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Puerto Rico - IDeA Networks of Biomedical Research Excellence

PRINBRE
IDeA Network of Biomedical Research Excellence

Python3 Part 3 – Crash Course in Python3 for Future STEM Coders

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- The following material is the result of PR-INBRE research and curriculum development effort to provide a set of educational materials for research training and curriculum changes in biology programs across the island to support PR-INBRE efforts to establish a Community of Practice in Bioinformatics that offers a fruitful environment to increase computational and bioinformatics skills among traditional researchers and students (undergraduate and graduate) in the island. They have been developed as a part of the NIH funded project "**Puerto Rico IDeA Network Biomedical Research Excellence (PRINBRE)**" (Award Number 5P20GM103475).

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Competencies

June 2, 2024 - Record and write simple and common **Python scripts to deal with Bioinformatic needs for biological data analyses** using a Jupyter Notebook

June 3, 2024 – Exploit **datatypes that can record objects**, as well as, reason **logical statements**

Today – ***create your own dataset using Python***

Objectives

- **Create** a dataset
- **Open** and **Read data** of different file formats using either a **for loop** or a **Python Library**
  - TXT File
  - CSV File
- **Write** to different file formats
  - TXT File
  - CSV File
- **Import** a **Python Library** to your code
- Using Panda Library, create a **Pandas DataFrame** with columns and **export the DataFrame as a CSV File**

Objectives

- Continue to use **Google Colab as an environment** to practice and learn common **Python** lines of code.

- **Create** a new file using the function open()

- **Write** information to a file using the write() function

- Using **for Loops** analyze **lines of a file**

- **import** python libraries

Target Audience

- This training is addressed to beginners, highly motivated (eager to learn what is needed in order to be competitive without the tendency to self-limit when learning computational skills by saying that is difficult) wanting to become familiar with the **Python** programming language and become the Script Master of their bioinformatic analysis.

The importance of Python

- R is great; however, you'll eventually run into the Python language
- No matter your field, python will be a necessity (chemistry, biology, engineering, ecology, mathematics, etc)
- Knowing Python gives you an edge when job searching and navigating graduate research
- The majority bioinformatic tools are python-based and will lead you to understand under the hood code in order to successfully execute said program's purpose.

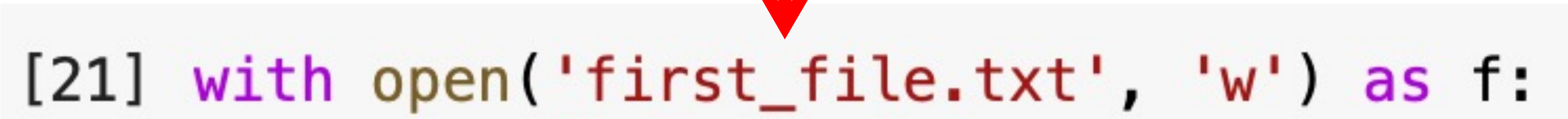
Lesson 3.0.0

Create Files

open() function facilitates creating a new file

1

Identify the name of your new file

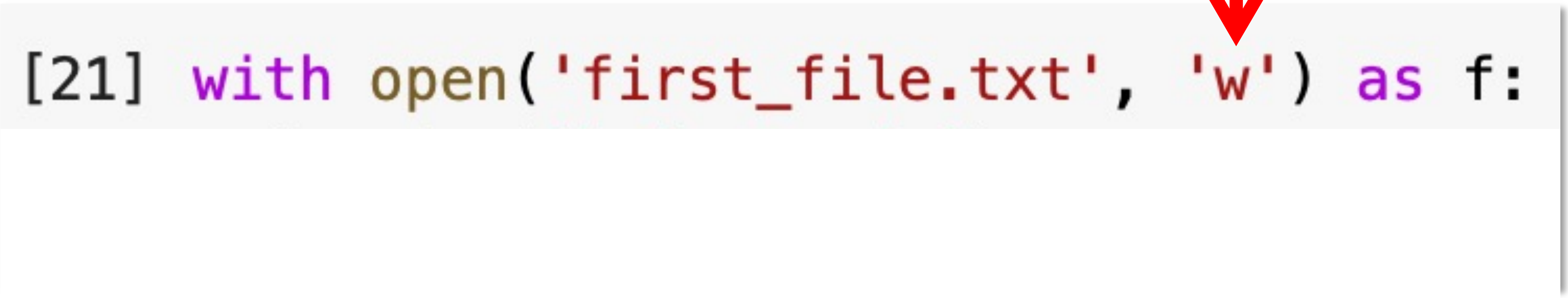


```
[21] with open('first_file.txt', 'w') as f:
```

open() function facilitates creating a new file

Indicate with ‘w’ that you want to write to this file

2

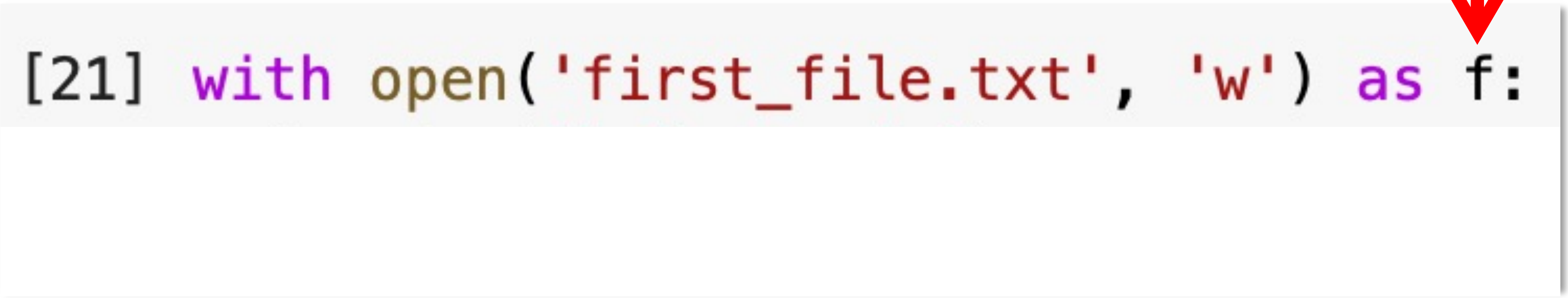


```
[21] with open('first_file.txt', 'w') as f:
```

open() function facilitates creating a new file

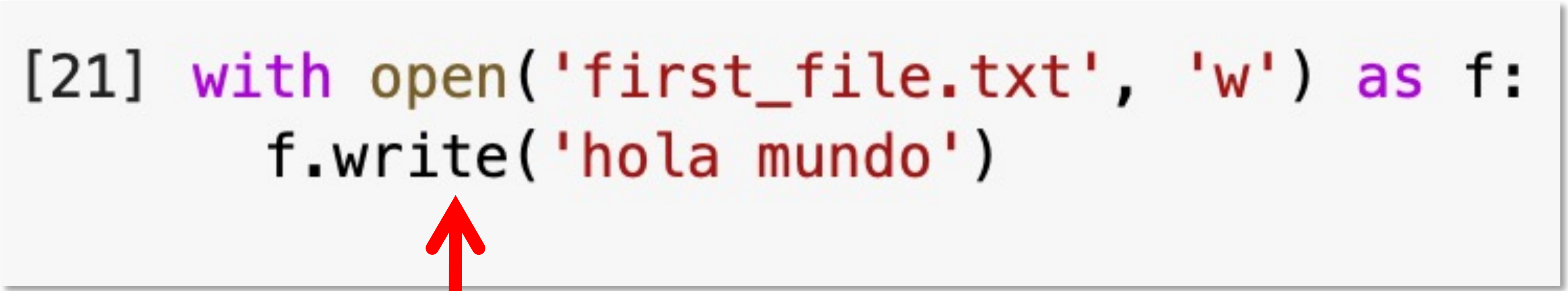
Assign a variable to this new file

3



```
[21] with open('first_file.txt', 'w') as f:
```

open() function facilitates creating a new file

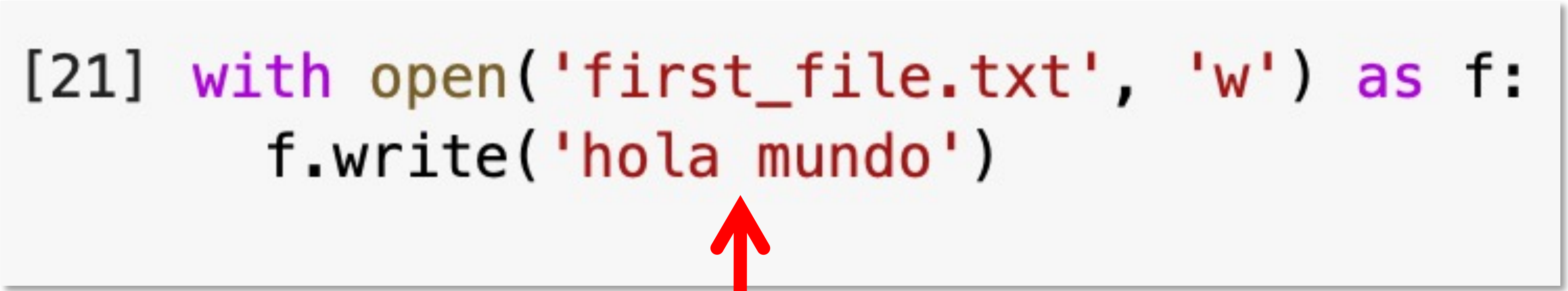


```
[21] with open('first_file.txt', 'w') as f:
         f.write('hola mundo')
```

4

write() will add content to a file

open() function facilitates creating a new file

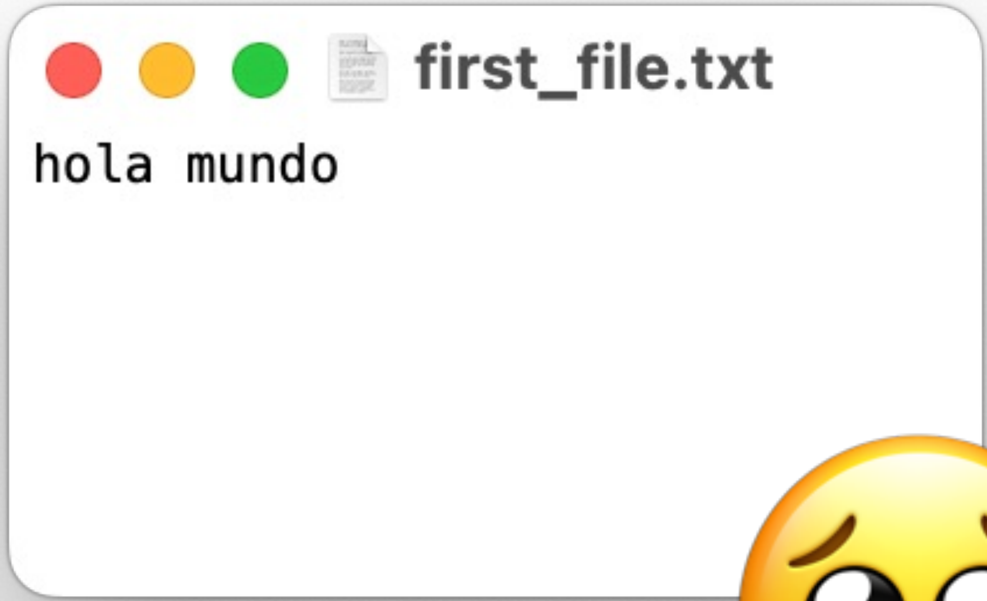


```
[21] with open('first_file.txt', 'w') as f:
         f.write('hola mundo')
```

5

Use write() to write 'hola mundo' to your new file called f

Success! Check out your first file!



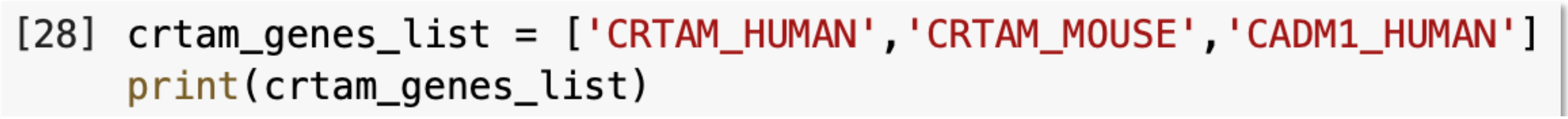
```
hola mundo
```

Exercise 3.0.0

Create a file with gene names found in a List

How can we create this txt file?

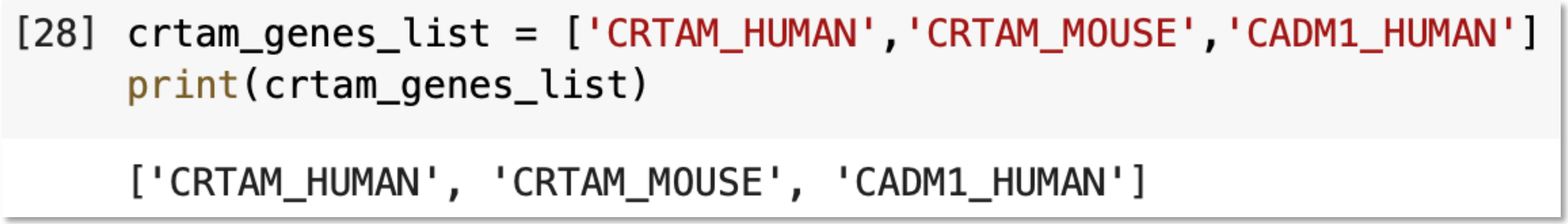
input is a list



```
[28] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     print(crtam_genes_list)
```

How can we create this txt file?

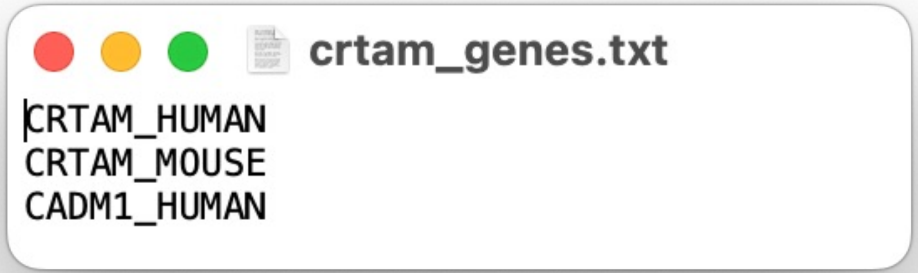
input is a list



```
[28] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     print(crtam_genes_list)

     ['CRTAM_HUMAN', 'CRTAM_MOUSE', 'CADM1_HUMAN']
```

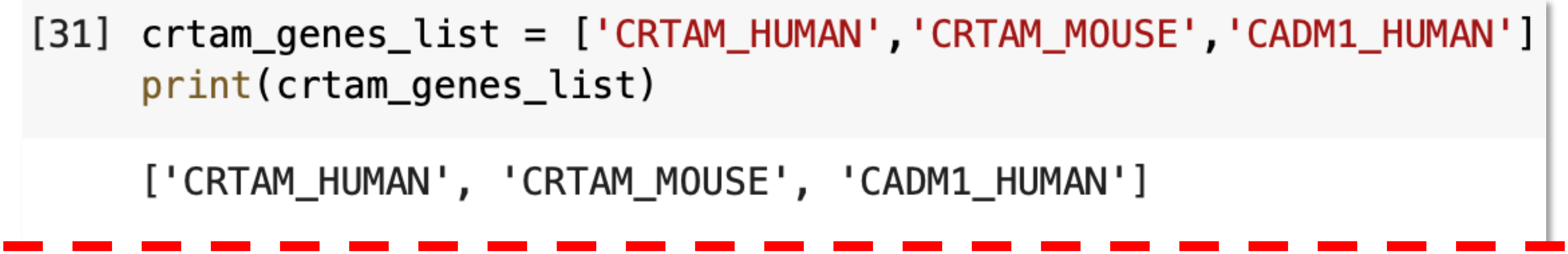
output the following txt file



```
CRTAM_HUMAN
CRTAM_MOUSE
CADM1_HUMAN
```

How can we create this txt file?

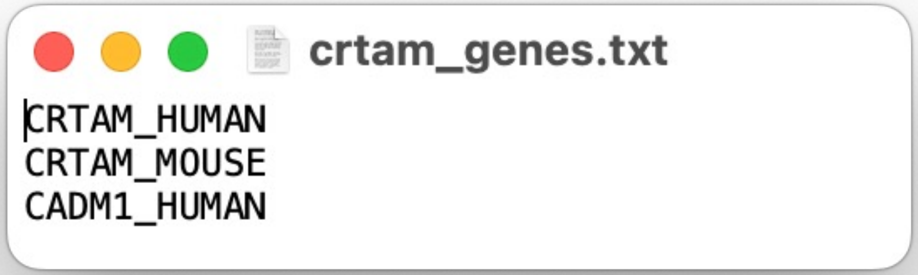
input is a list



```
[31] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     print(crtam_genes_list)

     ['CRTAM_HUMAN', 'CRTAM_MOUSE', 'CADM1_HUMAN']
```

Answer

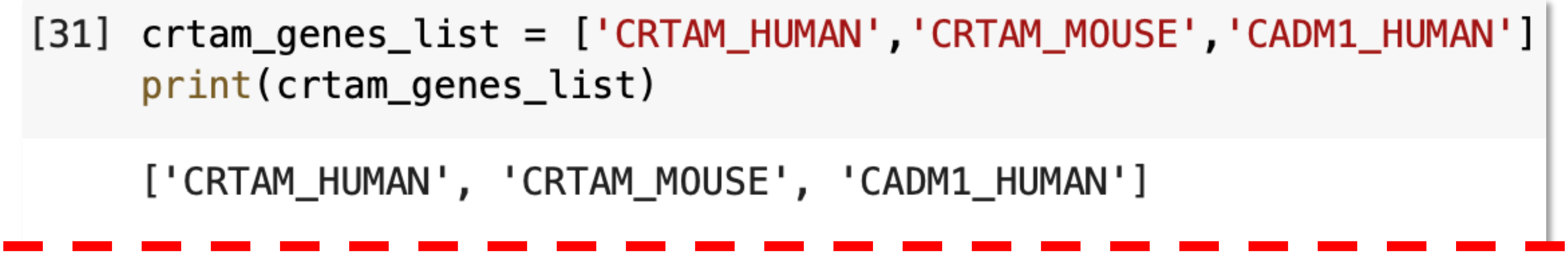


crtam_genes.txt

```
CRTAM_HUMAN
CRTAM_MOUSE
CADM1_HUMAN
```

How can we create this txt file?

input is a list

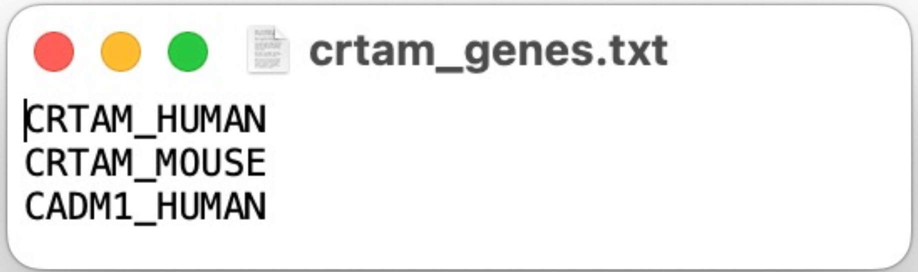


```
[31] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     print(crtam_genes_list)

     ['CRTAM_HUMAN', 'CRTAM_MOUSE', 'CADM1_HUMAN']
```

Answer

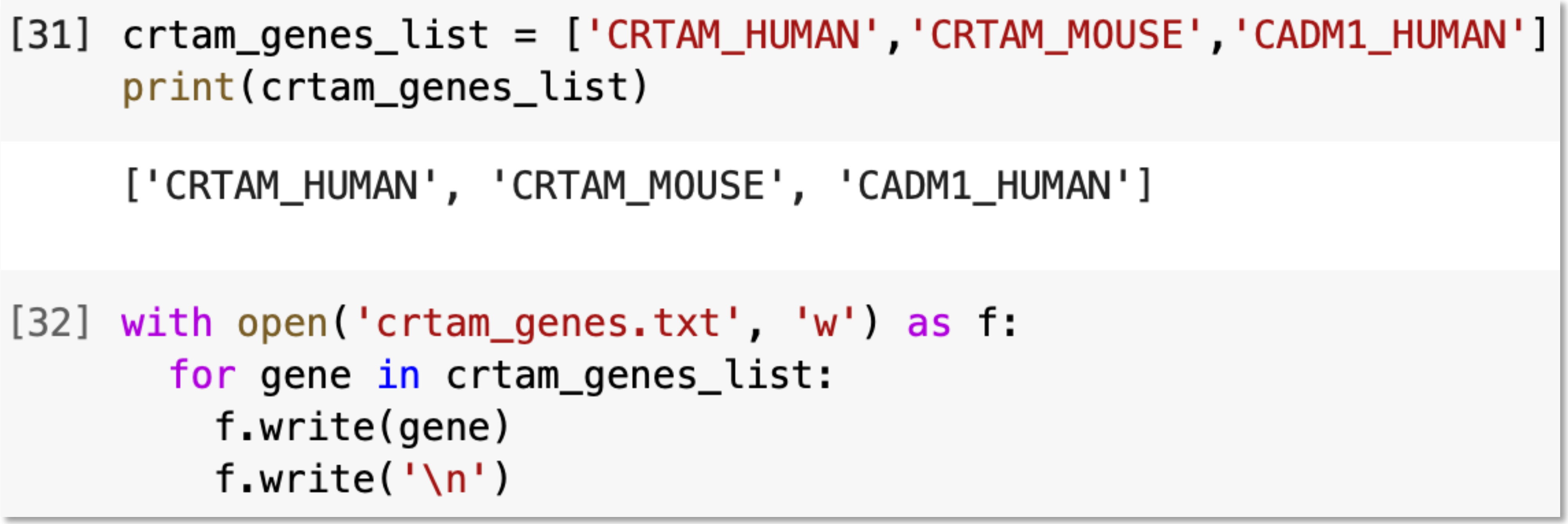
Tip: Use '\n' to indicate a new line



```
CRTAM_HUMAN
CRTAM_MOUSE
CADM1_HUMAN
```

How can we create this txt file?

