

MGnify API: accessing microbiome data computationally

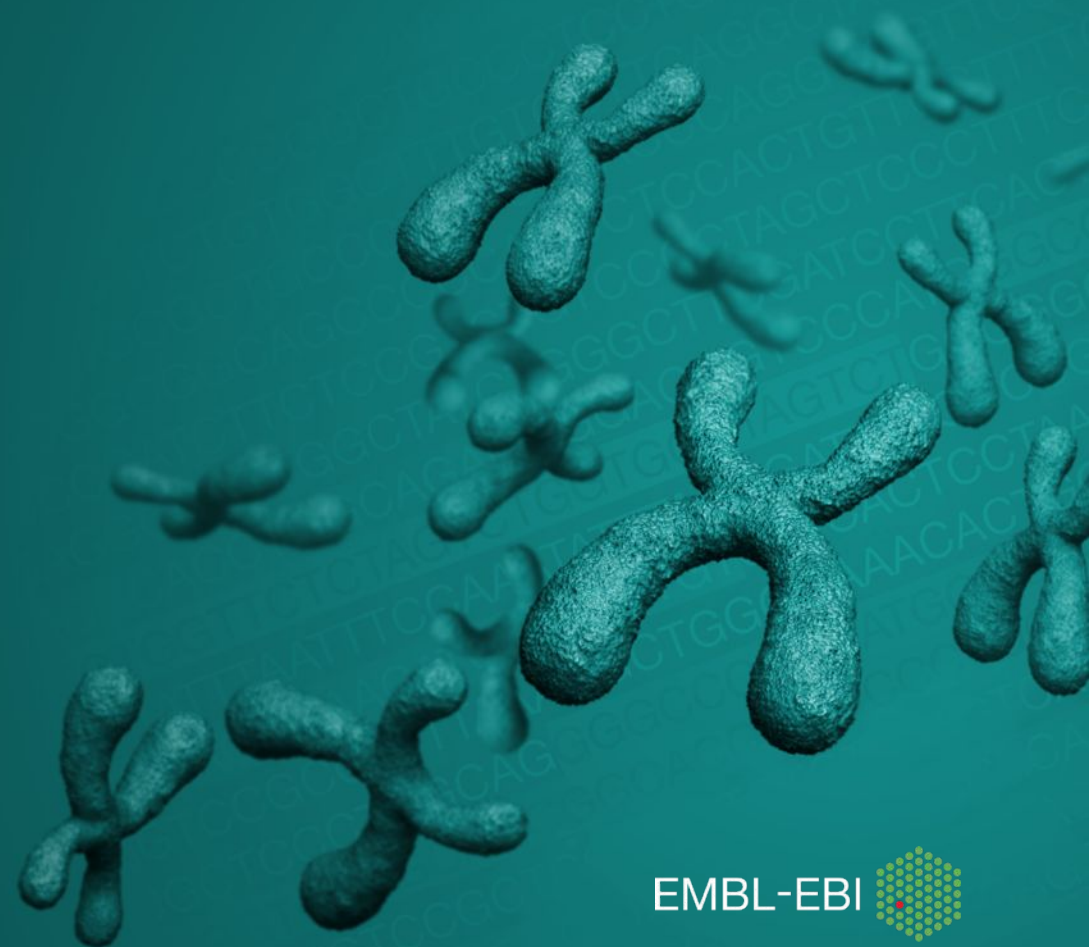
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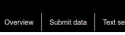
Objectives

- Understand how to interact with the MGnify API (Application Programming Interface)
- Learn how to write Python scripts to programmatically access data from MGnify API



A free resource for the assembly, analysis
and archiving of microbiome data

<https://www.ebi.ac.uk/metagenomics/>



Search

Example:

Overview Submit data Test search Sequence search Browse data Genomes API About Help 

Getting started

Search by

Name, biome, or keyword

[Text search](#)

Or by data type

348454	amplicon
30079	assemblies
2595	metabarcoding
32746	metagenomes
2204	metatranscriptomes

Or by selected biomes


Human
(140846)


Digestive system
(93555)


Aquatic
(44649)


Marine
(32299)


Digestive system
(31978)


Plants
(26476)


Soil
(22531)


Skin
(19501)


Wastewater
(3770)


Food production
(2676)

[Browse all biomes](#)

Request analysis of

Your data [Submit and/or Request](#)

A public dataset [Request](#)

Latest studies

- 1) Fungi, 2) Prescribed Burning, 3) Soil Targeted Locus (Loc)

We use Torrent Transcribed Interome Transcribed Spacer Region 1 (TSR1) amplicons to interrogate soil fungal community responses to long-term prescribed fire treatments in a loblolly pine forest on the Piedmont of Georgia. Our deep sequence data are in ...

