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Program Snapshot

The Common Fund's **Human Microbiome Project (HMP)** aims to characterize the microbial communities found at several different sites on the human body, including nasal passages, oral cavities, skin, gastrointestinal tract, and urogenital tract, and to analyze the role of these microbes in human health and disease. HMP includes the following initiatives.

- Development of a reference set of microbial genome sequences and preliminary characterization of the human microbiome
- Elucidation of the relationship between disease and changes in the human microbiome
- Development of new technologies for computational analysis
- Development of new tools for computational analysis
- Establishment of a data analysis and coordinating center (DACC)
- Establishment of resource repositories
- Examination of the ethical, legal and social implications (ELSI) of HMP research

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Program Highlights



NIH Human Microbiome Project Completes Seminal Study of Microbial Diversity in Healthy Volunteers

[Read more...](#)

[Listen to the BBC Frontiers radio program, 'Human Microbes', featuring HMP researchers as they talk about the research and its potential impact on understanding how microbes affect health and disease.](#) [EXIT Disclaimer](#)

Access the HMP data:

View the genomes of 100s of HMP reference strains in Gen Bank:

<http://www.ncbi.nlm.nih.gov/bioproject/28331>

Order an HMP reference strain:

<http://www.beiresources.org/>

View the HMP BioProjects page at NCBI with sequence and phenotype data:

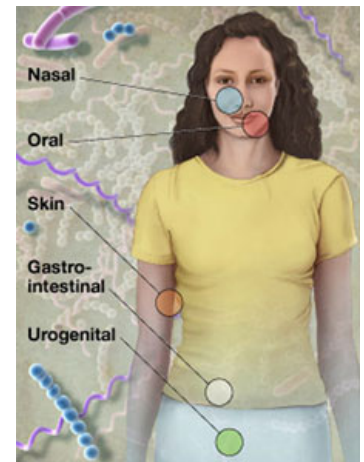
<http://www.ncbi.nlm.nih.gov/genomeprj/43021>

Visit the HMP Data Analysis and Coordination Center (DACC) site:

<http://www.hmpdacc.org>

WANTED: DEAD or ALIVE!

THE HUMAN MICROBIOME PROJECT (HMP) NEEDS YOUR HELP!!!



Researchers in the HMP are sampling and analyzing the genome of microbes from five sites on the human body: nasal passages, oral cavities, skin, gastrointestinal tract, and urogenital tract.

We're actively seeking microbes - bacterial, eukaryotic, and viral - that have been isolated from the human body and are available for sequencing as part of the HMP's reference genome collection. For a list of projects that have been targeted by the HMP, are underway, or have been completed, see the HMP [project catalog](#). [EXIT Disclaimer](#)

We're also maintaining a list of the ['most wanted'](#) [EXIT Disclaimer](#) bacteria for sequencing. Capture of these elusive bacteria for whole genome sequencing will help us to fill phylogenetic holes in the current reference genome collection. Amplified material from single cells will also be considered for sequencing.

To nominate strains for sequencing, please [click here](#) [EXIT Disclaimer](#). The deadline for nominations is November 1st, 2012!

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