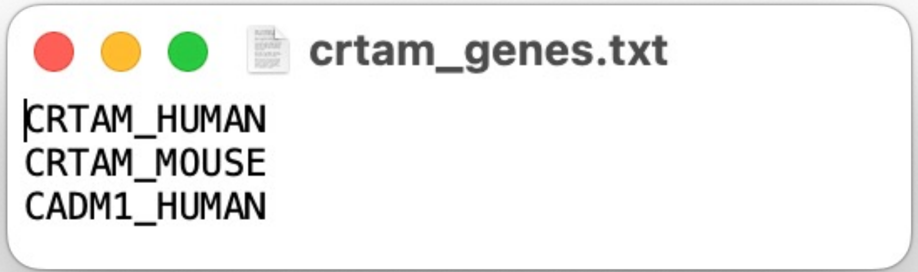
input is a list



```
[31] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     print(crtam_genes_list)

     ['CRTAM_HUMAN', 'CRTAM_MOUSE', 'CADM1_HUMAN']

[32] with open('crtam_genes.txt', 'w') as f:
       for gene in crtam_genes_list:
         f.write(gene)
         f.write('\n')
```



crtam_genes.txt

```
CRTAM_HUMAN
CRTAM_MOUSE
CADM1_HUMAN
```

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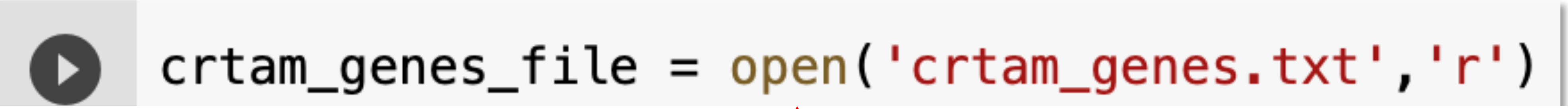
Lesson 3.1.0

Reading in your newly created files

Lesson 3.1.1

Read in the lines of a file using a For Loop

Read in your file using a for loop

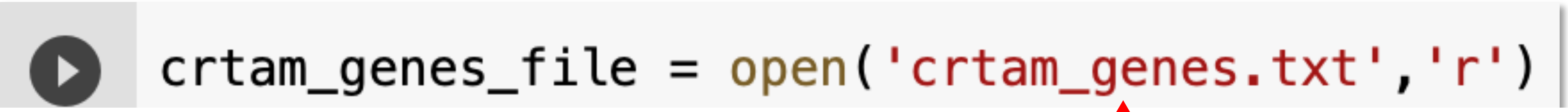


```
crtam_genes_file = open('crtam_genes.txt','r')
```

1

Use open() function

Read in your file using a for loop

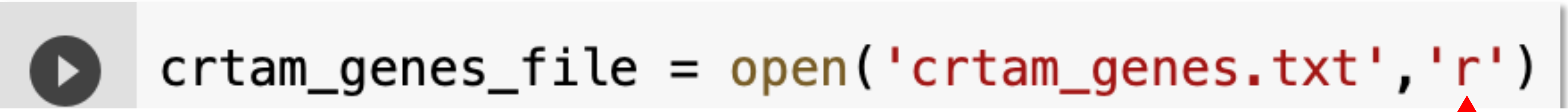


```
crtam_genes_file = open('crtam_genes.txt','r')
```

2

Identify your file of interest

Read in your file using a for loop

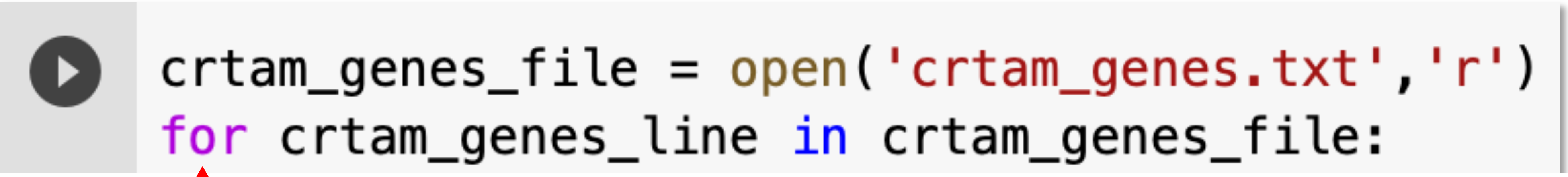


```
crtam_genes_file = open('crtam_genes.txt','r')
```

Indicate that you want to **read** the file with **‘r’**

3

Read in your file using a for loop

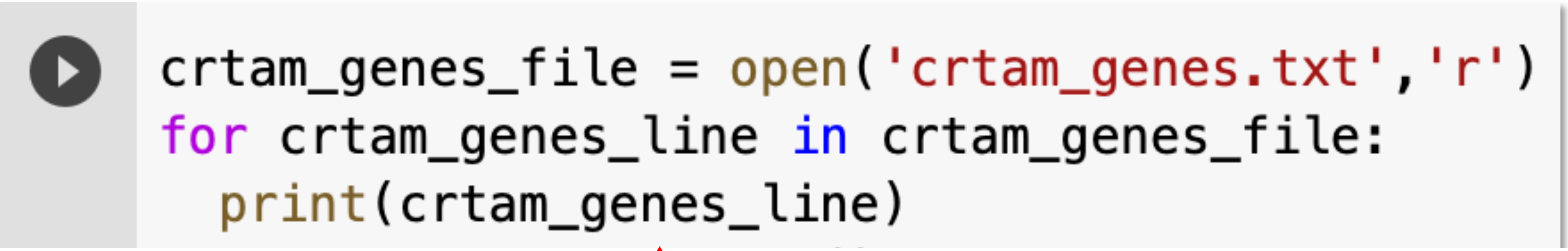


```
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
```

4

Use a for loop to loop through the lines in a file

Read in your file using a for loop

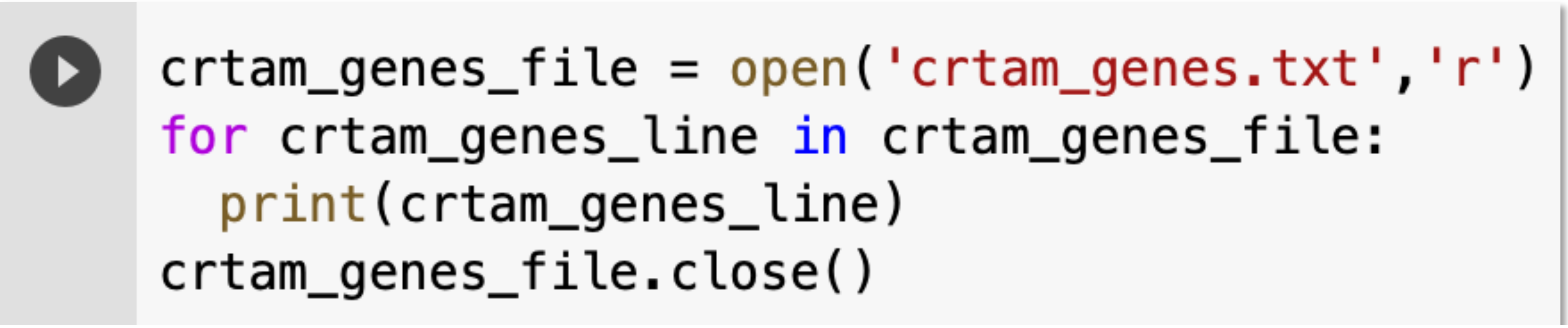


```
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
  print(crtam_genes_line)
```

print() each lines

5

Read in your file using a for loop

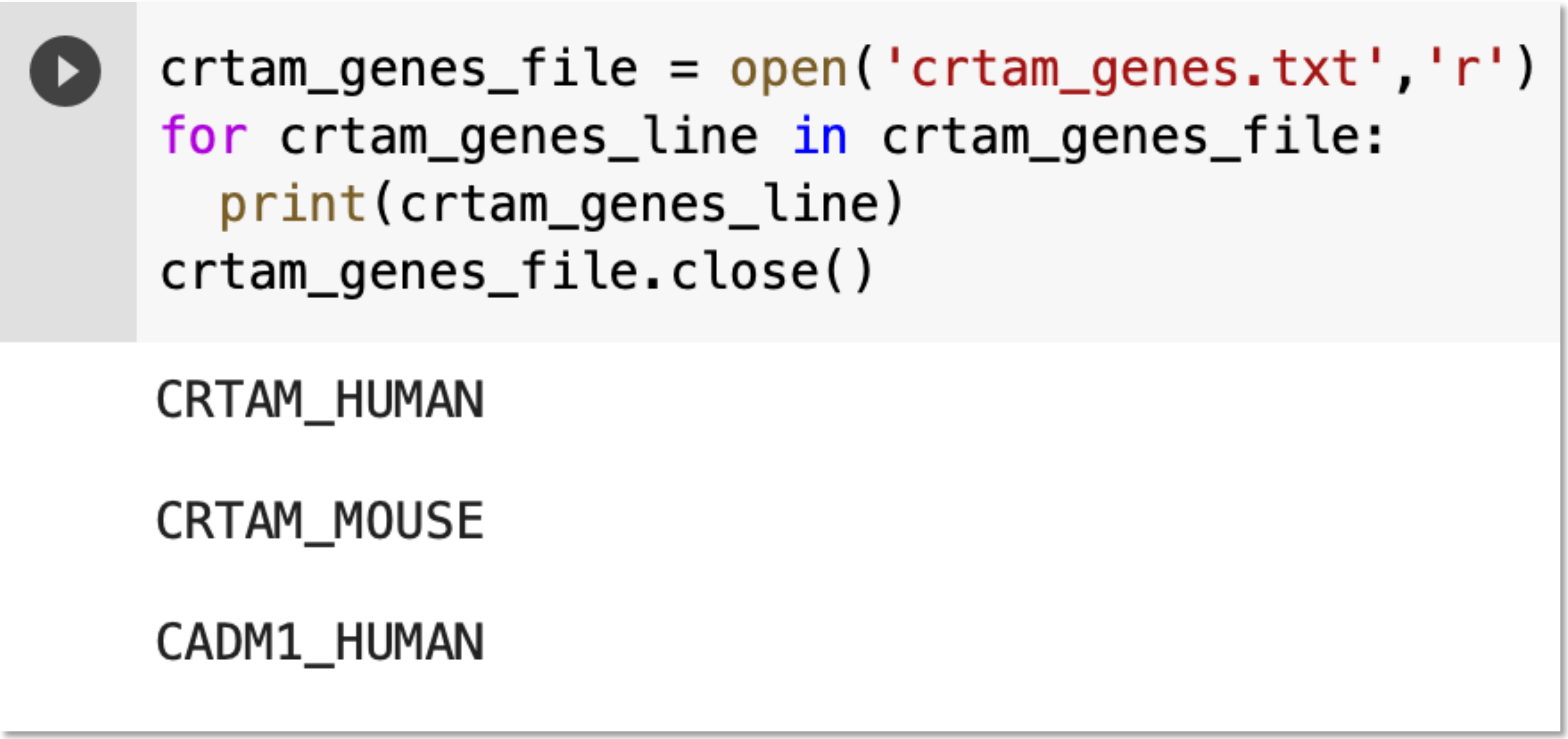


```python
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
  print(crtam_genes_line)
crtam_genes_file.close()
```

6

close() a file is important to prevent xyz

Read in your file using a for loop



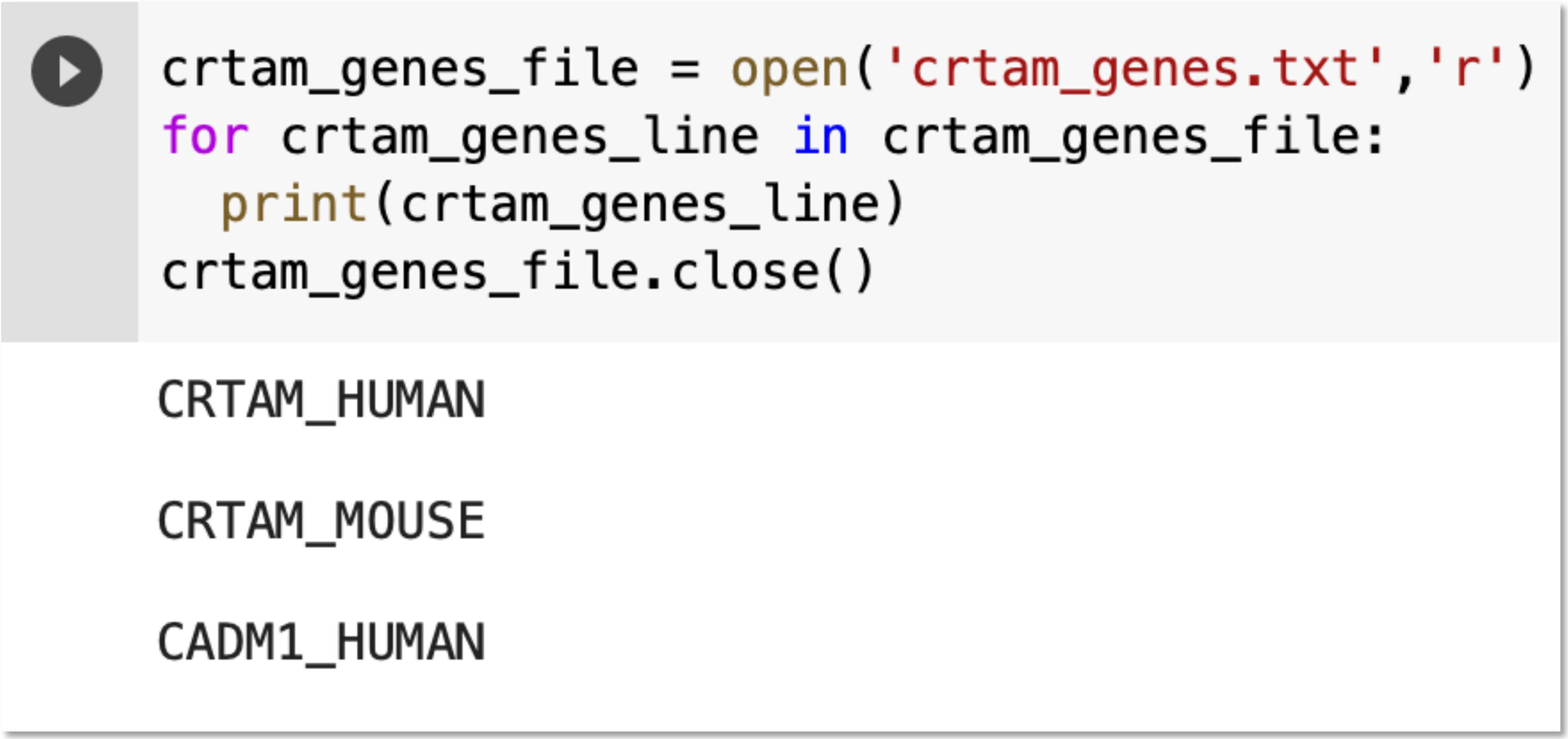
```python
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
  print(crtam_genes_line)
crtam_genes_file.close()
```

```
CRTAM_HUMAN

CRTAM_MOUSE

CADM1_HUMAN
```

How many lines are being printed out?



```
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
  print(crtam_genes_line)
crtam_genes_file.close()
```

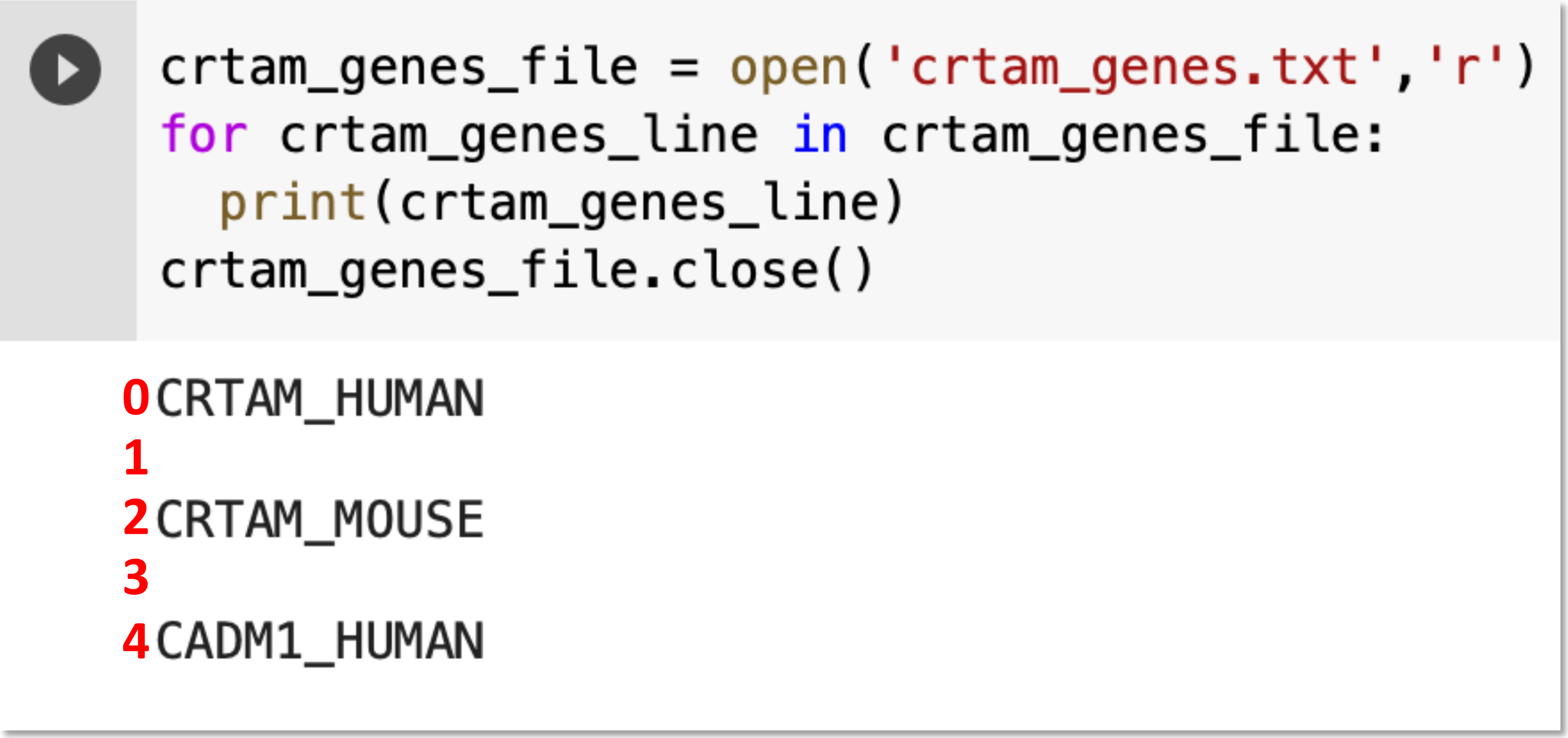
```
CRTAM_HUMAN

CRTAM_MOUSE

CADM1_HUMAN

