

# PARADIGM API

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## API Overview

This API is meant to provide users with a way to initiate PARADIGM runs programmatically. Users upload data files and pathways to the service, and then initiate a run specifying which files they'd like to use. The run can then be queried until completion at which point the results will be provided. The amount of time between run initiation and completion is variable, depending on current system queue and the size of the pathway provided.

## Obtaining an API Key

API keys can be obtained by creating a free account on Five3 and visiting the following URL (also available in the profile):

```
https://dna.five3genomics.com/account/apikey/
```

## Methods

All requests require authenticating, via username and api\_key sent as request variables (GET or POST parameters), for example:

```
https://dna.five3genomics.com/paradigm/api/v1/file/?  
username=jane&api_key=123456789
```

## Get uploaded files

```
https://dna.five3genomics.com/paradigm/api/v1/file/
```

**Method:** GET

**Response:** List of all the previously uploaded data files from this user

## Add uploaded file

```
https://dna.five3genomics.com/paradigm/api/v1/file/
```

**Method:** POST (Multipart)

### Required Parameters:

- format : a letter code describing the format
  - path : A pathway file
  - he : Tab delimited expression file with hugo in the first column and samples as subsequent columns
  - hcnv : Tab delimited copy-number file with hugo in the first column and samples as subsequent columns
- file : the file to upload

**Response:** \* file : The details of the file (md5 and filesize can be confirmed to assure transfer was successful)

## Get PARADIGM Runs

```
https://dna.five3genomics.com/paradigm/api/v1/run/
```

**Method:** GET

**Result:** List of all the paradigm runs that this user has initiated, and if they have results

## Start PARADIGM Run

```
https://dna.five3genomics.com/paradigm/api/v1/run/
```

**Method:** POST

### Required Parameters:

- name : the name of the paradigm run to initiate (no spaces allowed)
- files : the filename(s) of previously uploaded files. files should be specified multiple times in the request to include all the files the user wants  
(files=my\_pathway.tab&files=my\_expression\_file.txt). At minimum, this requires a single pathway and a single non-pathway data file (where format is “he” or “hcnv”)

### Response:

- run : The details of the run that was created

## Get PARADIGM Run Results

```
https://dna.five3genomics.com/paradigm/api/v1/run/{run.uuid}/
```

**Method:** GET

### Required Parameters:

- {run.uuid} : the uuid returned in paradigm/run/

### Response:

- result : If the run has finished, a JSON array of result row triples in the form of sample, feature, IPL
- run : The full details of the run object