

# Import a GEO / ENA project

- [How to import a study from GEO / ENA](#)
- [Common Issues](#)
  - [Error Message - The project did not yield any data. Double-check the project ID, or try importing the data manually](#)
  - [The project was imported, but the Analyses tab is empty and there are no FASTQ files](#)
  - [Something is missing or the import failed](#)
- [FAQ](#)
  - [What are GEO and ENA?](#)
  - [How do I know if a GEO project is also in ENA?](#)

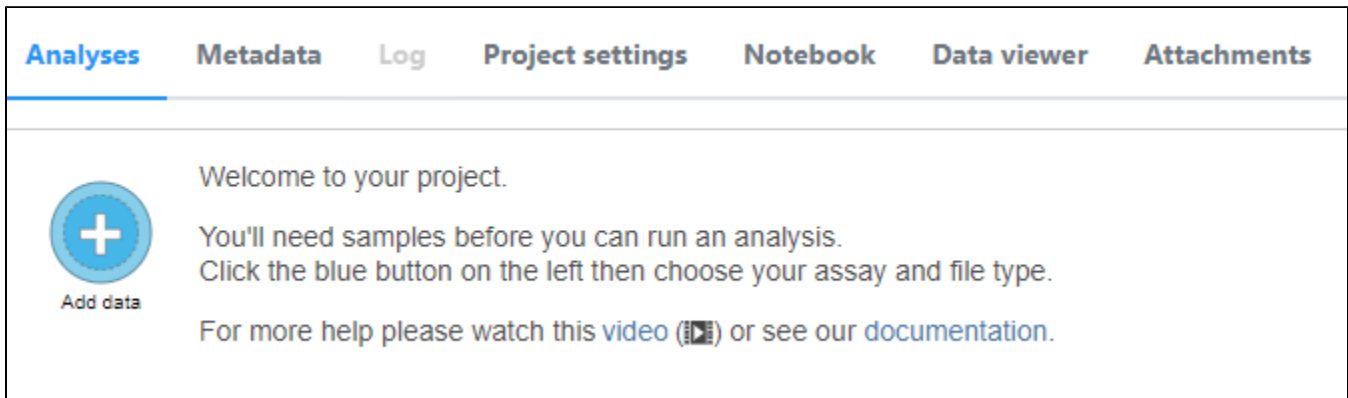
## How to import a study from GEO / ENA

If a project is publicly available in the Gene Expression Omnibus (GEO) and European Nucleotide Archive (ENA) databases, you can import associated FASTQ files and sample attributes automatically into Partek Flow.

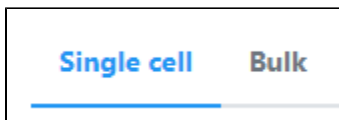
- On the Homepage click **New Project** to create a project and give the project a name



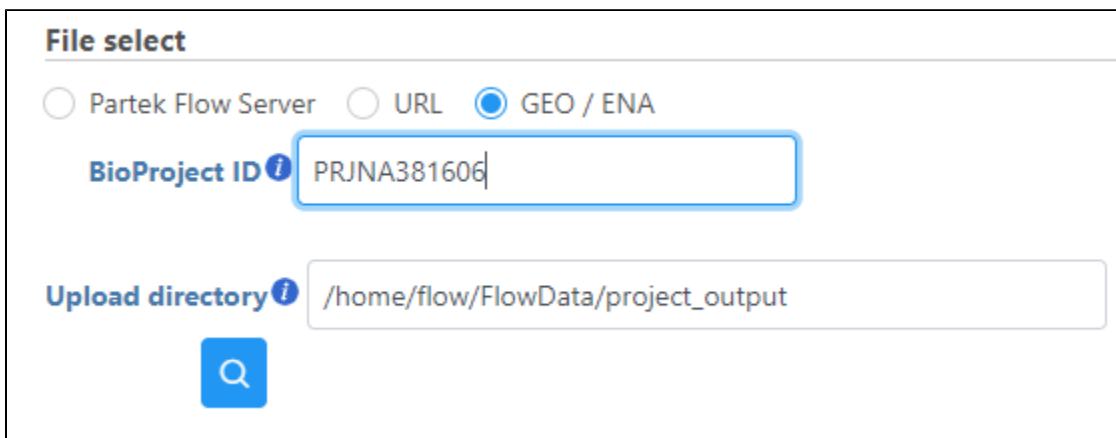
- Click **Add data**



- Select **fastq** as the file type after choosing between **Single cell** or **Bulk** as the assay types