```

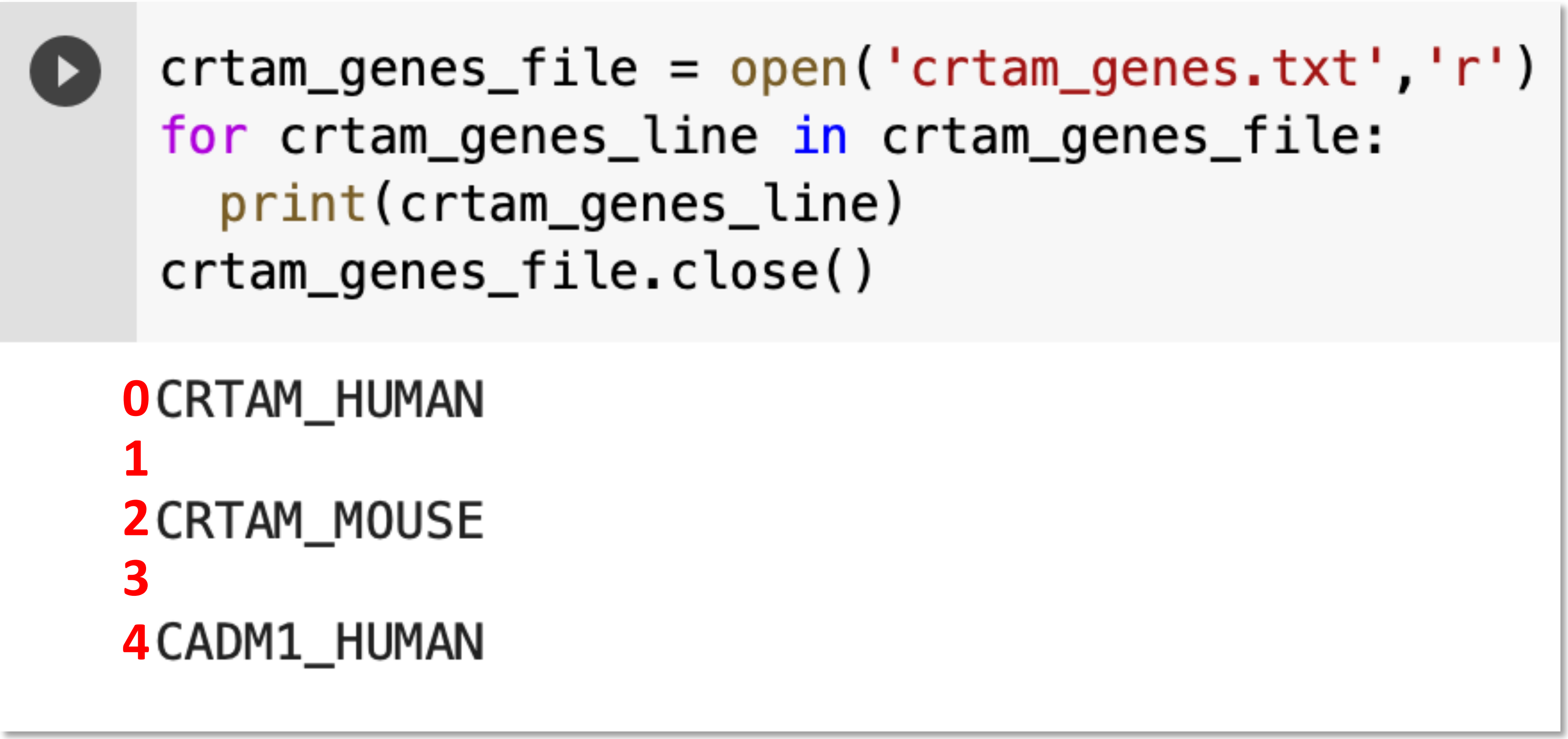
How many lines are being printed out?



```
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
  print(crtam_genes_line)
crtam_genes_file.close()
```

```
0 CRTAM_HUMAN
1
2 CRTAM_MOUSE
3
4 CADM1_HUMAN
```

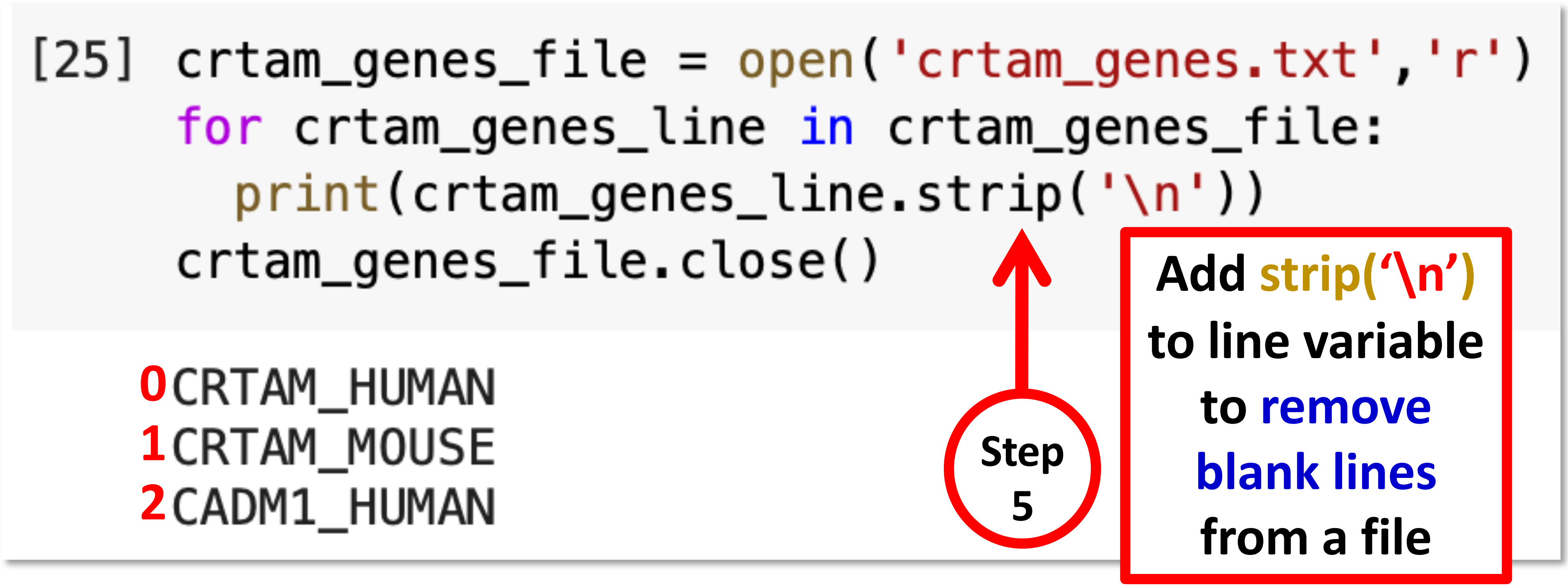
Remove these blank lines using strip()



```
crtam_genes_file = open('crtam_genes.txt','r')
for crtam_genes_line in crtam_genes_file:
  print(crtam_genes_line)
crtam_genes_file.close()
```

```
0 CRTAM_HUMAN
1
2 CRTAM_MOUSE
3
4 CADM1_HUMAN
```

Remove these blank lines using strip()



```
[25] crtam_genes_file = open('crtam_genes.txt','r')
     for crtam_genes_line in crtam_genes_file:
       print(crtam_genes_line.strip('\n'))
     crtam_genes_file.close()
```

```
0CRTAM_HUMAN
1CRTAM_MOUSE
2CADM1_HUMAN
```

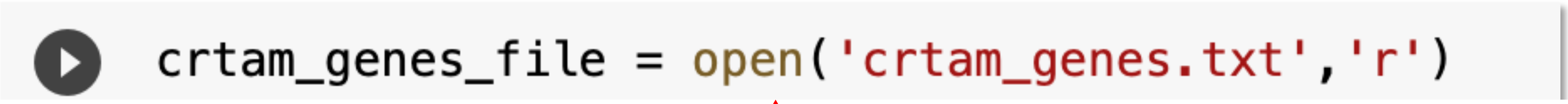
Step 5

Add strip('\n') to line variable to remove blank lines from a file

Lesson 3.1.2

Read in the lines of a file using a While Loop

Read in your file using a while loop

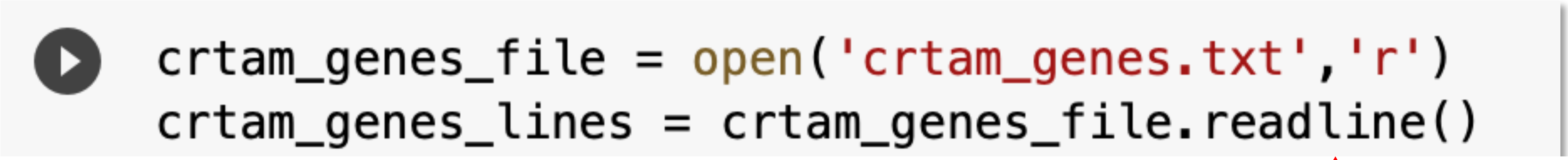


```
crtam_genes_file = open('crtam_genes.txt','r')
```

1

Use open() function

Read in your file using a while loop

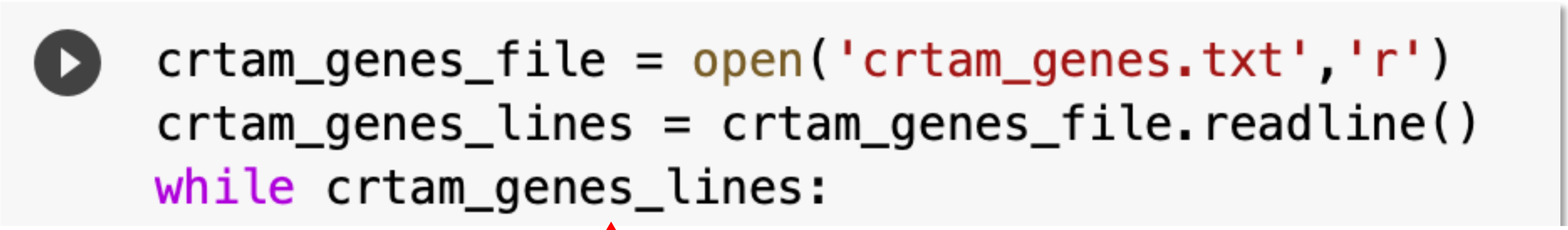


```
crtam_genes_file = open('crtam_genes.txt','r')
crtam_genes_lines = crtam_genes_file.readline()
```

Using **readline()** function will allow you to while loop the lines of a file

2

Read in your file using a while loop

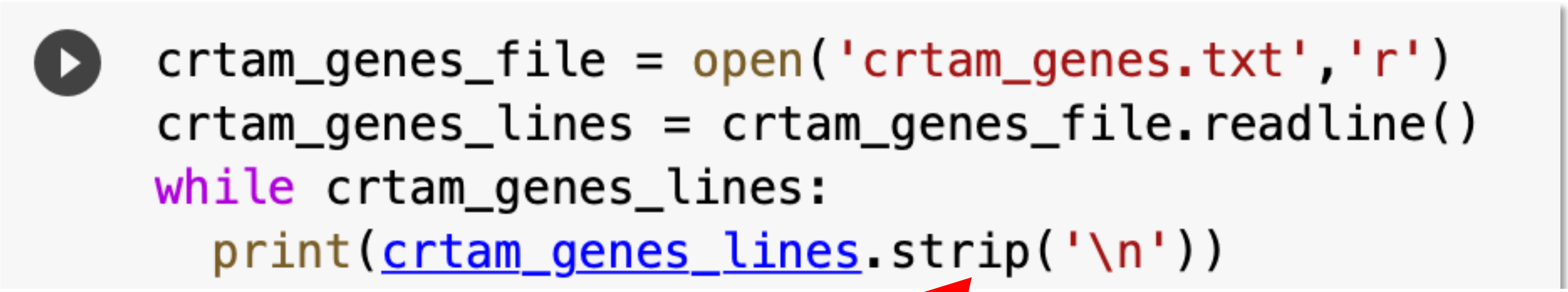


```
crtam_genes_file = open('crtam_genes.txt','r')
crtam_genes_lines = crtam_genes_file.readline()
while crtam_genes_lines:
```

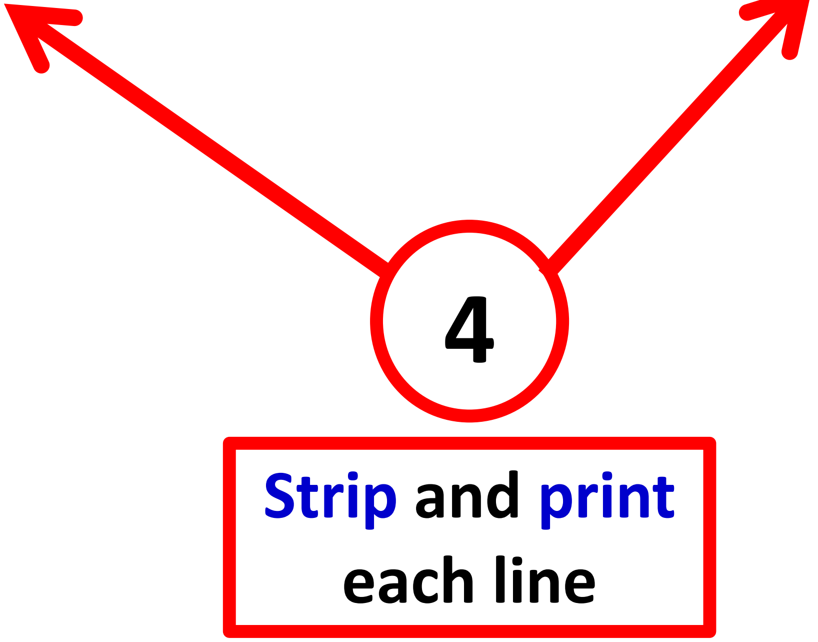
Perform while loop through lines of this file

3

Read in your file using a while loop



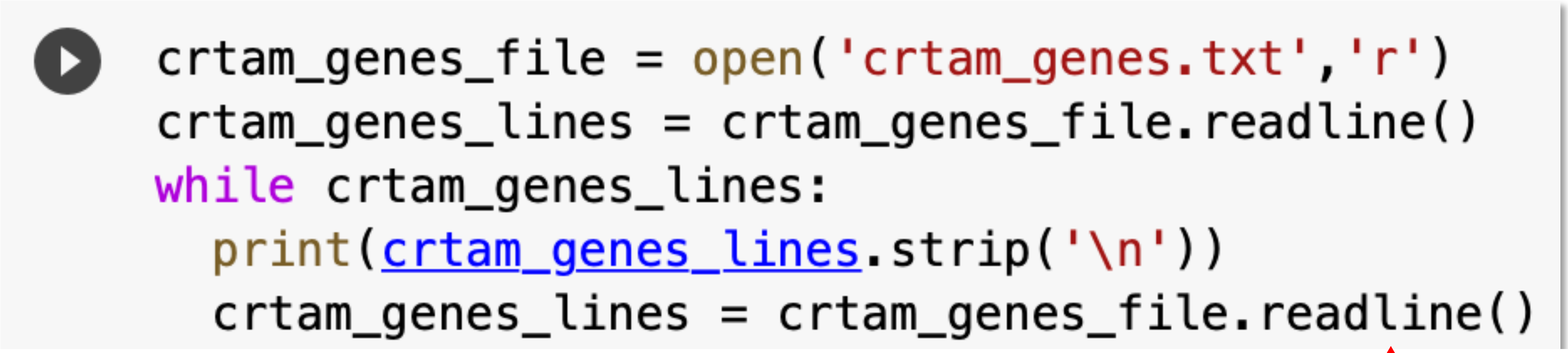
```
crtam_genes_file = open('crtam_genes.txt','r')
crtam_genes_lines = crtam_genes_file.readline()
while crtam_genes_lines:
  print(crtam_genes_lines.strip('\n'))
```



4

Strip and print each line

Read in your file using a while loop

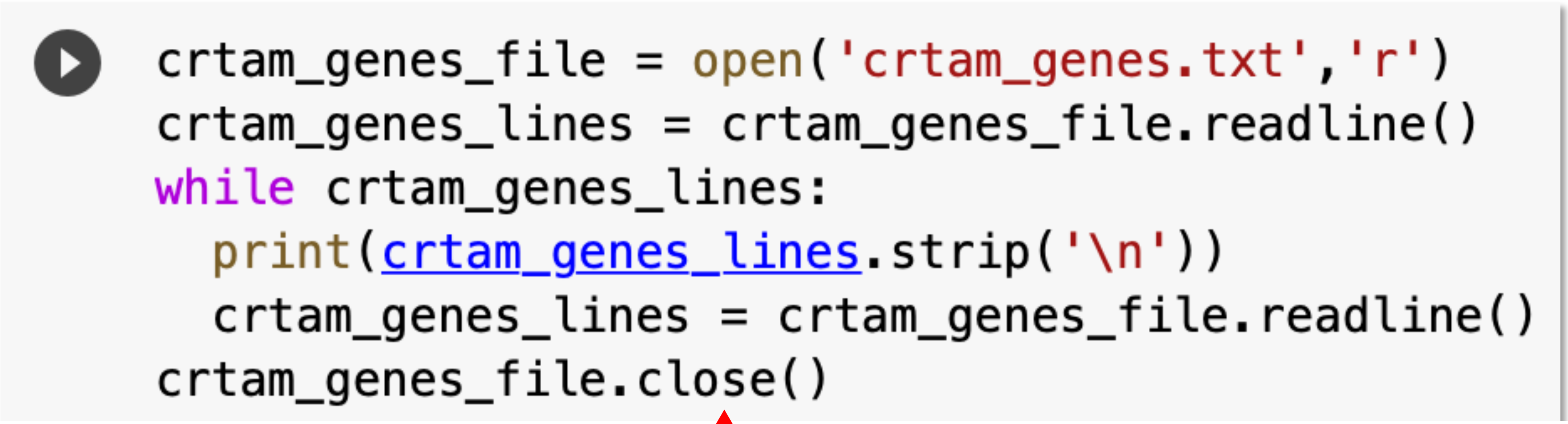


```
crtam_genes_file = open('crtam_genes.txt','r')
crtam_genes_lines = crtam_genes_file.readline()
while crtam_genes_lines:
  print(crtam_genes_lines.strip('\n'))
  crtam_genes_lines = crtam_genes_file.readline()
```