[View more - 1 samples](#)

- Complex community structure of ectomycorrhizal, arbuscular-mycorrhizal and root-endophytic fungi in a mixed subtropical forest of ectomycorrhizal and arbuscular-mycorrhizal plants

Most terrestrial plants interact with diverse clades of mycorrhizal and root-endophytic fungi in their roots. Through the below-ground plant_fungal association, dominant plants can benefit by interacting with host-specific mutualistic fungi, while s...

[View more - 1152 samples](#)

- Switchgrass rhizosphere

Characterization of bacterial and fungal communities in switchgrass rhizosphere

[View more - 588 samples](#)

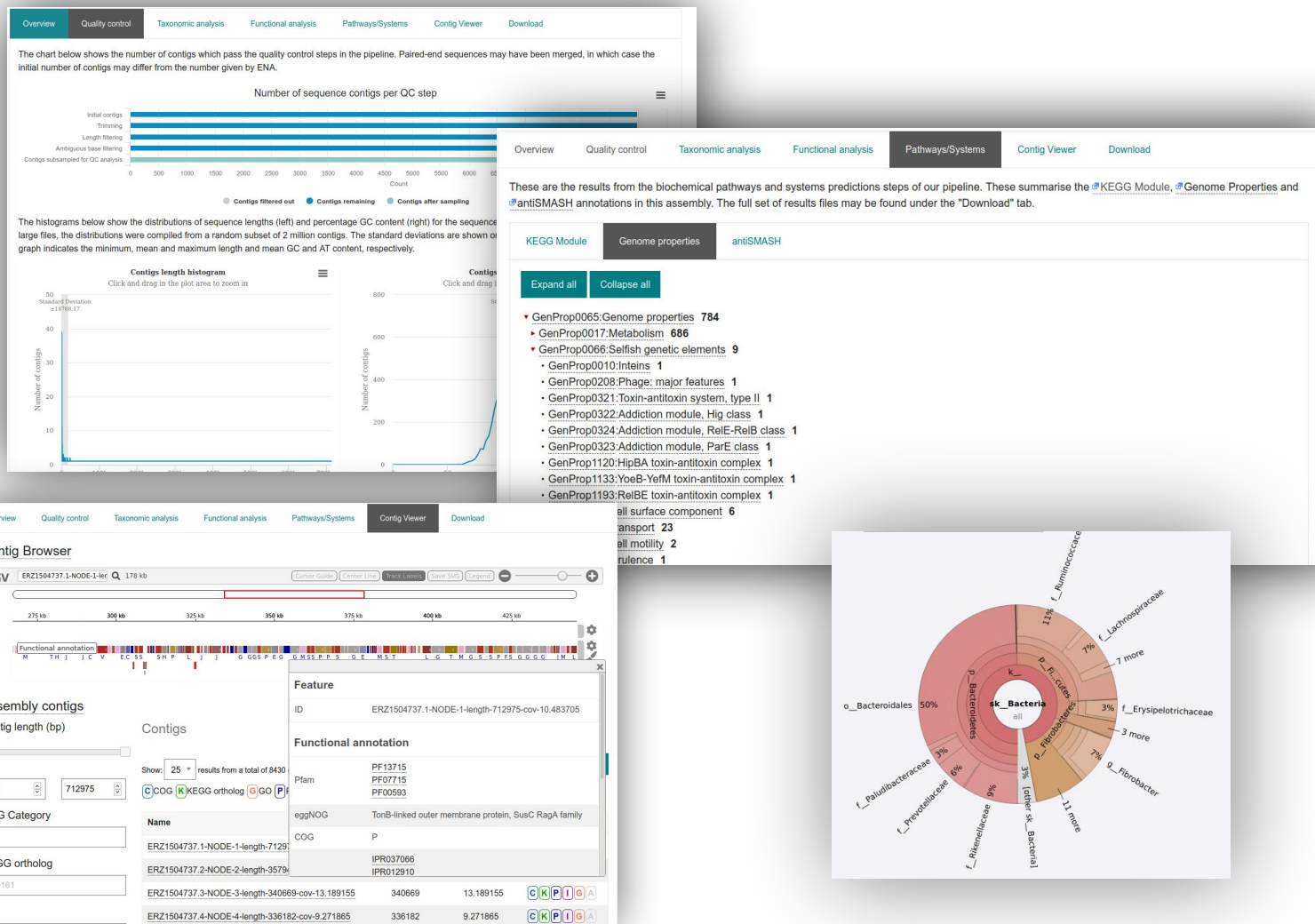
[View all studies](#)