- Click **Next**
- Choose GEO / ENA
- Enter the BioProject ID of the data set you would like to download. The format of a BioProject ID is PRJNA followed by one to six numbers (e.g. PRJNA381606)

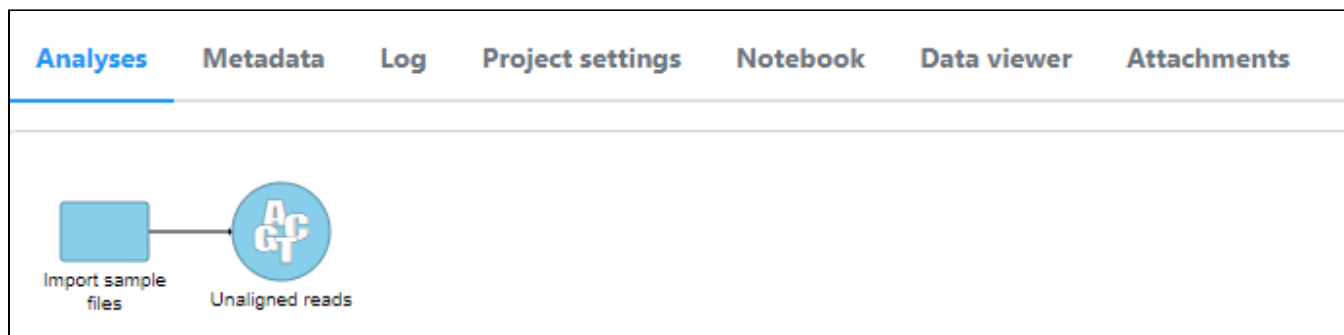


A GEO ID can also be used in the format GSE followed by one to five numbers (e.g. GSE71578).

- Click **Finish**

It may take a while for the download to complete depending on the size of the data. FASTQ files are downloaded from the ENA BioProject page.

- FASTQ files will be added as an Unaligned reads data node in the Analyses tab



## Common Issues

### Error Message - The project did not yield any data. Double-check the project ID, or try importing the data manually

If the study is not publicly available in both GEO and ENA, project import will not succeed.

### The project was imported, but the Analyses tab is empty and there are no FASTQ files

If there is an ENA project, but the FASTQ files are not available through ENA, the project will be created, but data will not be imported.

### Something is missing or the import failed

A variety of other issues and irregularities can cause imports to not succeed or partially succeed, including, but not limited to, a BioProject having multiple associated GSE IDs, incomplete information on the GEO or ENA page, and either the GEO or ENA project not being publicly available.

## FAQ

### What are GEO and ENA?

The Gene Expression Omnibus (GEO) and the European Nucleotide Archive (ENA) are web-accessible public repositories for genomic data and experiments. Access and learn more about their resources at their respective websites:

GEO - <https://www.ncbi.nlm.nih.gov/geo/>


ENA - <https://www.ebi.ac.uk/ena>

### How do I know if a GEO project is also in ENA?

- You can search ENA using the GEO ID (e.g., GSE71578) to check if there is a matching ENA project.

EMBL-EBI

[Services](#)
[Research](#)
[Training](#)
[About us](#)



Examples: [BN000065](#), [histone](#)
[Advanced](#)  
[Sequence](#)

[Home](#)
[Search & Browse](#)
[Submit & Update](#)
[Software](#)
[About ENA](#)
[Support](#)

Search results for *GSE97388*

Show more data from EMBL-EBI

**Study**  
Study (1)

**Submission**  
Submission (Read/Analysis) (1)

**Study (1 results found)**  
SRP103018 In vitro differentiation of human embryonic stem cells into ovarian follicle-like cells  
[View all 1 results](#)


**Submission (Read/Analysis) (1 results found)**  
SRA551479 Submitted by Gene Expression Omnibus on 05-JUL-2017  
[View all 1 results](#)

Powered by [EBI Search](#)