Reuse readline() to move on to the next line

5

Read in your file using a while loop

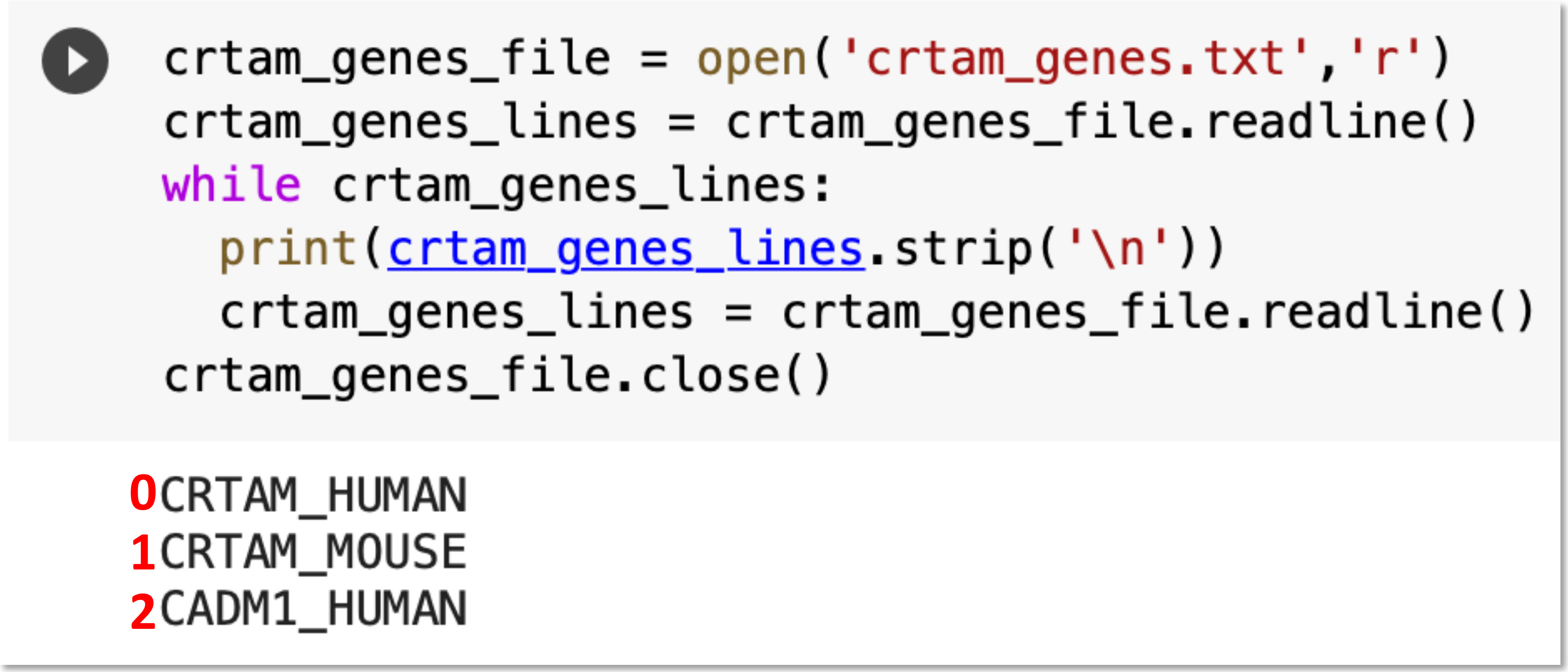


```
crtam_genes_file = open('crtam_genes.txt','r')
crtam_genes_lines = crtam_genes_file.readline()
while crtam_genes_lines:
  print(crtam_genes_lines.strip('\n'))
  crtam_genes_lines = crtam_genes_file.readline()
crtam_genes_file.close()
```

close() your file

6

Read in your file using a while loop



```
crtam_genes_file = open('crtam_genes.txt','r')
crtam_genes_lines = crtam_genes_file.readline()
while crtam_genes_lines:
  print(crtam_genes_lines.strip('\n'))
  crtam_genes_lines = crtam_genes_file.readline()
crtam_genes_file.close()
```

```
0CRTAM_HUMAN
1CRTAM_MOUSE
2CADM1_HUMAN
```

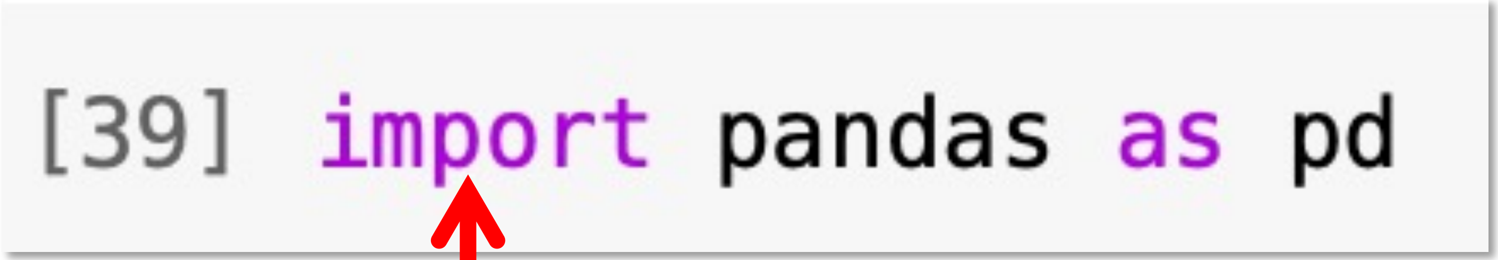
Lesson 3.2.0

Manipulate files the Panda way

Lesson 3.2.1

Import the Panda Library

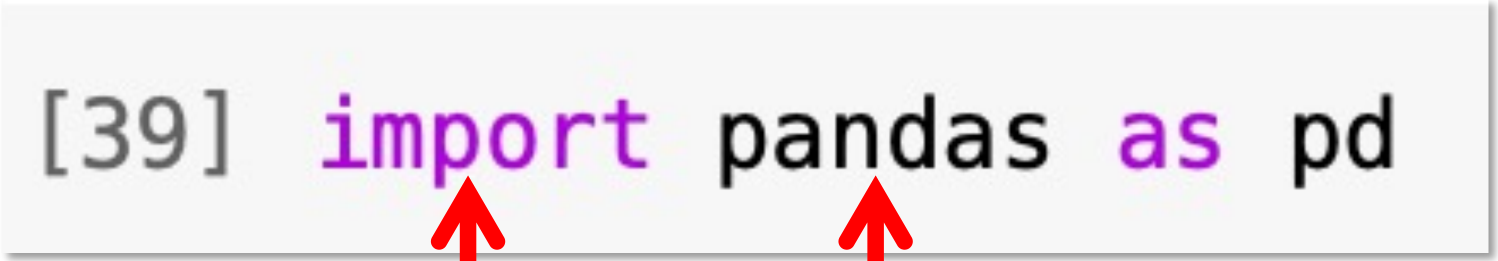
How to import a library



```
[39] import pandas as pd
```

Call import to use a library

How to import a library

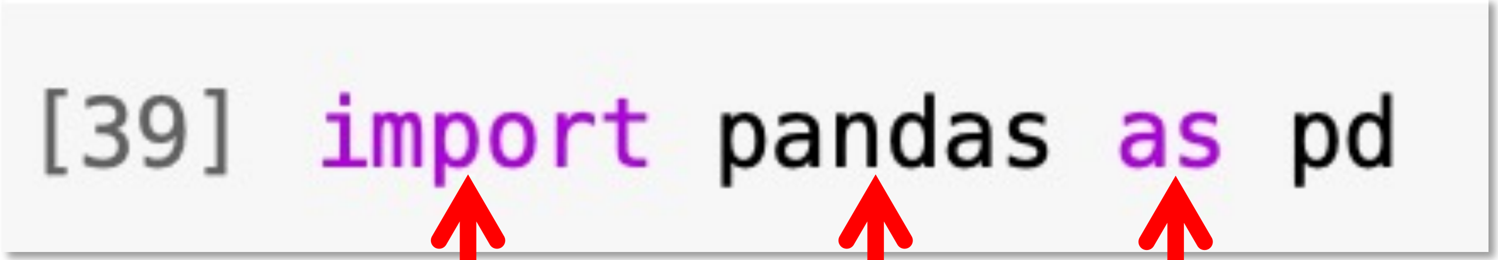


```
[39] import pandas as pd
```

Call import to use a library

Name your library of interest

How to import a library



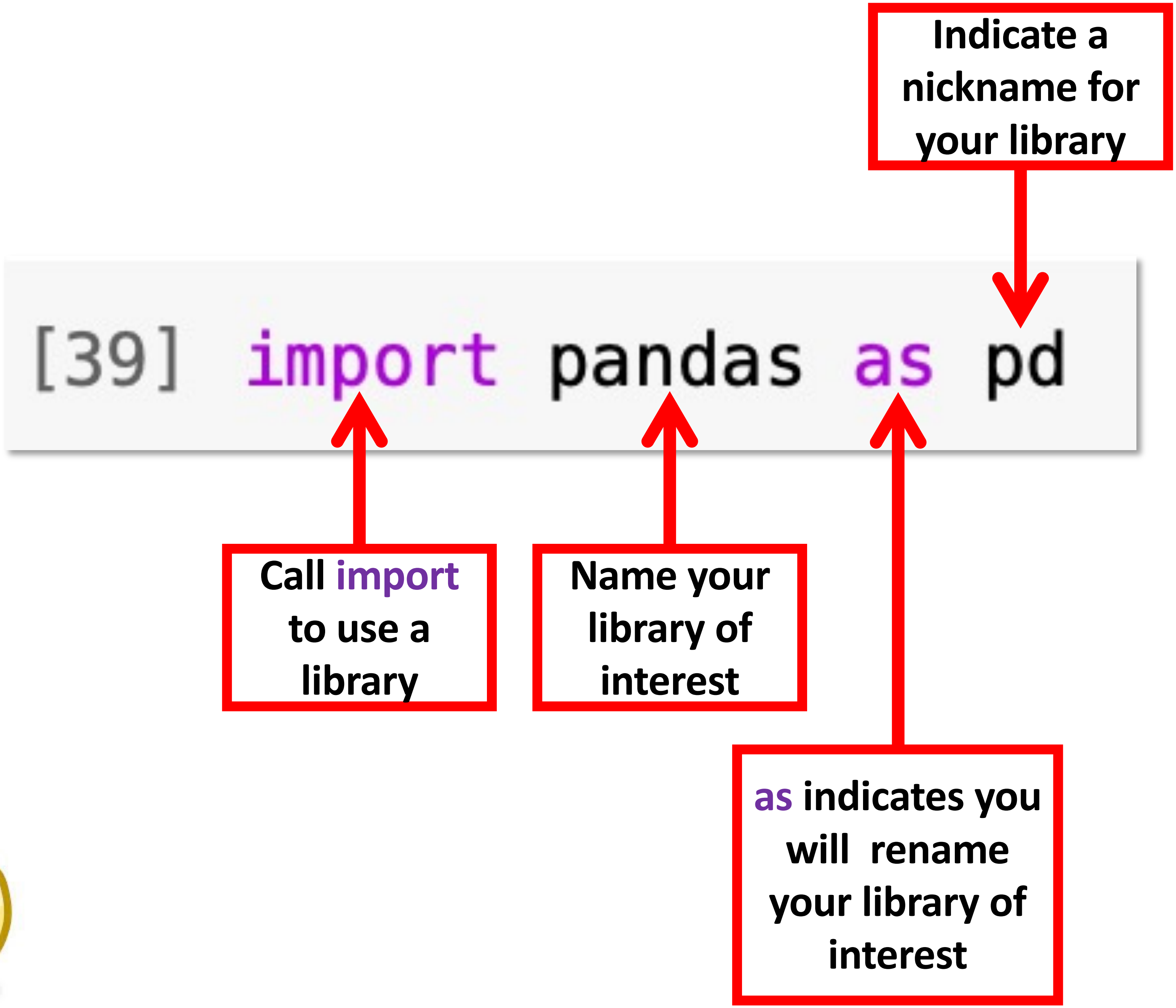
```
[39] import pandas as pd
```

Call import to use a library

Name your library of interest

as indicates you will rename your library of interest

How to import a library



```
[39] import pandas as pd
```

Indicate a nickname for your library

Call import to use a library

Name your library of interest

as indicates you will rename your library of interest

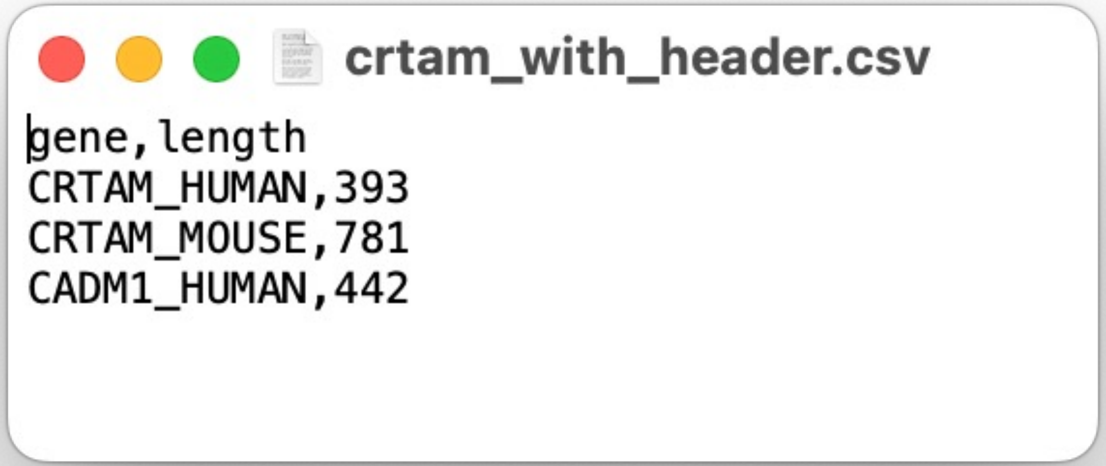
Lesson 3.2.2

Read in a CSV file using Panda Library

Lesson 3.2.2a

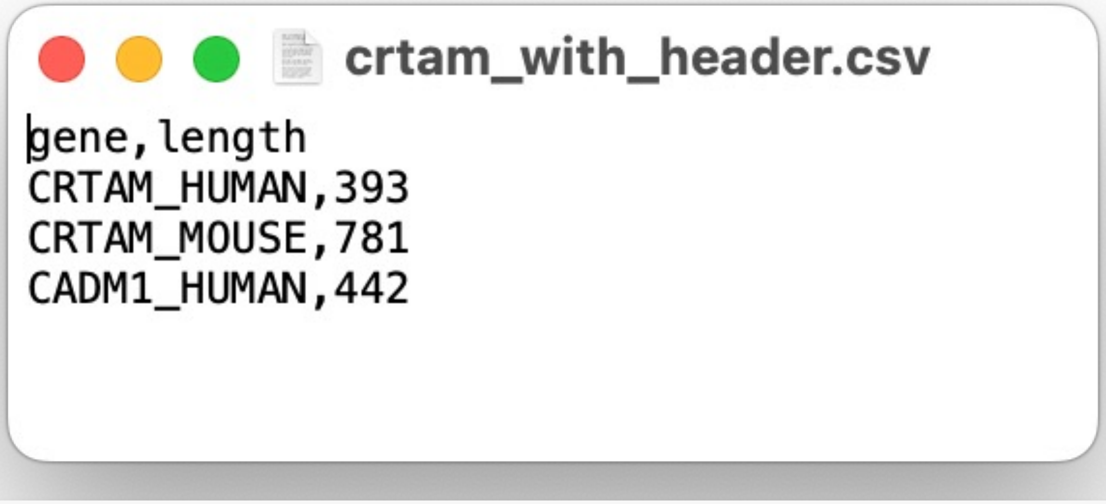
Reading in a CSV file with a header using Panda Library

CSV file with header



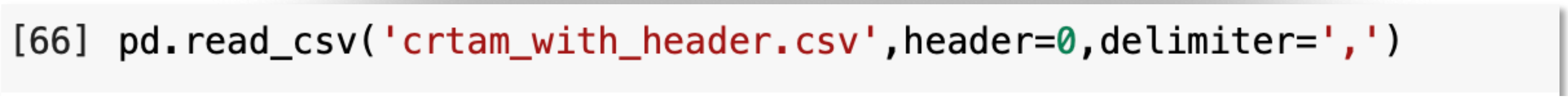
```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```

CSV file with header



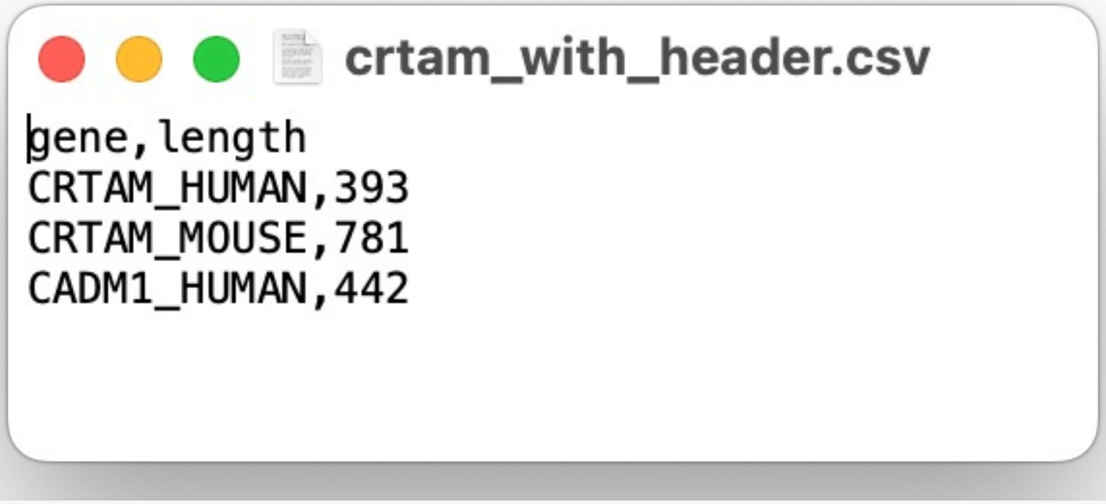
crtam_with_header.csv

```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```

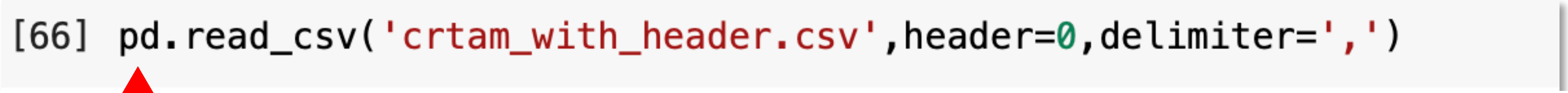


```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

CSV file with header



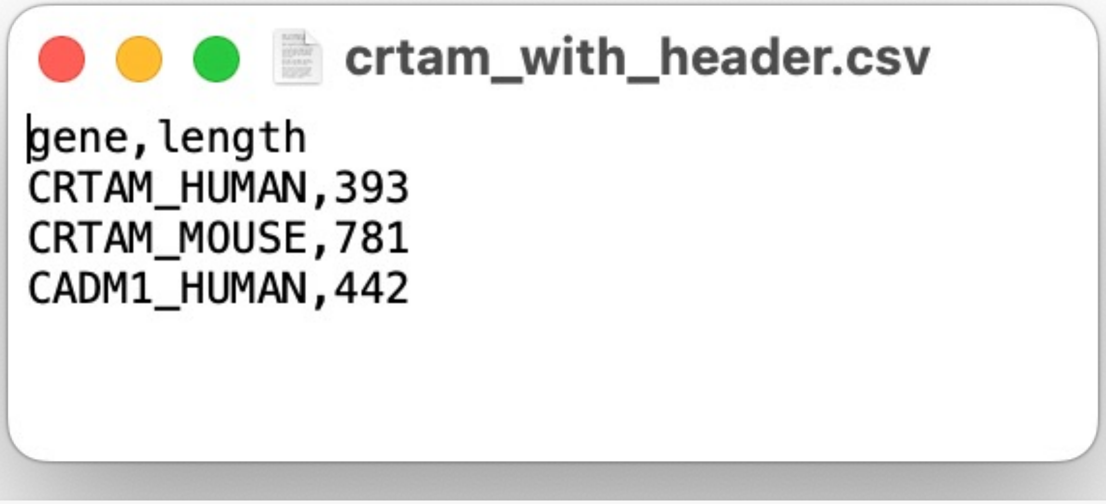
```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```



