



Reading Assignments for Wednesday

Human Microbiome Project (HMP) Published Papers

A series of coordinated scientific reports published on June 13, 2012, in *Nature* and several journals in the *Public Library of Science (PLOS)*

Nature Papers

- [Structure, function and diversity of the healthy human microbiome](#) 
- [A framework for human microbiome research](#) 

Public Library of Science (PLOS) Papers

- Fahad , Matt • [A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy](#)
- Devesh, Elena • [Complex Carbohydrate Utilization by the Healthy Human Microbiome](#)
- Lauren, Bing • [A case study for large-scale human microbiome analysis using JCVI's Metagenomics Reports \(METAREP\)](#)
- Asuka, Hannah • [A Core Human Microbiome as Viewed Through 16S rRNA Sequence Clusters](#)
- Adam, Minyueh • [Host genes related to Paneth cells and xenobiotic metabolism are associated with shifts in human ileum-associated microbial composition](#)
- Graham, Sam • [Inflammatory bowel diseases phenotype, C. difficile and NOD2 genotype are associated with shifts in human ileum associated microbial composition](#)
- Huan • [Analyses of the Microbial Diversity across the Human Microbiome](#)
- Meihua • [Optimizing Read Mapping to Reference Genomes to Determine Composition and Species Prevalence in Microbial Communities](#)
- Jason • [Novel Bacterial Taxa in the Human Microbiome](#)
- Justin • [Evaluation of 16S rDNA-based community profiling for human microbiome research](#)
- Molly • [Sequence Analysis of the Human Virome in Febrile and Afebrile Children](#)
- James • [Metabolic reconstruction for metagenomic data and its application to the human microbiome](#)
- Ben • [Diverse CRISPRs evolving in human microbiomes](#)
- Dean • [Reducing the effects of PCR amplification and sequencing artifacts on 16S rRNA-based studies](#)