Spotlight

The Earth Microbiome Project

Tools

The Mnify protein database -



Web API

A web Application Programming Interface (API) is a tool to access data from a web resource.

It's possible to explore/consume MGNify data using its API. This allows more extensive and personalized analyses.

- Data exchange
- Data mining

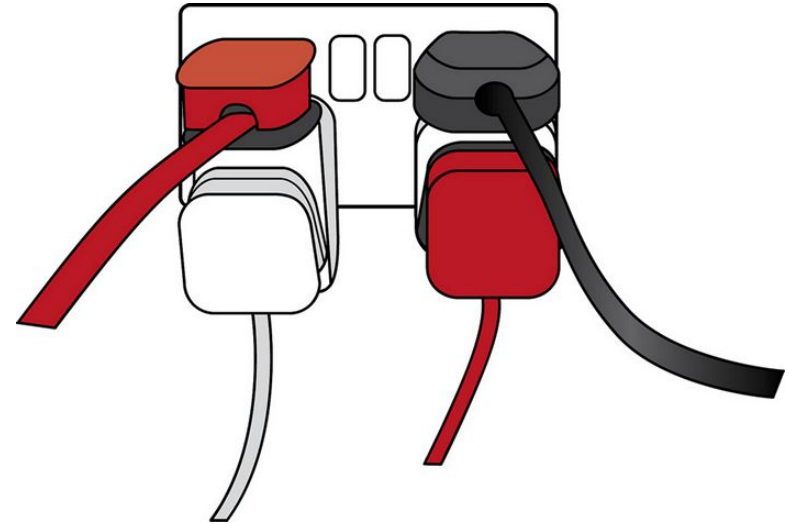
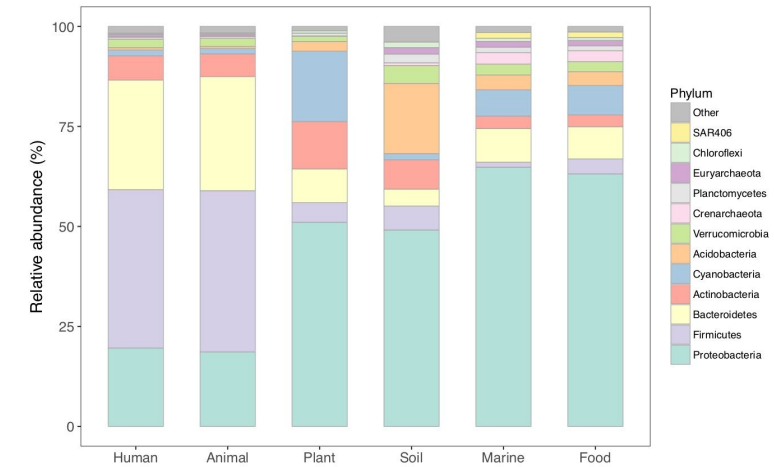
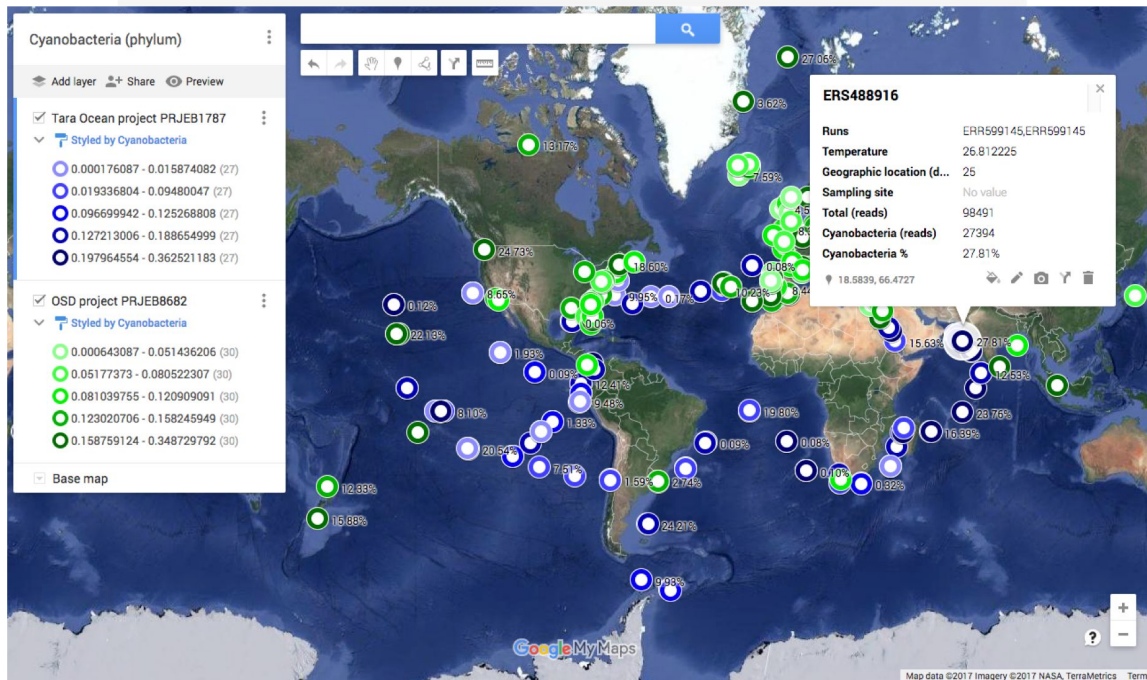