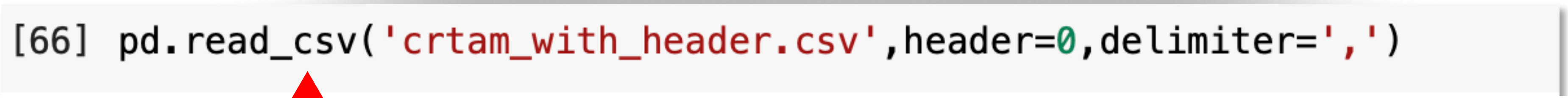
```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

Call **pandas** library by its nickname

CSV file with header



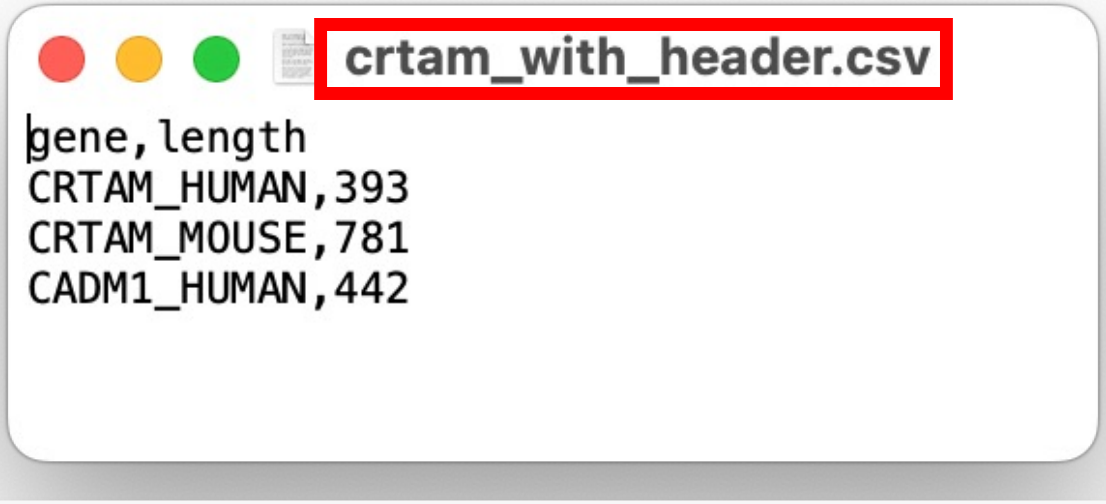
```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```



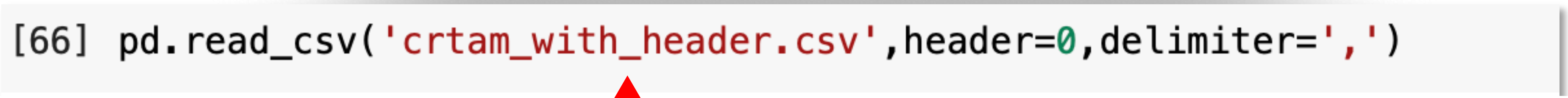
```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

Call **read_csv()** function for a csv file

CSV file with header


crtam_with_header.csv

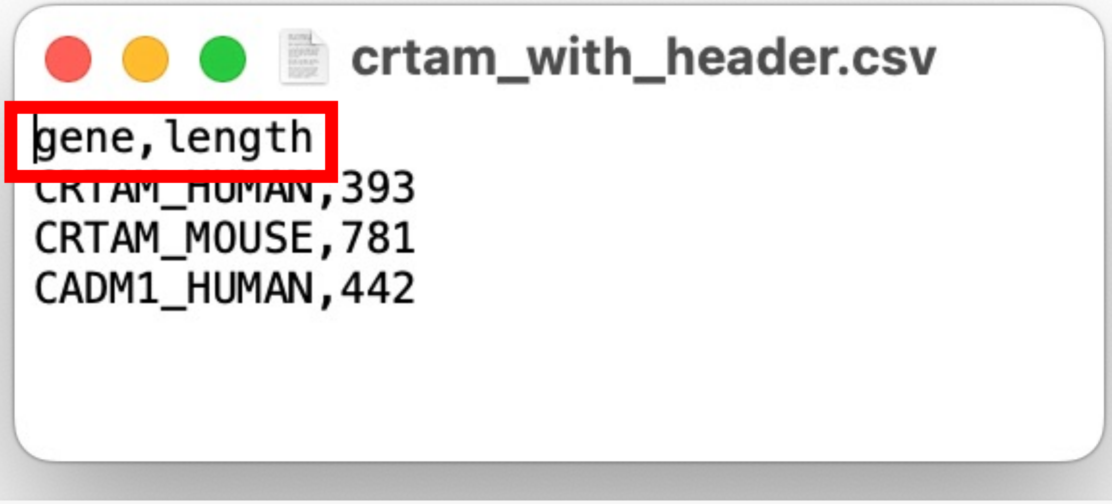
```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```



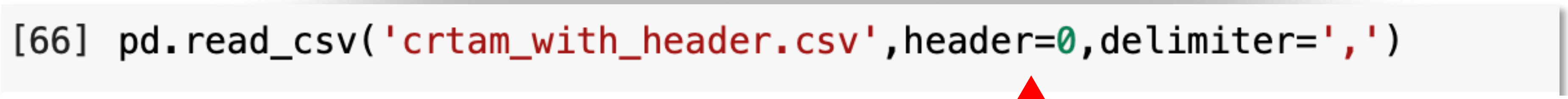
```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

Name your file of interest

CSV file with header

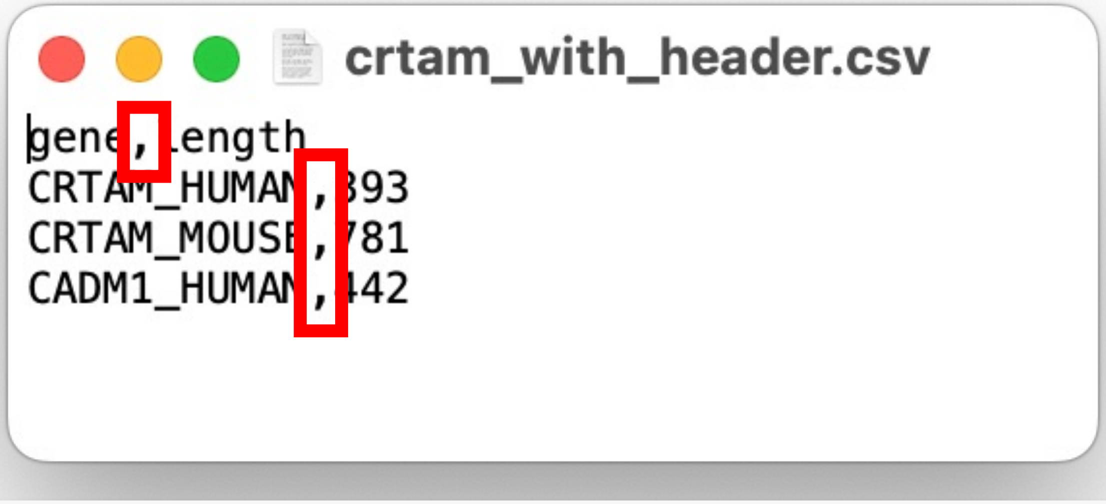

crtam_with_header.csv

```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```


```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

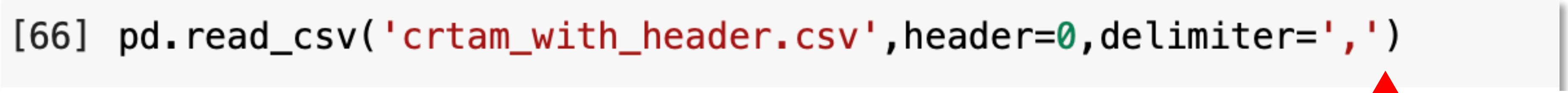
Indicate that there is a header exist

CSV file with header



crtam_with_header.csv

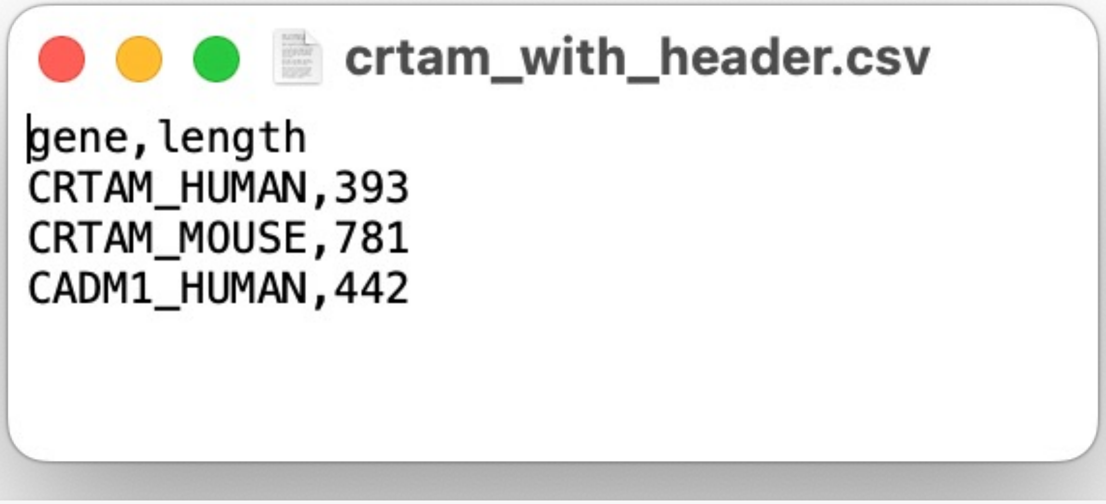
```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```



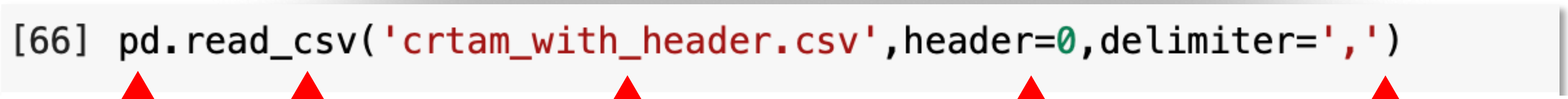
```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

Indicate the type of **delimiter** is **‘,’**

CSV file with header



```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```



```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

Call **pandas** library by its nickname

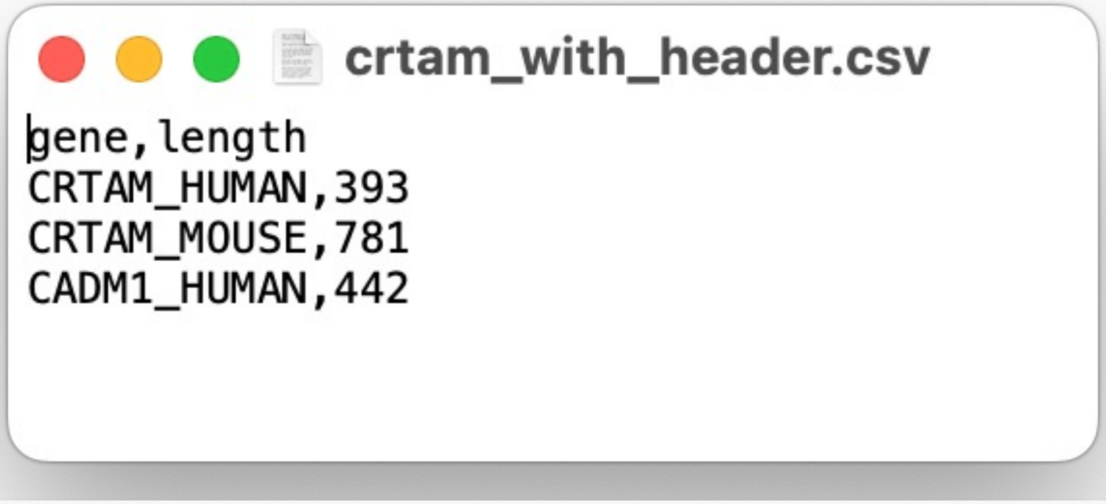
Call **read_csv()** function for a csv file

Name your file of interest

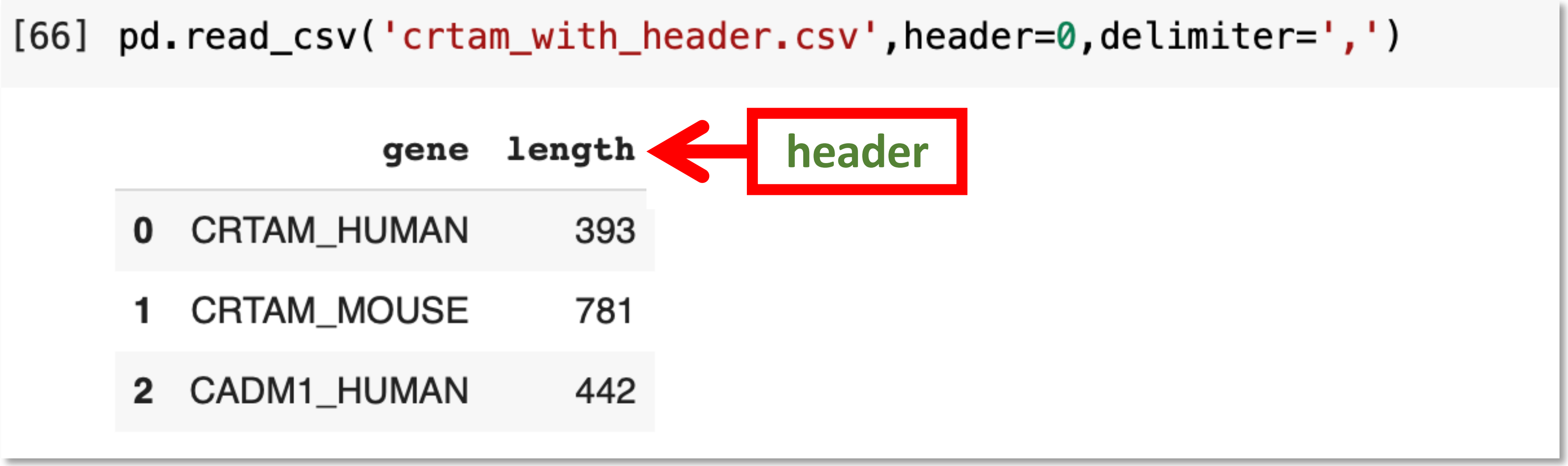
Indicate that there is a **header** exist

Indicate the type of **delimiter** is **‘,’**

CSV file with header


crtam_with_header.csv

```
gene,length
CRTAM_HUMAN,393
CRTAM_MOUSE,781
CADM1_HUMAN,442
```


```
[66] pd.read_csv('crtam_with_header.csv',header=0,delimiter=',')
```

	gene	length
0	CRTAM_HUMAN	393
1	CRTAM_MOUSE	781
2	CADM1_HUMAN	442

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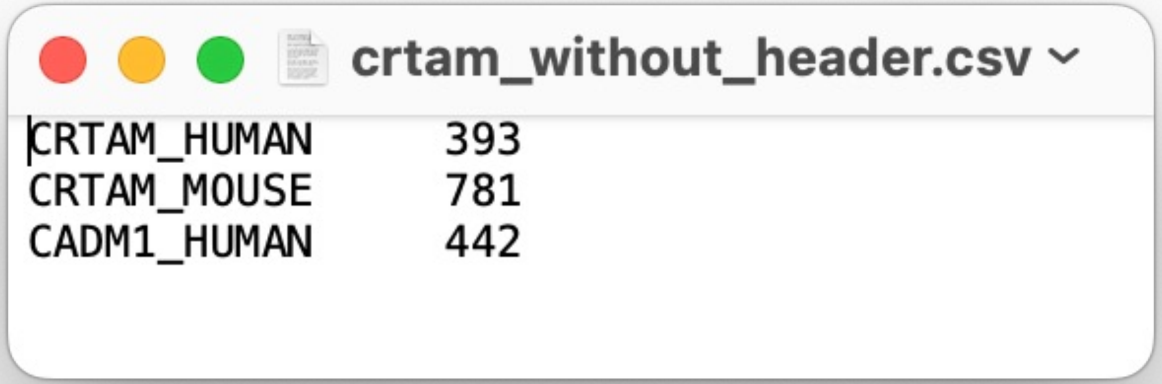
Lesson 3.2.2b

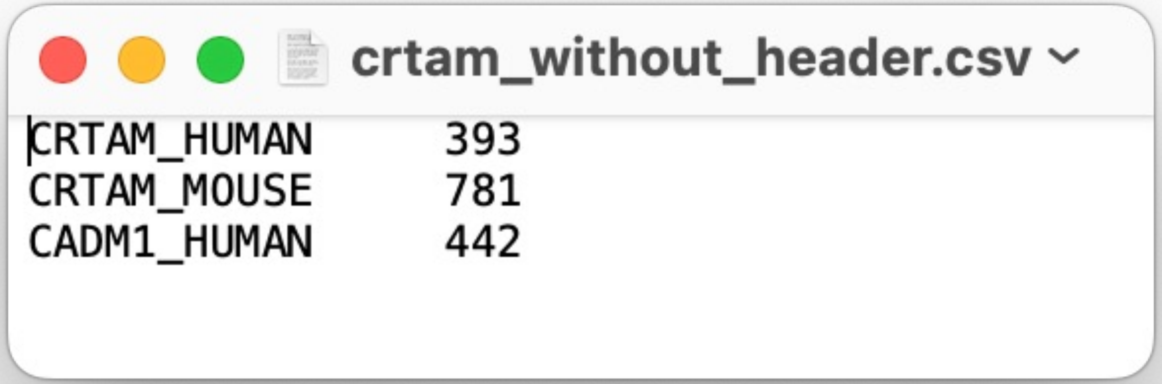
Reading in a CSV file with no header using Panda Library

CSV file with no header

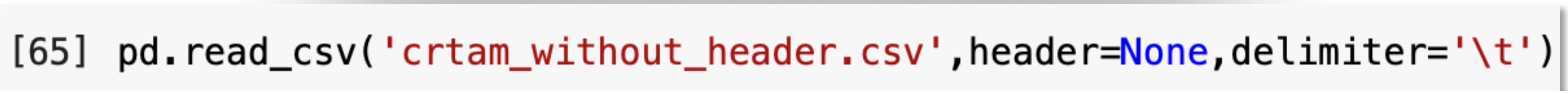


```
CRTAM_HUMAN      393
CRTAM_MOUSE      781
CADM1_HUMAN      442
```

CSV file with no header

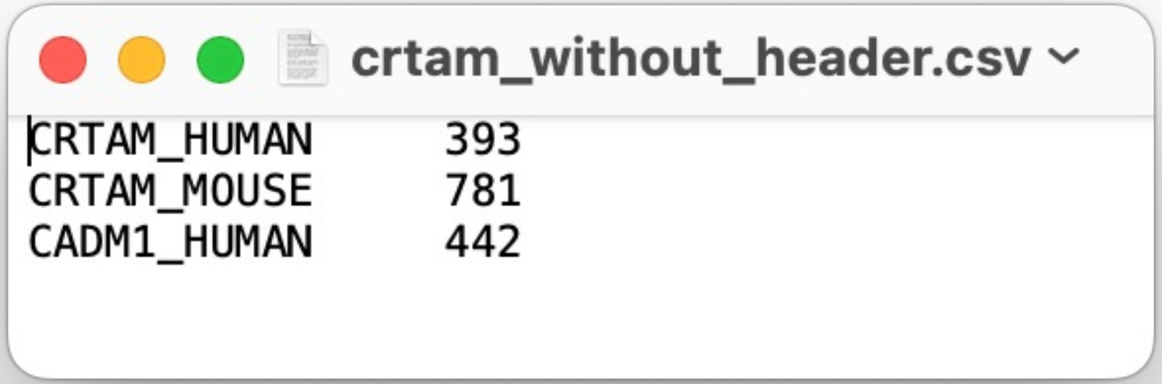


```
CRTAM_HUMAN      393
CRTAM_MOUSE      781
CADM1_HUMAN      442
```

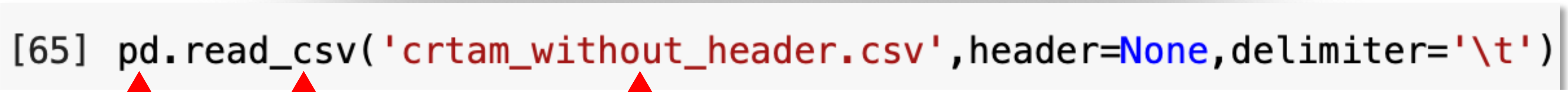


```
[65] pd.read_csv('crtam_without_header.csv',header=None,delimiter='\t')
```

CSV file with no header



