MG-RAST Data

If using Chordomics for metagenomics or metatranscriptomics samples one must first upload the data to MG-RAST.

Chordomics allows the user to enter just their MG-RAST dataset ID (beginning with "mgm") and it will download and process the data automatically. Alternatively users can manually download the appropriate files and upload them manually to Chordomics. This walkthrough will explain how to get them.
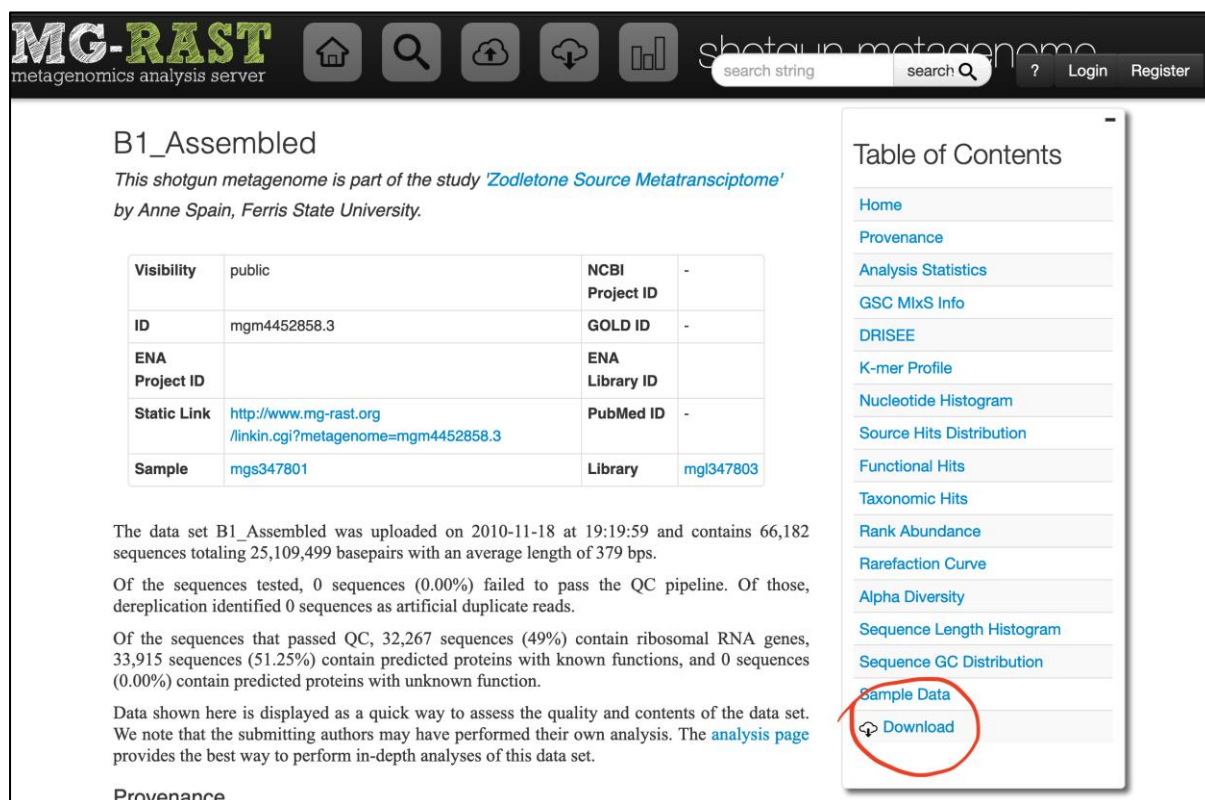
Chordomics requires 3 files:

- COG ontology file
- Organism file e.g. RefSeq
- Original fasta input

Walkthrough

Go to dataset page of the sample you want to download.

Click on the "Download" link on the panel on the right as shown.

Under the heading "Annotation Downloads" select and download the taxonomy file from Annotation Type – organism and your Data Source of choice. We recommend RefSeq.

Similarly select and download the functional file from Annotation Type – ontology and Data Source COG.

The input fasta file can be downloaded just below this from Step 0.