

# Resource Summary Report

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## Human Gut Microbiome Initiative

RRID:SCR\_008137

Type: Tool

### Proper Citation

Human Gut Microbiome Initiative (RRID:SCR\_008137)

### Resource Information

**URL:** <http://genome.wustl.edu/projects/detail/human-gut-microbiome/>

**Proper Citation:** Human Gut Microbiome Initiative (RRID:SCR\_008137)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 19, 2022. Human Gut Microbiome Initiative (HGMI) seeks to provide simply annotated, deep draft genome sequences for 100 cultured representatives of the phylogenetic diversity documented by 16S rRNA surveys of the human gut microbiota. Humans are supra-organisms, composed of 10 times more microbial cells than human cells. Therefore, it seems appropriate to consider ourselves as a composite of many species - human, bacterial, and archaeal - and our genome as an amalgamation of human genes and the genes in "our" microbial genomes ("microbiome"). In the same sense, our metabolome can be considered to be a synthesis of co-evolved human and microbial traits. The total number of genes present in the human microbiome likely exceeds the number of our *H. sapiens* genes by orders of magnitude. Thus, without an understanding of our microbiota and microbiome, it not possible to obtain a complete picture of our genetic diversity and of our normal physiology. Our intestine is home to our largest collections of microbes: bacterial densities in the colon (up to 1 trillion cells/ml of luminal contents) are the highest recorded for any known ecosystem. The vast majority of phylogenetic types in the distal gut microbiota belong to just two divisions (phyla) of the domain Bacteria - the Bacteroidetes and the Firmicutes. Members of eight other divisions have also been identified using culture-independent 16S rRNA gene-based surveys. Metagenomic studies of complex microbial communities residing in our various body habitats are limited by the availability of suitable reference genomes for confident assignment of short sequence reads generated by highly parallel DNA sequencers, and by knowledge of the professions (niches) of community members. Therefore, HGMI, which represents a collaboration between Washington University's Genome Center and its Center for Genome Sciences, seeks to provide simply annotated, deep draft genome sequences for 100 cultured representatives of the phylogenetic diversity documented by 16S rRNA surveys of the human gut microbiota.

**Synonyms:** HGMI

**Resource Type:** portal, topical portal, database, data or information resource

**Keywords:** ecosystem, firmicutes, bacterial, bacteroidetes, body, cell, diversity, genome, gut, habitat, human, metabolom, microbial, microbiome, microbiota, phylogenetic, rna, sequence, specie, synthesis

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** Human Gut Microbiome Initiative

**Resource ID:** SCR\_008137

**Alternate IDs:** nif-0000-20960

**Old URLs:** <http://genome.wustl.edu/projects/athaliana/>

**Record Creation Time:** 20220129T080245+0000

**Record Last Update:** 20260807T042706+0000

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## Ratings and Alerts

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

No alerts have been found for Human Gut Microbiome Initiative.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.