```
CRTAM_HUMAN     393
CRTAM_MOUSE     781
CADM1_HUMAN     442
```



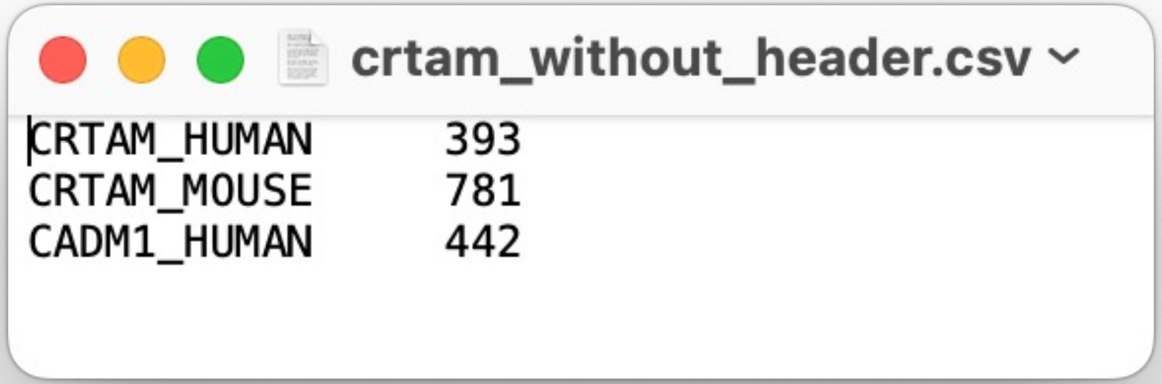
```
[65] pd.read_csv('crtam_without_header.csv',header=None,delimiter='\t')
```

Call pandas library by its nickname

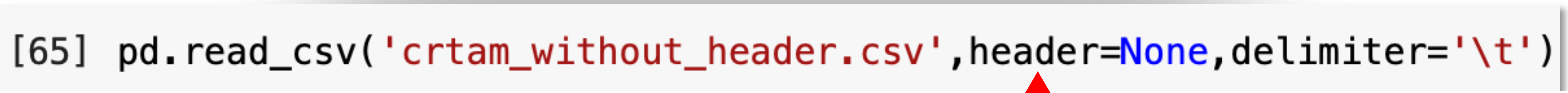
Name your file of interest

Call read_csv() function for a csv file

CSV file with no header



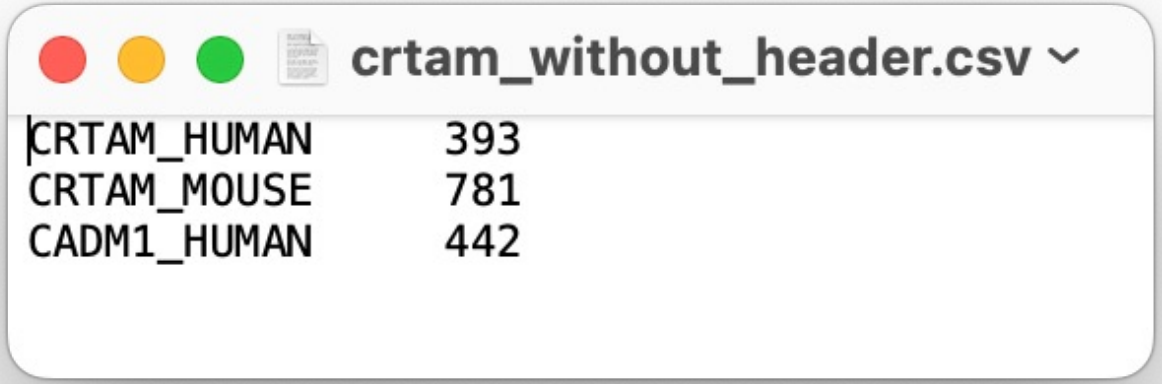
```
CRTAM_HUMAN	393
CRTAM_MOUSE	781
CADM1_HUMAN	442
```



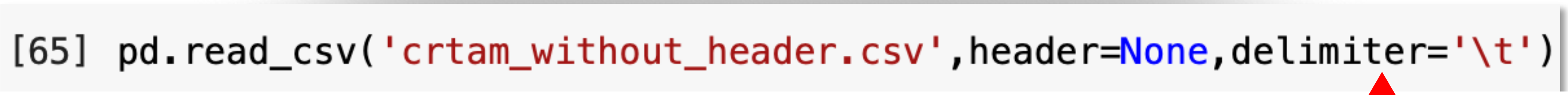
```
[65] pd.read_csv('crtam_without_header.csv',header=None,delimiter='\t')
```

Indicate that there is no header exist

CSV file with no header



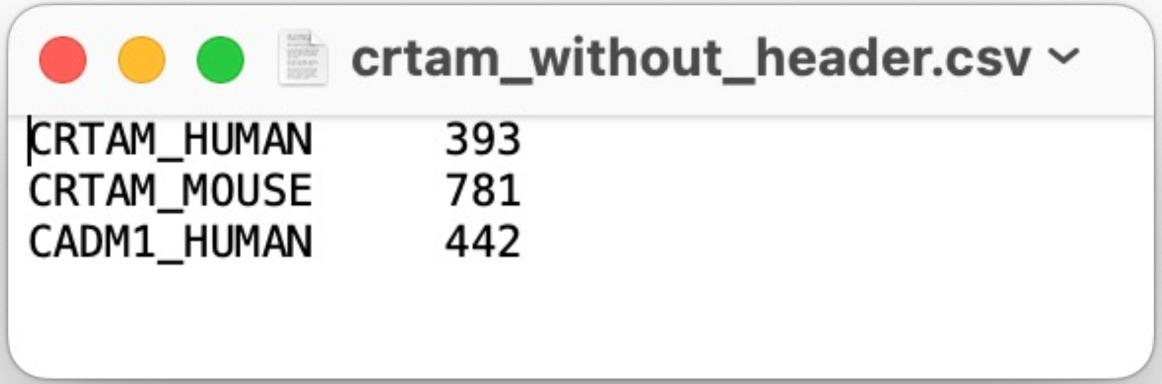
```
CRTAM_HUMAN	393
CRTAM_MOUSE	781
CADM1_HUMAN	442
```



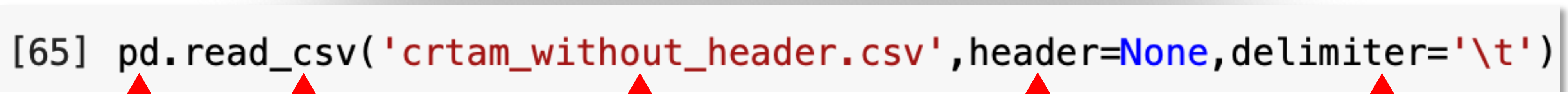
```
[65] pd.read_csv('crtam_without_header.csv',header=None,delimiter='\t')
```

Indicate the type of delimiter is ‘\t’

CSV file with no header



```
CRTAM_HUMAN     393
CRTAM_MOUSE     781
CADM1_HUMAN     442
```



```
[65] pd.read_csv('crtam_without_header.csv',header=None,delimiter='\t')
```

Call pandas library by its nickname

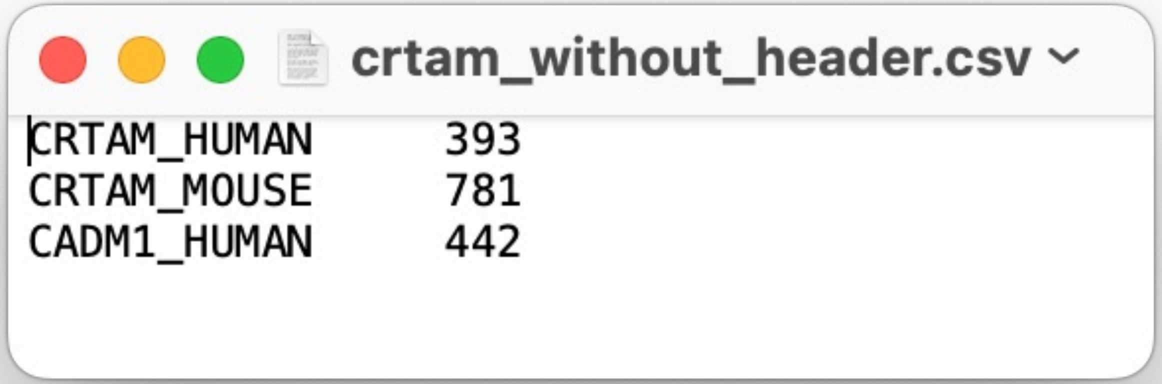
Call read_csv() function for a csv file

Name your file of interest

Indicate that there is no header exist

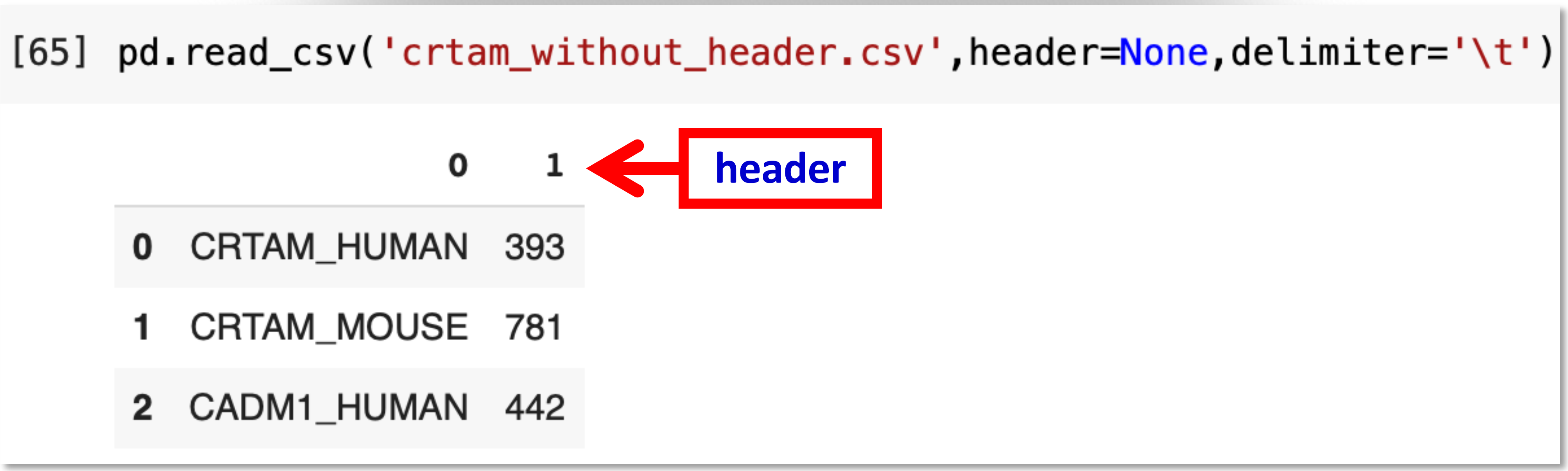
Indicate the type of delimiter is '\t'

CSV file with no header



crtam_without_header.csv

```
CRTAM_HUMAN      393
CRTAM_MOUSE      781
CADM1_HUMAN      442
```



```
[65] pd.read_csv('crtam_without_header.csv',header=None,delimiter='\t')
```

	0	1
0	CRTAM_HUMAN	393
1	CRTAM_MOUSE	781
2	CADM1_HUMAN	442

header

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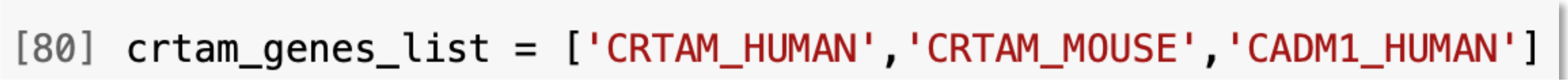
Lesson 3.2.3

Create a DataFrame and export a new CSV file using Panda Library

Lesson 3.2.3a

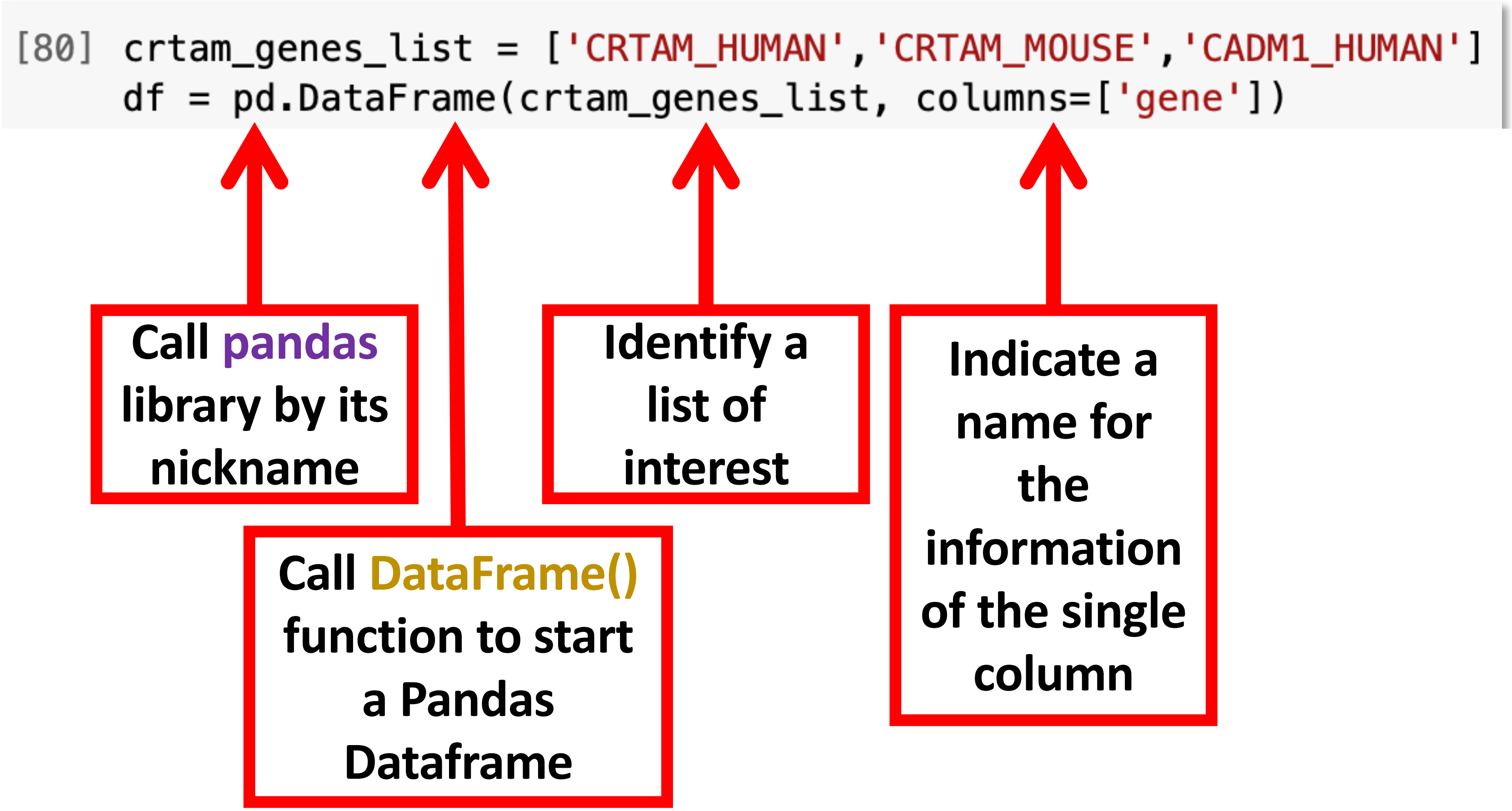
Create a Panda DataFrame from a single List

Convert a simple list into a Pandas Dataframe



```
[80] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
```

Convert a simple list into a Pandas Dataframe



```
[80] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     df = pd.DataFrame(crtam_genes_list, columns=['gene'])
```

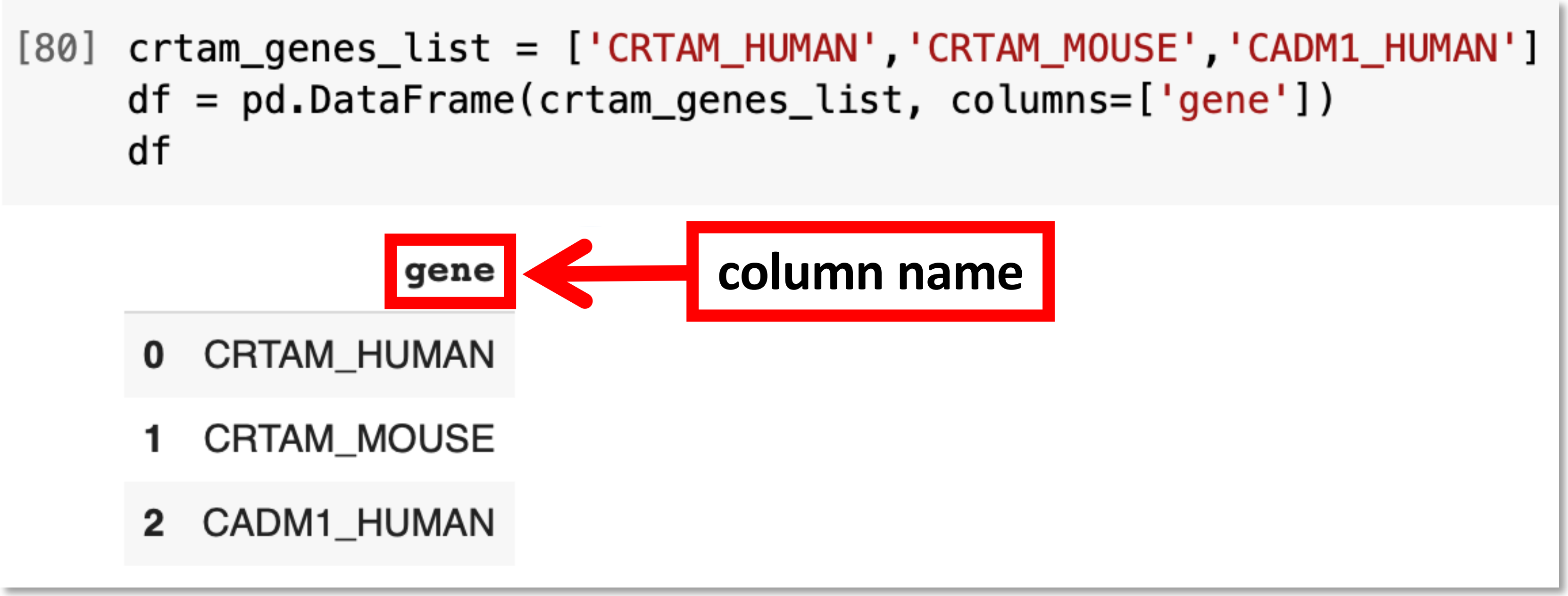
Call pandas library by its nickname

Call DataFrame() function to start a Pandas Dataframe

Identify a list of interest

Indicate a name for the information of the single column

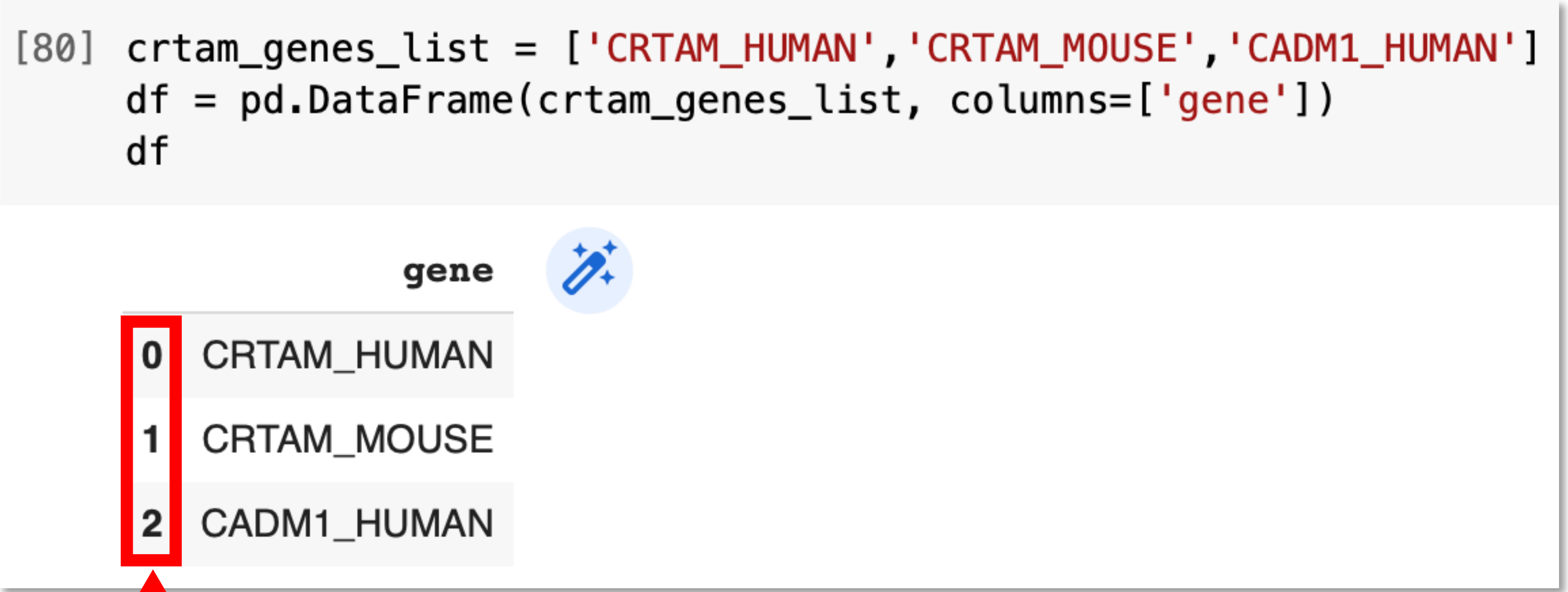
Convert a simple list into a Pandas Dataframe