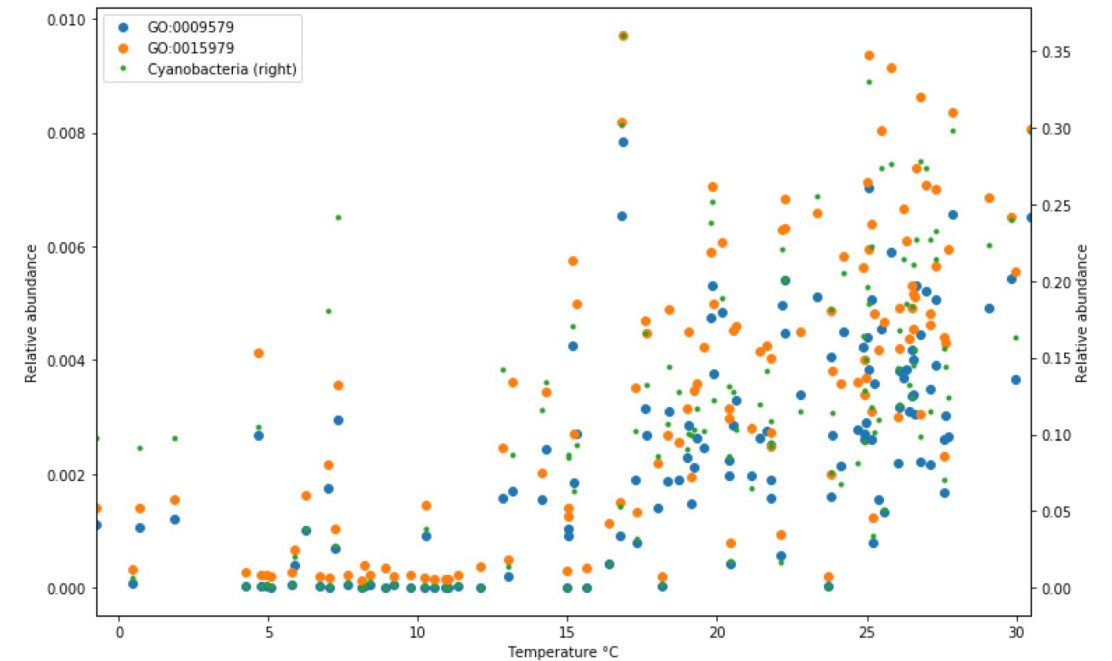
Image source: [Overloaded plug socket](#) by [The Clear Communication People](#), on Flickr.

