This document contains a few SRA datasets that may be worth investigating. Each of these data sets will not apply to every project, you should still look for data sets that relate closely to the virus/ARG you are investigating.

**PRJNA43021 (**[**link**](https://www.ncbi.nlm.nih.gov/bioproject/?term=PRJNA43021)**) – Human Microbiome Project**

|  |  |
| --- | --- |
| Project Type | Number of Sub-Projects |
| Umbrella project | 4 |
| | **BioProject accession** | **Name** | **Title** | | --- | --- | --- | | PRJNA48489 | Human Microbiome Project (HMP) 16S rRNA Gene Diversity | Examining the diversity of 16S ribosomal RNA genes in the human microbiome for the Human Microbiome Project (HMP) (NIH Human Microbiome Consortium) | | [PRJNA46305](https://www.ncbi.nlm.nih.gov/bioproject/46305) | Human Microbiome Project (HMP) Demonstration Projects | The human microbiome and human health and disease (NIH Human Microbiome Consortium) | | [PRJNA43017](https://www.ncbi.nlm.nih.gov/bioproject/43017) | Human Microbiome Project (HMP) Metagenome Projects | Deeper shotgun sequencing of human microbiome samples for the Human Microbiome Project (HMP) (NIH Human Microbiome Consortium) | | [PRJNA28331](https://www.ncbi.nlm.nih.gov/bioproject/28331) | Human Microbiome Project (HMP) Reference Genomes | Genomes of microorganisms that have been isolated in and on the human body, to be used as Reference Genomes for the Human Microbiome Project (HMP) (NIH Human Microbiome Consortium) | | |

**PRJNA32089 (**[**link**](https://www.ncbi.nlm.nih.gov/bioproject/32089)**) – Gut microbiomes from obese and lean twins**

Abstract: Total community DNA was isolated from the feces of monozygotic and dizygotic twins and their mothers. We have characterized the fecal microbial communities of adult female monozygotic and dizygotic twin pairs concordant for leanness or obesity, and their mothers. The results demonstrate that a diversity of organismal assemblages can nonetheless yield a core microbiome at a functional level, and that deviations from this core are associated with different physiologic states (obese versus lean).

**ERP003228 (**[link](https://www.ncbi.nlm.nih.gov/bioproject/397906)**) – Gut microbiome samples of melanoma cancer patients receiving immune checkpoint inhibitor therapy (side effects include diarrhea, rash, hepatitis)**

Abstract: (from related study) A major breakthrough in cancer immunotherapy was the discovery of immune checkpoint proteins, which function to effectively inhibit the immune system through various mechanisms. The first of such molecules shown to inhibit both T-cell proliferation and IL-2 production was cytotoxic T-lymphocyte associated protein 4 (CTLA-4). With this discovery, efforts turned to blocking this inhibitory pathway in an attempt to activate dormant T-cells directed at cancer cells. The first antibody directed against CTLA-4, ipilimumab, was quickly ushered into clinical trials and was approved by the US Food and Drug Administration (FDA) for the treatment of metastatic melanoma in 2011. Following the success of ipilimumab, other immune checkpoints were studied as possible targets for inhibition. One such interaction was that of the programmed cell death-1 (PD-1) T-cell receptor and its ligand found on many cancer cells, programmed death-ligand 1 (PD-L1). Unfortunately, the untoward effects of blocking the immune system's natural inhibitory mechanisms have manifested clinically as diarrhea, rash, and hepatitis. Nevertheless, the exciting field of immune checkpoint inhibitors offers a potential curative option for many cancer patients who previously had a more dismal prognosis. The authors aim to provide a comprehensive review of the literature and update on the use of CTLA-4, PD-1 and PD-L1 targeted therapy in the treatment of cancer and other molecules still in the early development phase.

**ERP003228 (**[link](https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=ERP003228)**) – Gut samples from one patient in ICU throughout stay and 9 months after**

Abstract: To study the effect of antibiotic therapy during patient hospitalization on the antibiotic resistance gene (ARG) reservoir (‘the resistome’) formed by the human microbiota, conventional clinical culturing methods are insufficient. Here, we apply functional metagenomics (using large-insert fosmid libraries in Escherichia coli) and metagenomic shotgun sequencing to examine resistome dynamics in a patient admitted to an Intensive Care Unit, throughout hospital stay and nine months after hospital discharge. Our data indicate that selection for antibiotic resistance, specifically among anaerobic gut commensals, occurs during hospital stay. Functional metagenomics provided data on the genetic context of the resistance genes, which are frequently associated with putative mobile genetic elements. Metagenomic sequencing allowed the identification and relative quantification of many ARGs (between one and eleven for each antibiotic family) per sampled time-point. We suggest that metagenomic shotgun sequencing may be applied as a monitoring tool to detect and quantify ARGs in patient microbiota.

**PRJNA421881 (**[link](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA421881)**) – Gut microbiomes of Vegans, Vegetarians, and Omnivores**

Abstract: human gut metagenome of vegetarians, vegans and omnivores (that’s all they wrote)

**SRP002523 (**[link](https://trace.ncbi.nlm.nih.gov/Traces/sra/?study=SRP002523)**) – Viromes of 4 monozygotic twins and their mothers derived from fecal samples at 3 time points over a year.**

Abstract: The human gut contains our largest collection of viruses, which infect the bacteria, archaea, and small eukaryotes that comprise its microbiota. Viral diversity and lifecycles are poorly understood in this as well as other body habitats. Therefore, we sequenced the viromes (metagnomes) of virus-like particles (VLPs) isolated from fecal samples that were collected from 4 pairs of adult female monozygotic (MZ) twins and their mothers at three different time points over the course of a year. These datasets were compared to datasets of sequenced bacterial 16S rRNA gene amplicons and total fecal community DNA. While our previous metagenomic analyses demonstrated that co-twins and their mothers share a greater degree of similarity in their fecal bacterial communities than unrelated individuals1, the current study shows that viromes, which encode diverse metabolic functions, are unique to individuals regardless of family relationships. Moreover, viromes are dominated by temperate phage that exhibit remarkable stability over the one year study period. Together these results indicate that the virome is a highly individualistic component of our gut ecosystems, even among people with identical human genotypes.

**PRJNA375935 (**[link](https://www.ncbi.nlm.nih.gov/bioproject/375935)**) – Gut metagenomes from 97 patients with ankylosing spondylitis and 104 healthy controls**

Abstract: To reveal the relationship between the gut microbiome and ankylosing spondylitis, a quantitative metagenomics study that was based on deep shotgun sequencing of the gut microbial DNA from 211 Chinese individuals (97 patients and 104 healthy controls) was carried out. A total of 23,709 genes and 16 metagenomic species that were differentially abundant in the two groups were identified

**All PARTIE Identified WGS metagenomes in the SRA (**[link](https://github.com/linsalrob/partie)**) – 60,000+ data sets of various ecosystems**

Abstract: PARTIE is a random forest classifier that reads DNA from a dataset and classifies it as WGS, 16s or Other. As we all now know, SRA labels are not exact - a 16s metagenome may be labeled as WGS-Random. Please talk to me if you want this list. It is absolutely a possibility for this project to search all of these data sets, but not every project will benefit from such a broad search.