```
[80] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     df = pd.DataFrame(crtam_genes_list, columns=['gene'])
     df
```

```
          gene
0  CRTAM_HUMAN
1  CRTAM_MOUSE
2  CADM1_HUMAN
```

Convert a simple list into a Pandas Dataframe



```
[80] crtam_genes_list = ['CRTAM_HUMAN','CRTAM_MOUSE','CADM1_HUMAN']
     df = pd.DataFrame(crtam_genes_list, columns=['gene'])
     df
```

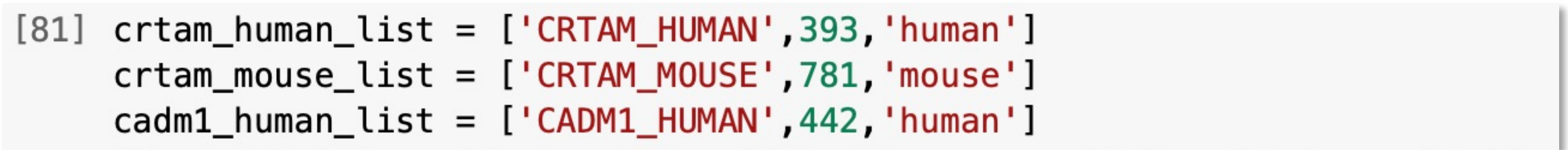
```
          gene
0  CRTAM_HUMAN
1  CRTAM_MOUSE
2  CADM1_HUMAN
```

index

Lesson 3.2.3b

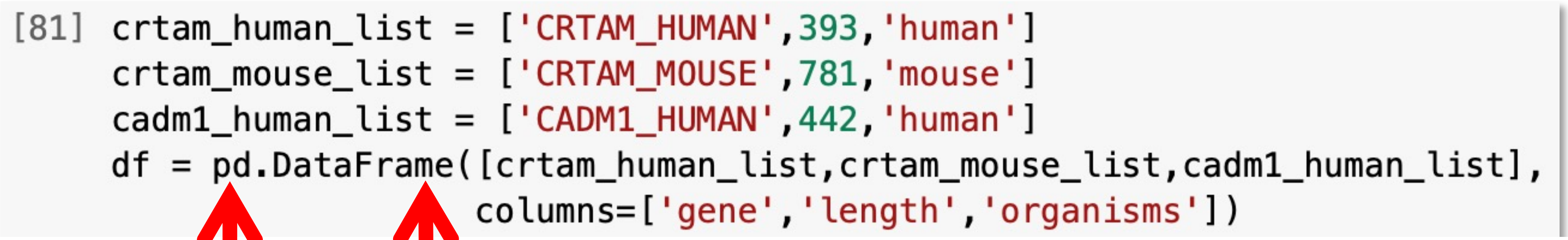
Create a Panda DataFrame from multiple Lists

Convert multiple lists into a Pandas Dataframe



```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
```

Convert multiple lists into a Pandas Dataframe

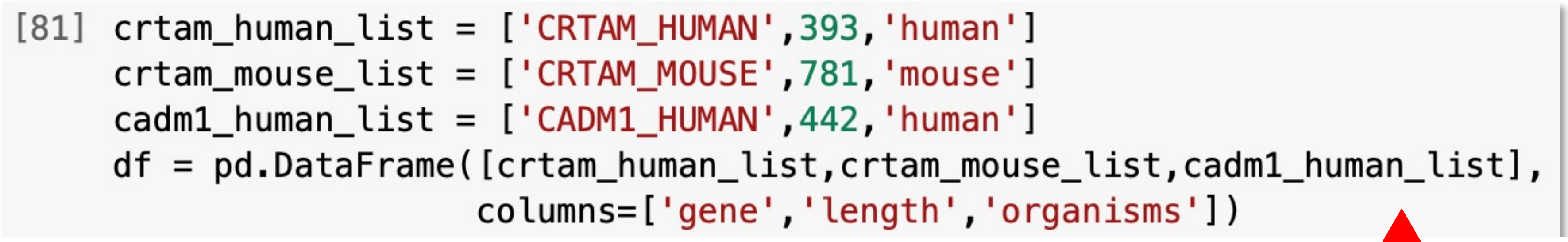


```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
```

Call pandas library by its nickname

Call DataFrame() function to start a Pandas Dataframe

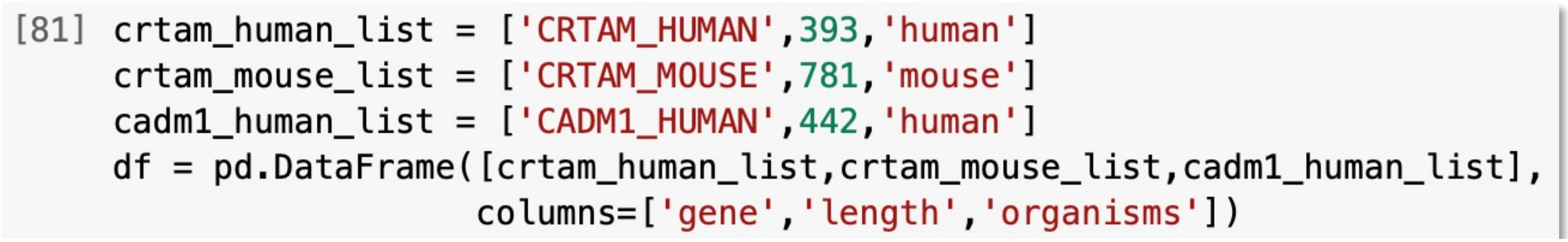
Convert multiple lists into a Pandas Dataframe



```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
```

List of Lists

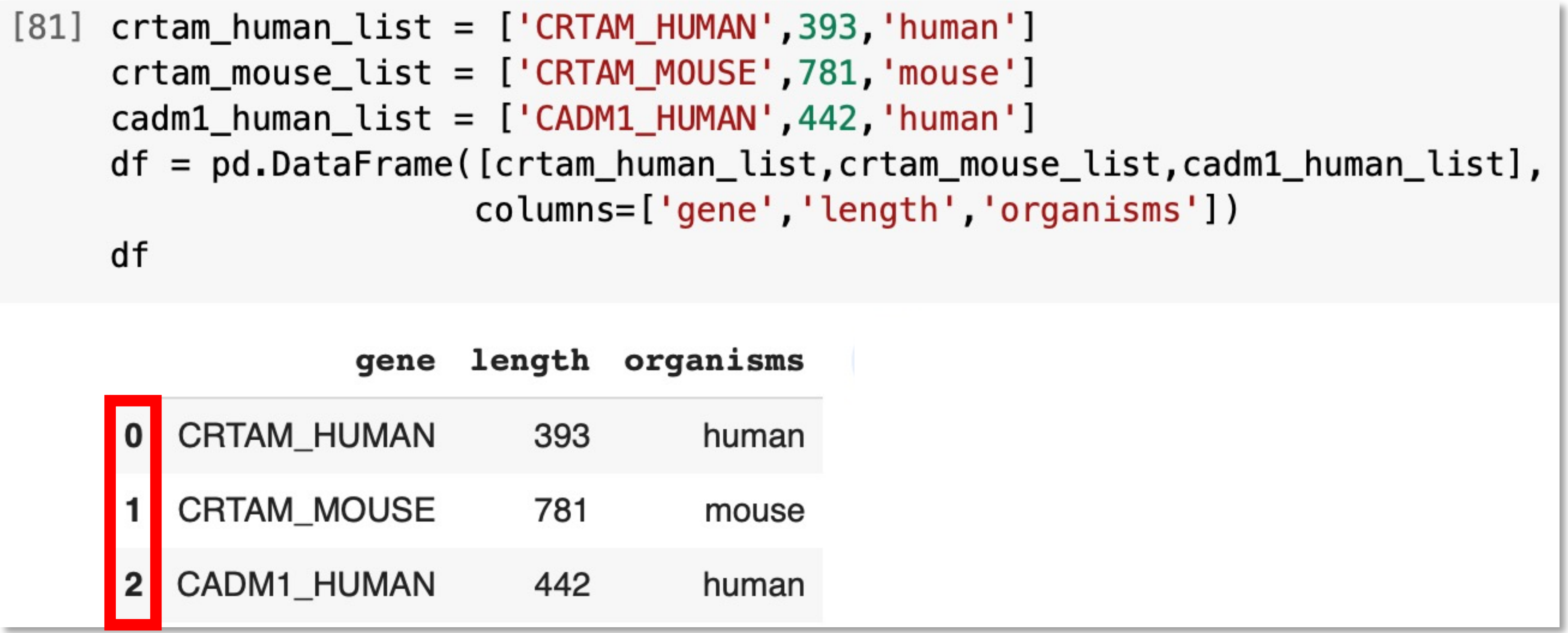
Convert multiple lists into a Pandas Dataframe



```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
```

Naming columns

Convert multiple lists into a Pandas Dataframe

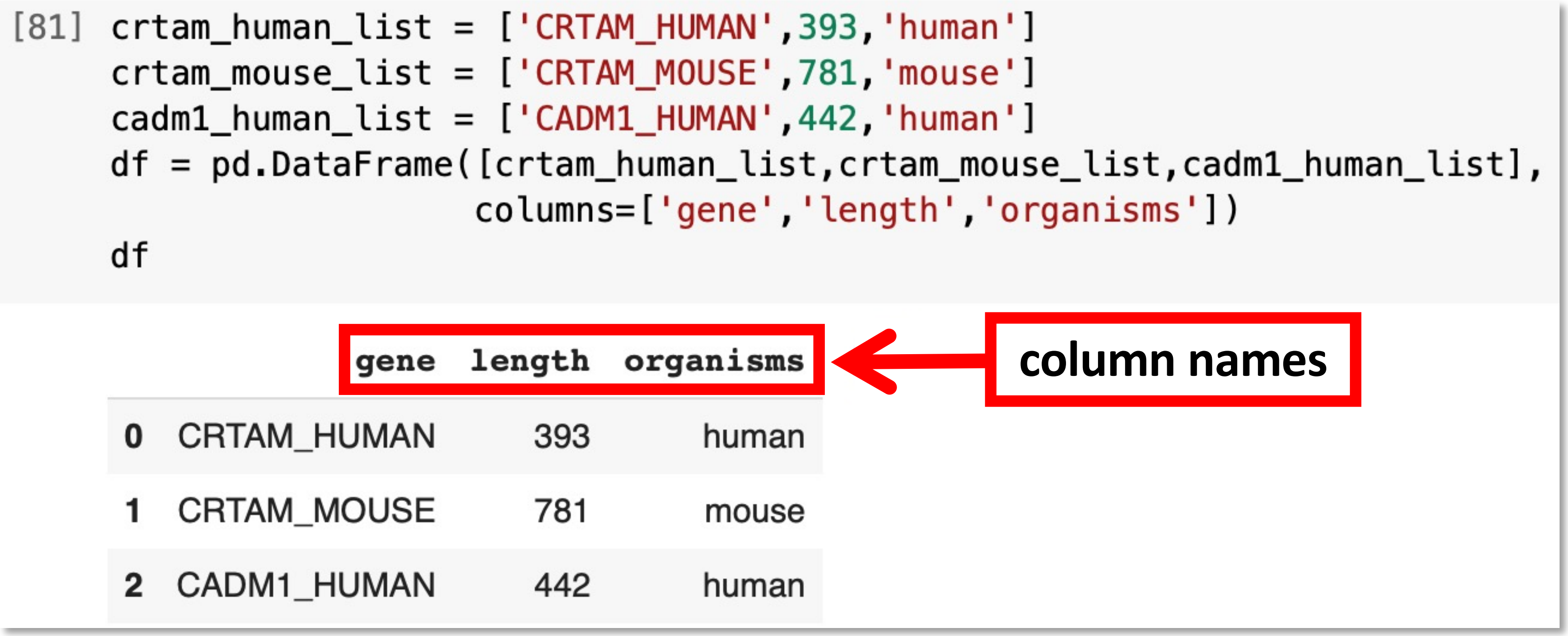


```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
     df
```

	gene	length	organisms
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

index

Convert multiple lists into a Pandas Dataframe

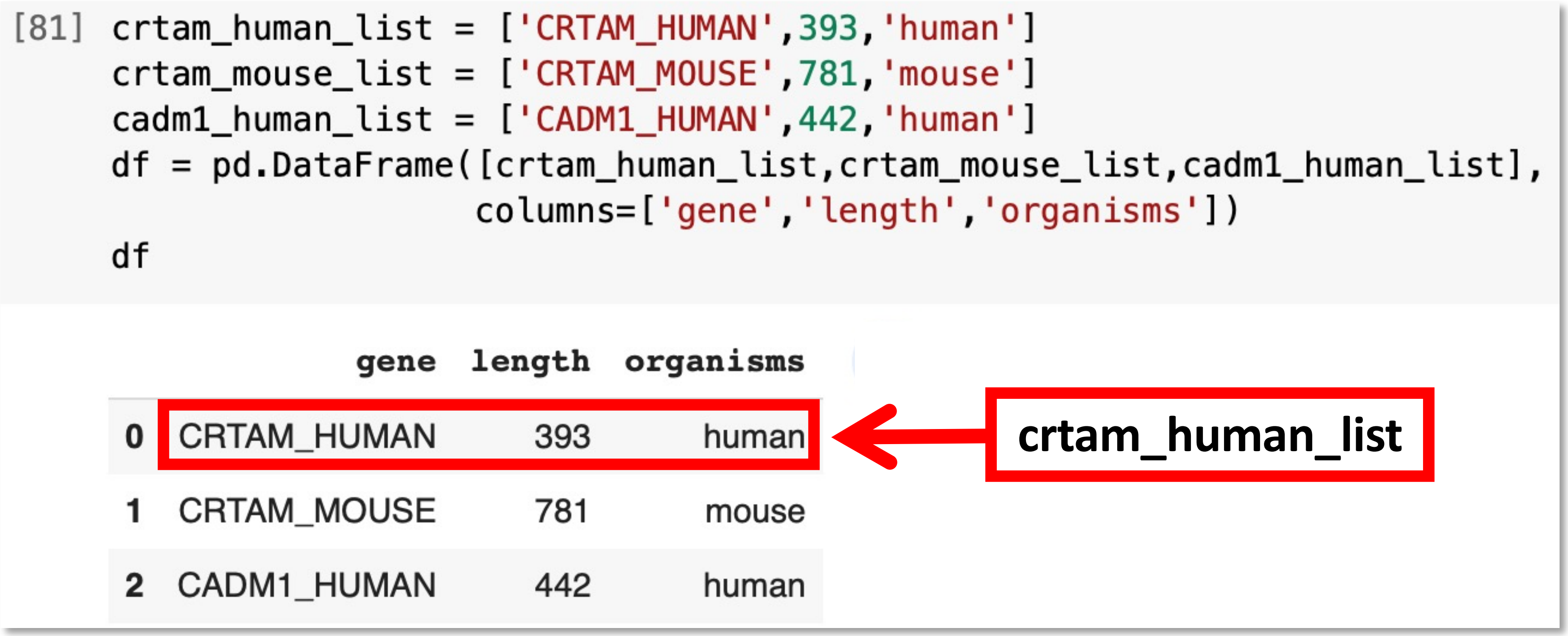


```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
     df
```

	gene	length	organisms
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

column names

Convert multiple lists into a Pandas Dataframe

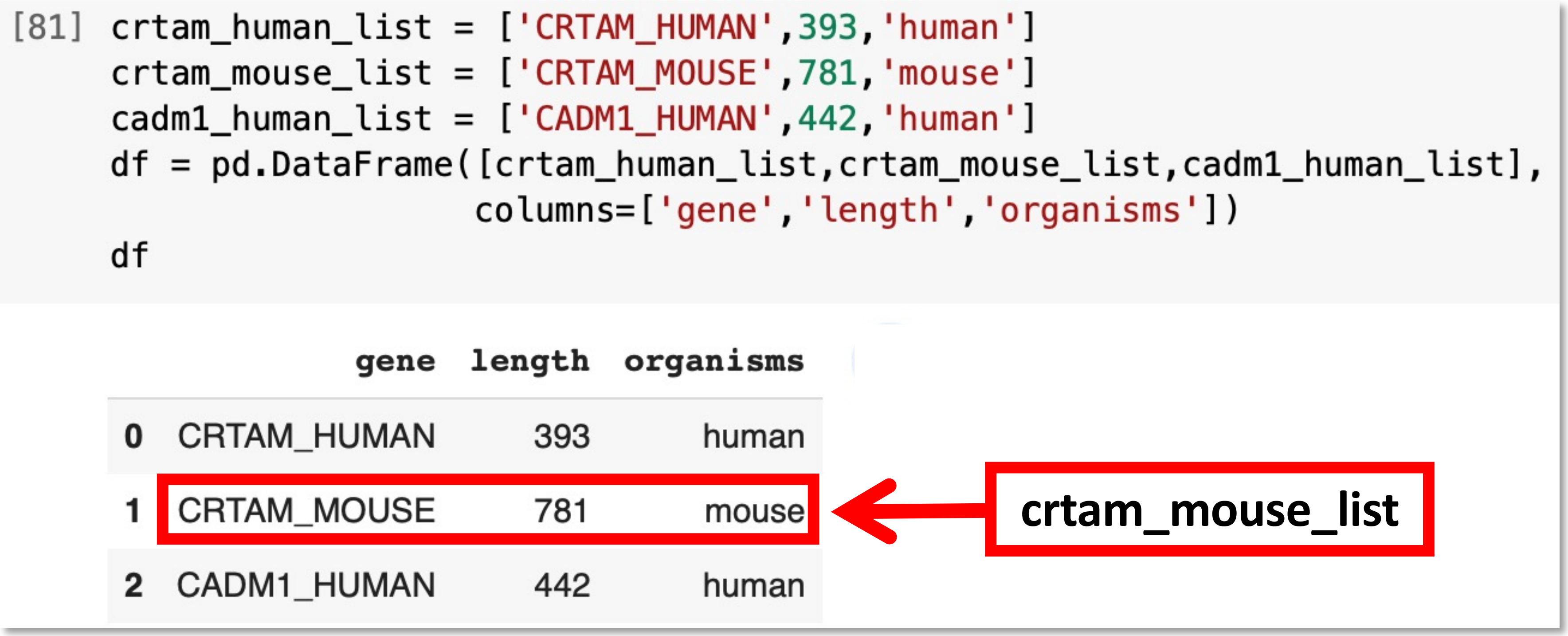