Data visualization

accession	sample name	biome	temperature	depth	location	latitude
ERS1569005	Arctic seawater metagenome, 12 m	Oceanic	1.0376	12	Arctic Ocean	72.7978
ERS1568998	Arctic seawater metagenome, 57 m	Oceanic	1.7079	57	Arctic Ocean	72.9989
ERS1568997	Arctic seawater metagenome, 57 m	Oceanic	1.7079	57	Arctic Ocean	72.9989
ERS1569006	Arctic seawater metagenome, 12 m	Oceanic	1.0376	12	Arctic Ocean	72.7978
ERS1568999	Arctic seawater metagenome, 25 m	Oceanic	1.6423	25	Arctic Ocean	72.9989
ERS493460	TARA_20111019T1928Z_133_Combined-EVENTS_CAST_M...	Oceanic	4.936634 °C	650 m	None	35.2698
ERS493372	TARA_20111005T2047Z_132_Combined-EVENTS_CAST_M...	Oceanic	6.689724 °C	550 m	None	31.5280
ERS493705	TARA_20111203T1433Z_137_Combined-EVENTS_CAST_M...	Oceanic	8.911481 °C	375 m	None	14.2025



Microbiome diversity in different environments at the phylum level



How to browse the MGnify API?

Base URL:

- <https://www.ebi.ac.uk/metagenomics/api>

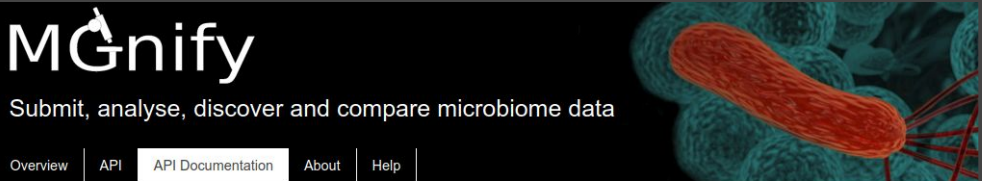
API Documentation:

- <https://www.ebi.ac.uk/metagenomics/api/docs>

Features:

- **Hypermedia** driven REST API
- **JSON API** - defined data structure
- Provides schema using **Open API Specification**

Open API Documentation



MGnify
Submit, analyse, discover and compare microbiome data

Overview | API | **API Documentation** | About | Help

HOME / API BROWSER / **API DOCUMENTATION**

MGnify API

<https://www.ebi.ac.uk/metagenomics/api/schema?format=openapi>

MGnify API documentation is available on Read the Docs site on <https://emg-docs.readthedocs.io/en/latest/api.html>

- [analyses >](#)
- [annotations >](#)
- [antismash-geneclusters >](#)
- [assemblies >](#)
- [banner-message >](#)
- [biomes >](#)
- [cogs >](#)
- [ebi-search-download >](#)
- [experiment-types >](#)
- [genomes >](#)
- [genomeset >](#)
- [kegg-classes >](#)

<https://www.ebi.ac.uk/metagenomics/api/docs/>

genomes ▾

GET </metagenomics/api/v1/genomes>

GET </metagenomics/api/v1/genomes/{accession}>

GET </metagenomics/api/v1/genomes/{accession}/antismash-genecluster>

GET </metagenomics/api/v1/genomes/{accession}/cogs>

GET </metagenomics/api/v1/genomes/{accession}/downloads> Retrieves list of static summary files

GET </metagenomics/api/v1/genomes/{accession}/downloads/{alias}>

GET </metagenomics/api/v1/genomes/{accession}/kegg-class>

GET </metagenomics/api/v1/genomes/{accession}/kegg-module>

GET </metagenomics/api/v1/genomes/{accession}/releases>

Useful links

Documentation

<https://emg-docs.readthedocs.io/en/latest/api.html#restful-api>

Code examples

<https://github.com/EBI-Metagenomics/examples>

Contact us

<https://www.ebi.ac.uk/support/metagenomics>

Follow us on twitter

<https://twitter.com/MGnifyDB>

Acknowledgements



- Rob Finn
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