Update Date: February 2023

Metagenome - SIP Projects in GOLD

Introduction

Metagenome Stable Isotope Probing (Metagenome - SIP) projects are experiments designed to analyze metabolically active microbial population growth through assimilation of stable isotope-labeled media (e.g. ¹³C, ¹⁵N, ¹⁸O, etc). SIP Projects are composed of "SIP Parent" samples, which are metagenomic DNA extracted from microbial populations grown with unlabeled substrates (i.e. controls) or isotope-labeled compounds (i.e. treatments). Metabolically active microbial populations will assimilate isotope labels into biomass and DNA. To analyze the distribution of stable isotope assimilation, SIP Parent samples are separated by density gradient fractionation into "SIP Fraction" samples. For JGI Metagenome - SIP projects, SIP Fractions that originate from the same SIP Parent are co-assembled with metaSPAdes. In addition, all SIP Fractions project-wide are co-assembled with MetaHipMer. All co-assemblies, with either metaSPAdes or MetaHipMer, are assigned their own Analysis Project IDs (AP IDs) in the JGI IMG database.

This document will help guide users to the information about SIP projects, SIP Parents, and SIP Fractions metadata in the Genomes Online Database (GOLD). It will cover three search paths:

- 1. SIP projects on the GOLD homepage.
- 2. SIP projects via Search by Sequencing Strategy.
- 3. SIP Fraction metadata via Biosample ID.

1. SIP projects on the GOLD homepage.

One way to access SIP projects is the GOLD homepage e.g. by clicking on the count of "Combined Assembly SIP Metagenome" analysis projects in the Analysis Projects section:

Analysis Projects

Genome Analysis (Isolate) 215,039

Metagenome Analysis 105,211

Metagenome - Cell Enrichment 2,525

Metagenome - Single Particle Sort 6,552

Metagenome - Assembled Genome (MAG) 18,186

Metatranscriptome Analysis 16,517

Combined Assembly 732

Combined Assembly SIP Metagenome 6

Single Cell - Screened (SAG) 2,505

Single Cell - Unscreened (SAG) 7,963

Transcriptome Analysis 818

2. SIP projects via Search by Sequencing Strategy

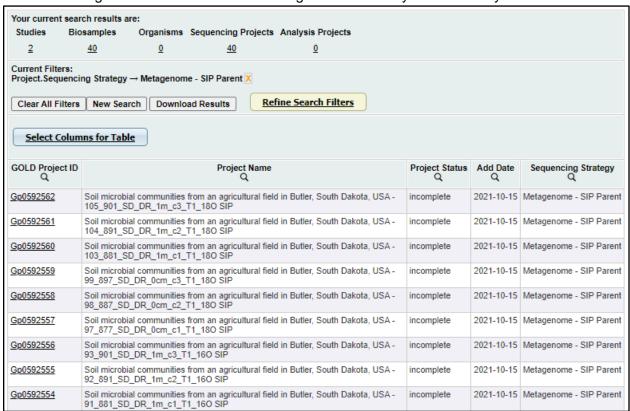
a. A more specific way to access SIP data is with GOLD's Advanced Search in the Search option of the menu bar:



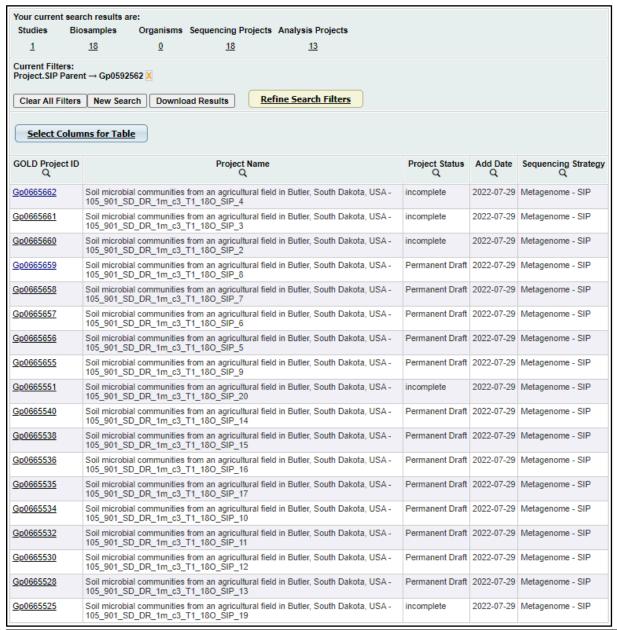
- To specify SIP projects in the Advanced Search, in the Project Fields filter you may select "Metagenome - SIP" or "Metagenome - SIP Parent" as the desired Sequencing Strategy.
- c. When you submit your search, the results will be summarized:



d. Clicking on the numbers in these categories will show you a table of your results:



e. To view individual SIP Fractions, click on the GOLD Project ID and scroll to the Project Composition section of the Project Information tab, then click on the number of SIP Fractions:

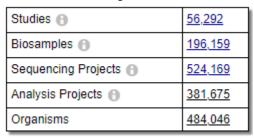


PROJECT COMPOSITION	
Study	Soil microbial communities from agricultural fields across the midwestern and eastern USA
Biosample	Soil microbial communities from an agricultural field in Butler, South Dakota, USA- 105 901 SD DR 1m c3 T1 180 SIP 8
Analysis Projects	Soil microbial communities from an agricultural field in Butler, South Dakota, USA- 105 901 SD DR 1m c3 T1 180 SIP 8
SIP Projects	SIP Parent <u>Gp0592562</u> → <u>18 SIP Fractions</u>
Number of Analysis Projects (AP)	1
Number of Derived Analyis Projects (DAP)	0

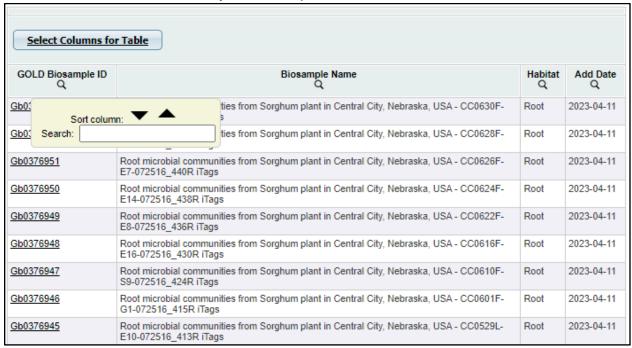
3. SIP Fraction metadata via Biosample ID

SIP Fraction specific metadata is associated with the Biosample in GOLD. If you already know the GOLD Biosample ID for the SIP fraction of interest, you can navigate to the metadata with the following steps:

a. If you are starting from an Advanced Search results page, you can skip to part 3b. If you are starting from the GOLD homepage, click on the "Biosamples" count:



b. From the list of Biosamples, click on the search button under the "GOLD Biosample ID" column header and enter your Biosample ID and/or click on the ID link:



c. Once on the "Biosample Information" page, click on the "Biosample Source" tab to view fraction specific SIP metadata:

