (2023) Development of the oral resistome during the first decade of life. *Nature communications*, 14(1), 1291.

Zhang XL, et al. (2023) Characterization of Gut Microbiota Compositions along the Intestinal Tract in CD163/pAPN Double Knockout Piglets and Their Potential Roles in Iron Absorption. *Microbiology spectrum*, 11(1), e0190622.

Lai S, et al. (2023) Enterotypes of the human gut mycobiome. *Microbiome*, 11(1), 179.