- Open the Study result to view the BioProject ID (e.g., PRJNA381606) and a table with information about the samples and files included in the project

EMBL-EBI

[Services](#)
[Research](#)
[Training](#)
[About us](#)



Examples: [BN000065](#), [histone](#)
[Advanced](#)  
[Sequence](#)

[Home](#)
[Search & Browse](#)
[Submit & Update](#)
[Software](#)
[About ENA](#)
[Support](#)

Study: PRJNA381606

[Contact Helpdesk](#)

In vitro differentiation of human embryonic stem cells into ovarian follicle-like cells

View: [Project XML](#) [Study XML](#)
Download: [Project XML](#) [Study XML](#)

<b>Name</b>	<b>Submitting Centre</b>	<b>Organism</b>
Homo sapiens	Basic Medical Sciences, Tsinghua University	<a href="#">Homo sapiens</a>

**Secondary accession(s)**  
SRP103018

**Description**  

Understanding the unique mechanisms of human oogenesis necessitates the development of an in vitro system of stem cell differentiation into oocytes. Specialized cell types and organoids have been derived from human pluripotent stem cells in vitro, but generating a human ovarian follicle remains a challenge. Here we report that human embryonic stem cells (hESCs) can be induced to differentiate into ovarian follicle-like cells in vitro. First, we find that two RNA-binding proteins specifically expressed in germ cells, DAZL and BOULE, regulate the exit from pluripotency and entry into meiosis. By expressing DAZL and BOULE with recombinant human GDF9 and BMP15, these meiotic germ cells are further induced to form ovarian follicle-like cells (FLCs), including oocytes and granulosa cells. This robust in vitro differentiation system will allow the study of the unique molecular mechanisms underlying human pluripotent stem cell differentiation into late PGCs, meiotic germ cells, and ovarian follicles. Overall design: Including 6 samples, 4 controls: ES\_1, ES\_2, SDE\_1, SDE\_2; 2 samples: FLC\_1 (HSF6), FLC\_2 (H9)

**Lineage**  
[Eukaryota](#), [Metazoa](#), [Chordata](#), [Craniata](#), [Vertebrata](#), [Euteleostomi](#), [Mammalia](#), [Eutheria](#), [Euarchontoglires](#), [Primates](#), [Haplorrhini](#), [Catarrhini](#), [Hominidae](#), [Homo](#)

Navigation

Read Files

Portal

Attributes

Publications

Parent Projects

Bulk Download Files

(If the downloader app doesn't open, please try using Firefox to launch it.)

Download:  -  of 6 results in [TEXT](#)

[Select columns](#)

Showing results 1 - 6 of 6 results

Study accession	Sample accession	Secondary sample accession	Experiment accession	Run accession	Tax ID	Scientific name	Instrument model	Library layout	FASTQ files (FTP)	FASTQ files (Galaxy)	Submitted files (FTP)	Submitted files (Galaxy)	NCBI SRA file (FTP)	NCBI SRA file (Galaxy)	CRAM Index files (FTP)	CRAM Index files (Galaxy)
<a href="#">PRJNA381606</a>	<a href="#">SAMN06681557</a>	<a href="#">SRS2098866</a>	<a href="#">SRX2705208</a>	<a href="#">SRR5413258</a>	<a href="#">9606</a>	<a href="#">Homo sapiens</a>	Illumina HiSeq 2500	PAIRED	<a href="#">File 1</a> <a href="#">File 2</a>	<a href="#">File 1</a> <a href="#">File 2</a>			<a href="#">File 1</a>	<a href="#">File 1</a>		
<a href="#">PRJNA381606</a>	<a href="#">SAMN06681556</a>	<a href="#">SRS2098867</a>	<a href="#">SRX2705209</a>	<a href="#">SRR5413259</a>	<a href="#">9606</a>	<a href="#">Homo sapiens</a>	Illumina HiSeq 2500	PAIRED	<a href="#">File 1</a> <a href="#">File 2</a>	<a href="#">File 1</a> <a href="#">File 2</a>			<a href="#">File 1</a>	<a href="#">File 1</a>		

# Additional Assistance

If you need additional assistance, please visit [our support page](#) to submit a help ticket or find phone numbers for regional support.



Your Rating: Results: 1 rates