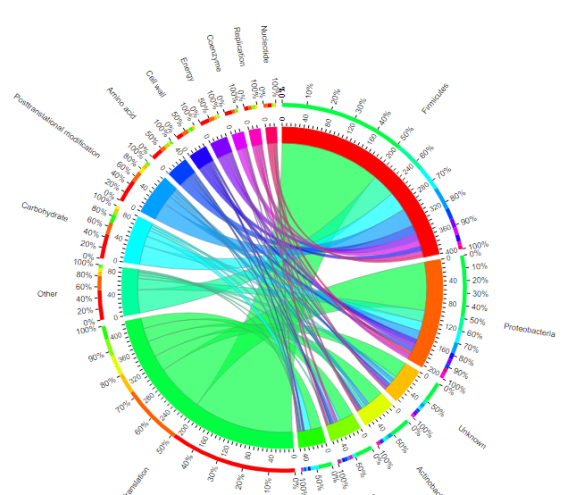


# Metaproteomics Data Processing

To process your data from the MPA click on Tab 3: Metaproteomics Data Processing.

Chordomics1. Metagenomics/Metatranscriptomics Data Processing2. Metaproteomics Data Processing3. Processed File Upload4. Chord Plot

Welcome to Chordomics!  
Chordomics is a tool for visualising the link between taxonomy and function in meta-omics data. We also provide a pipeline for correct file formatting.  
For more information visit us on [GitHub](#).  
Please navigate to the required tab:  
**1. Metagenomics/Metatranscriptomics Data Processing**  
Here users can join their MG-RAST organism and ontology files. The processed files can then be uploaded into Tab 3 for analysis.  
**2. Metaproteomics Data Processing**  
Here the user can annotate their MetaProteomeAnalyzer datasets with COG ID's using the UniProt API. The processed files can then be uploaded into Tab 3 for analysis.  
**3. Processed File Upload**  
Here users can upload their processed files from Tabs 1 and 2 or a manually formatted file for analysis and visualisation on Tab 4.  
Ensure the file types are csv format and contain headings of taxonomic rank (Superkingdom, Kingdom, Phylum, Class, Order, Family, Genus and/or Species) and function (COG\_Category and/or COG\_Name).  
**4. Chord Plot**  
Interact with your uploaded data here or select 'Load Example Data' to see an example.



Upload the Metaproteins output file from the MPA to Chordomics via the sidebar panel on the left.

Chordomics1. Metagenomics/Metatranscriptomics Data Processing2. Metaproteomics Data Processing3. Processed File Upload4. Chord Plot

Upload MPA CSVs here  
Browse... No file selected  
  
Prepare Data

### Metaproteomics Data Processing

Before data can be explored using chordomics it must be presented in the correct format. Use this utility to get functional (COG) information using the UniProt API as well as format your data for the next step (Tab 3).

Please upload a MetaProteomeAnalyzer(MPA) dataset to the panel on the left. For more information visit us on [GitHub](#). Once the dataset is entered press Prepare Data.

A download button will appear once the file is ready.

Progress:

Once a dataset has been uploaded, pressing the Prepare Data button begins the processing.

The Progress window will post updates of what is happening in the processing pipeline.

Note large datasets will take a long time to process.

Once the data is ready a Download button will appear. Use this to save the processed file.

The processed data can then be uploaded to Tab 3: Processed File Upload for visualisation.

Chordomics

1. Metagenomics/Metatranscriptomics Data Processing

2. Metaproteomics Data Processing

3. Processed File Upload

4. Chord Plot

Upload MPA CSVs here

Browse...

day1R1\_curated\_Head.csv

Upload complete

Prepare Data

Download

### Metaproteomics Data Processing

Before data can be explored using chordomics it must be presented in the correct format. Use this utility to get functional (COG) information using the UniProt API as well as format your data for the next step (Tab 3).

Please upload a MetaProteomeAnalyzer(MPA) dataset to the panel on the left. For more information visit us on [GiltHub](#). Once the dataset is entered press Prepare Data.

A download button will appear once the file is ready.

Progress:

Read in Data

Getting data from UniProt

Complete

Add extra rows if needed

Add labels to COG ids

File ready to download!

Click the 'Download' button on the side panel.