```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
     df
```

```
          gene  length  organisms
0  CRTAM_HUMAN     393      human
1  CRTAM_MOUSE     781      mouse
2  CADM1_HUMAN     442      human
```

crtam_human_list

Convert multiple lists into a Pandas Dataframe

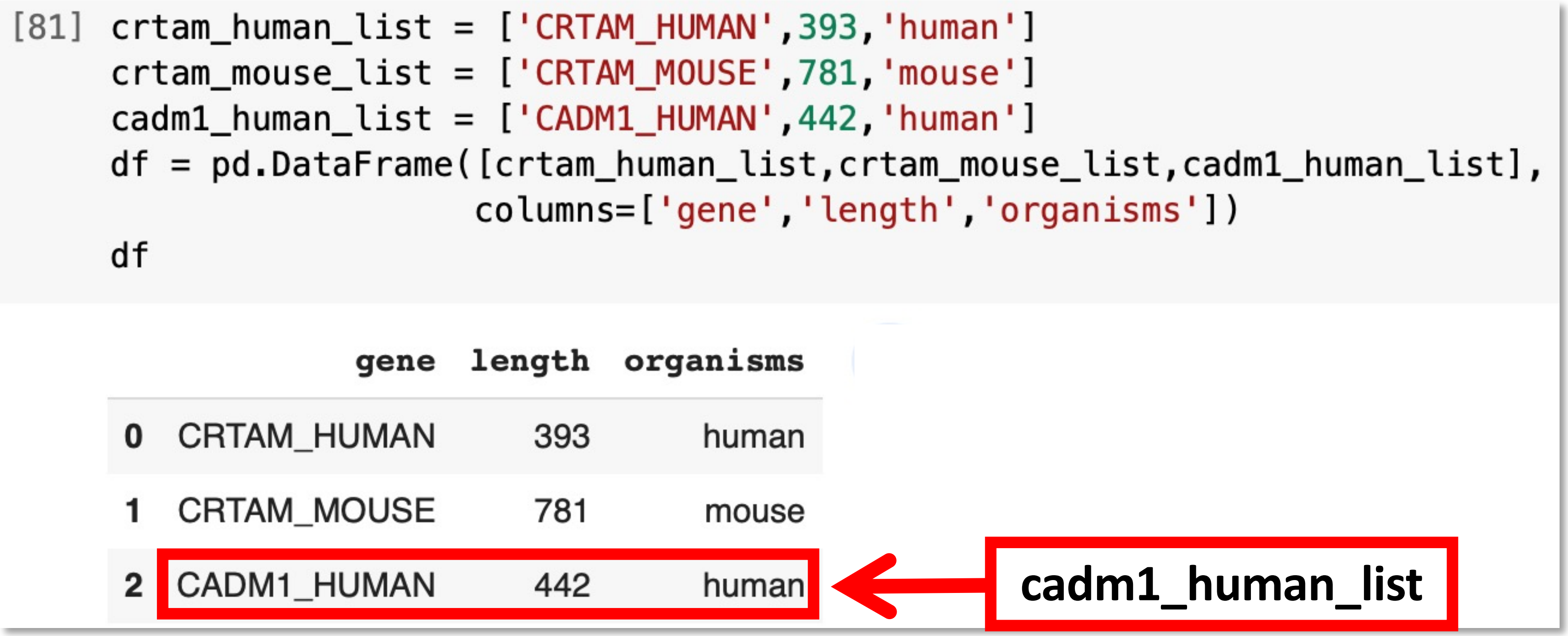


```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
     df
```

```
          gene  length  organisms
0  CRTAM_HUMAN     393      human
1  CRTAM_MOUSE     781      mouse
2  CADM1_HUMAN     442      human
```

crtam_mouse_list

Convert multiple lists into a Pandas Dataframe



```
[81] crtam_human_list = ['CRTAM_HUMAN',393,'human']
     crtam_mouse_list = ['CRTAM_MOUSE',781,'mouse']
     cadm1_human_list = ['CADM1_HUMAN',442,'human']
     df = pd.DataFrame([crtam_human_list,crtam_mouse_list,cadm1_human_list],
                       columns=['gene','length','organisms'])
     df
```

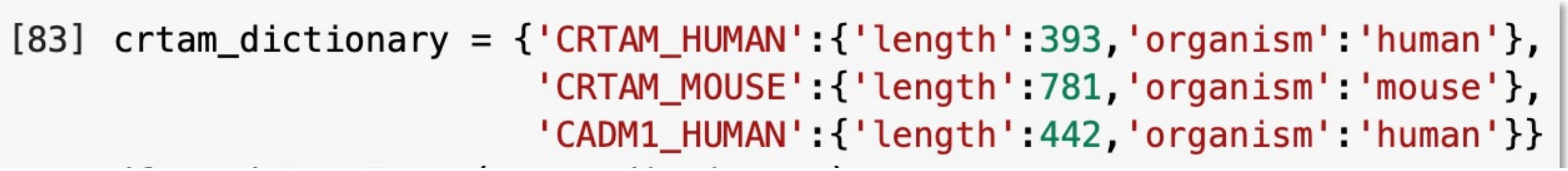
```
          gene  length  organisms
0  CRTAM_HUMAN     393      human
1  CRTAM_MOUSE     781      mouse
2  CADM1_HUMAN     442      human
```

cadm1_human_list

Lesson 3.2.3c

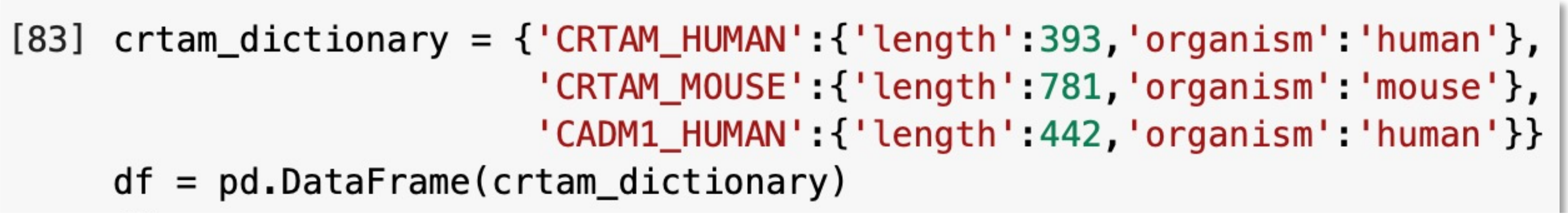
Create a Pandas DataFrame from a Nested Dictionary

Convert a nested dictionary into a Panda DataFrame



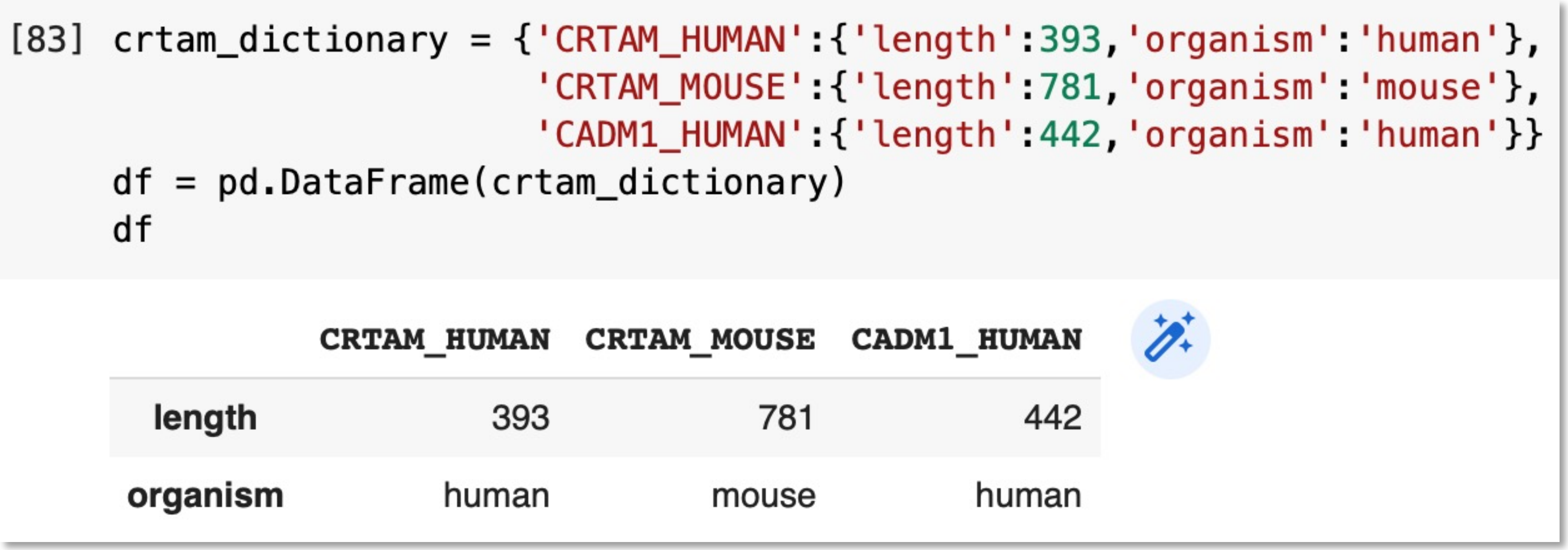
```
[83] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
```

Convert a nested dictionary into a Panda DataFrame



```
[83] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary)
```

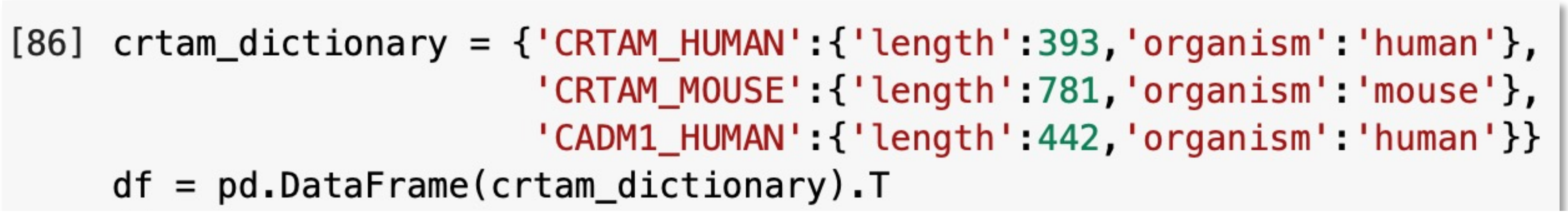
Convert a nested dictionary into a Panda DataFrame



```
[83] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary)
     df
```

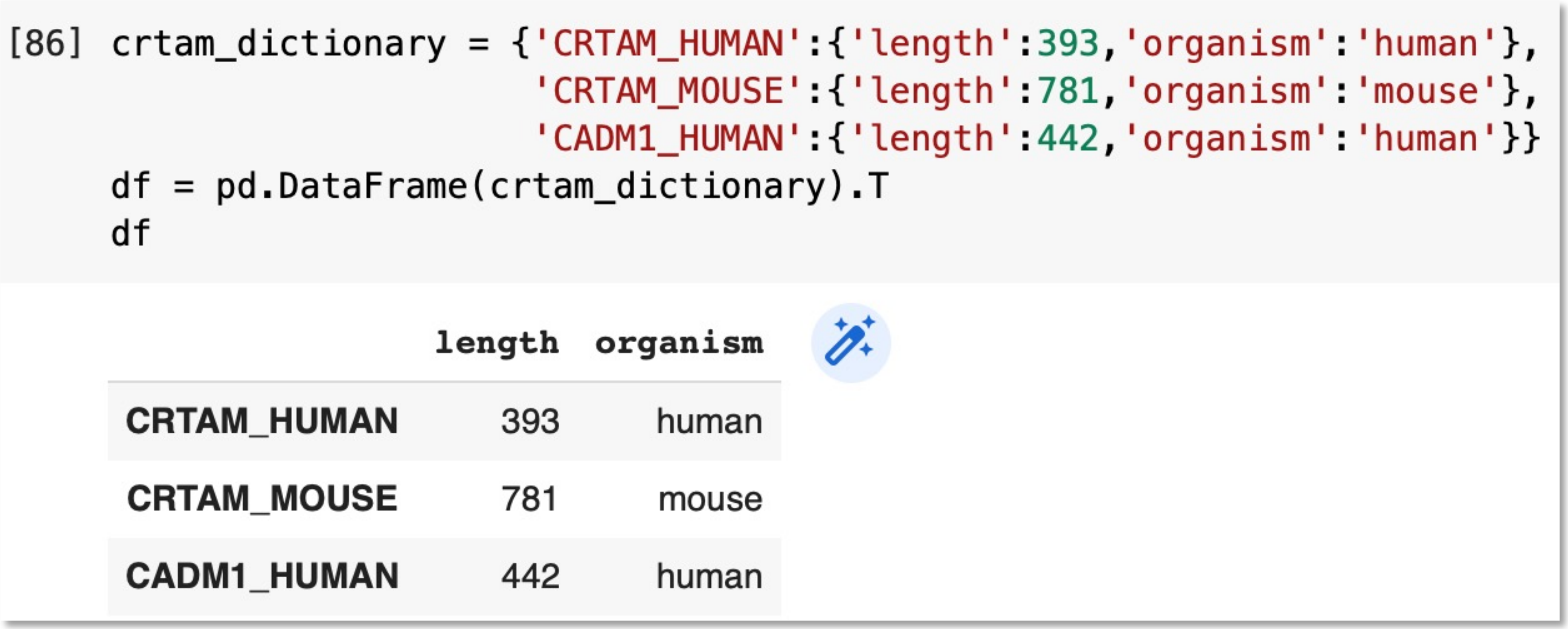
	CRTAM_HUMAN	CRTAM_MOUSE	CADM1_HUMAN
length	393	781	442
organism	human	mouse	human

Convert a nested dictionary into a Panda DataFrame



```
[86] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                        'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                        'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T
```

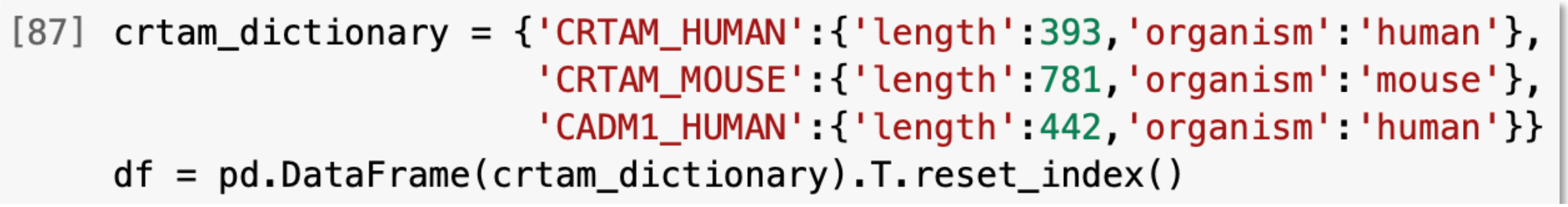
Convert a nested dictionary into a Panda DataFrame



```
[86] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T
     df
```

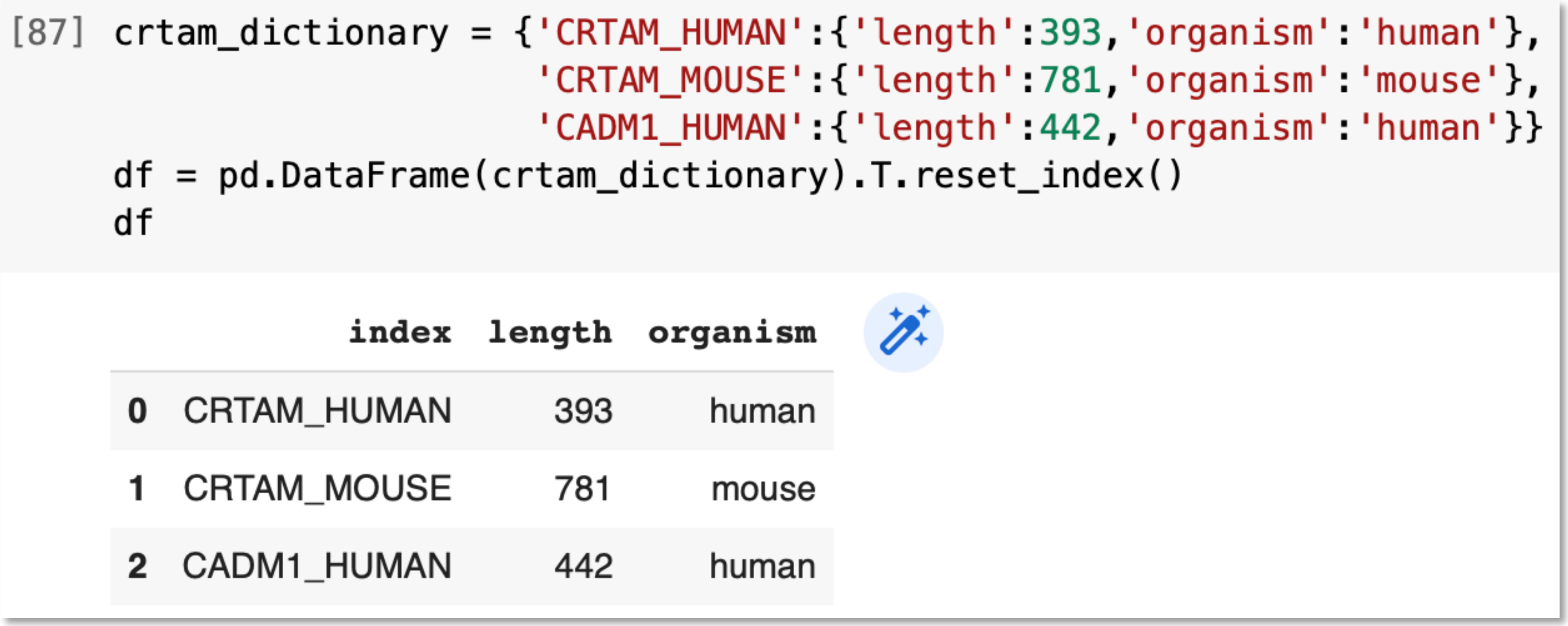
	length	organism
CRTAM_HUMAN	393	human
CRTAM_MOUSE	781	mouse
CADM1_HUMAN	442	human

Convert a nested dictionary into a Panda DataFrame



```
[87] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                        'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                        'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T.reset_index()
```

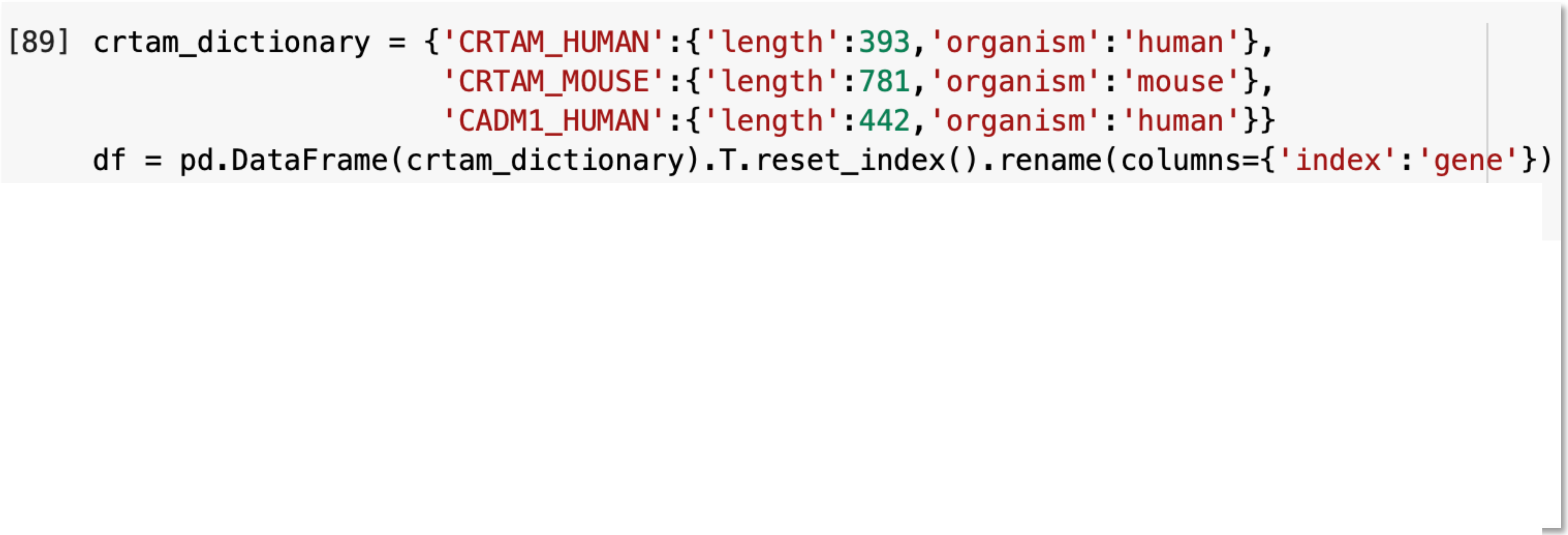
Convert a nested dictionary into a Panda DataFrame



```
[87] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T.reset_index()
     df
```

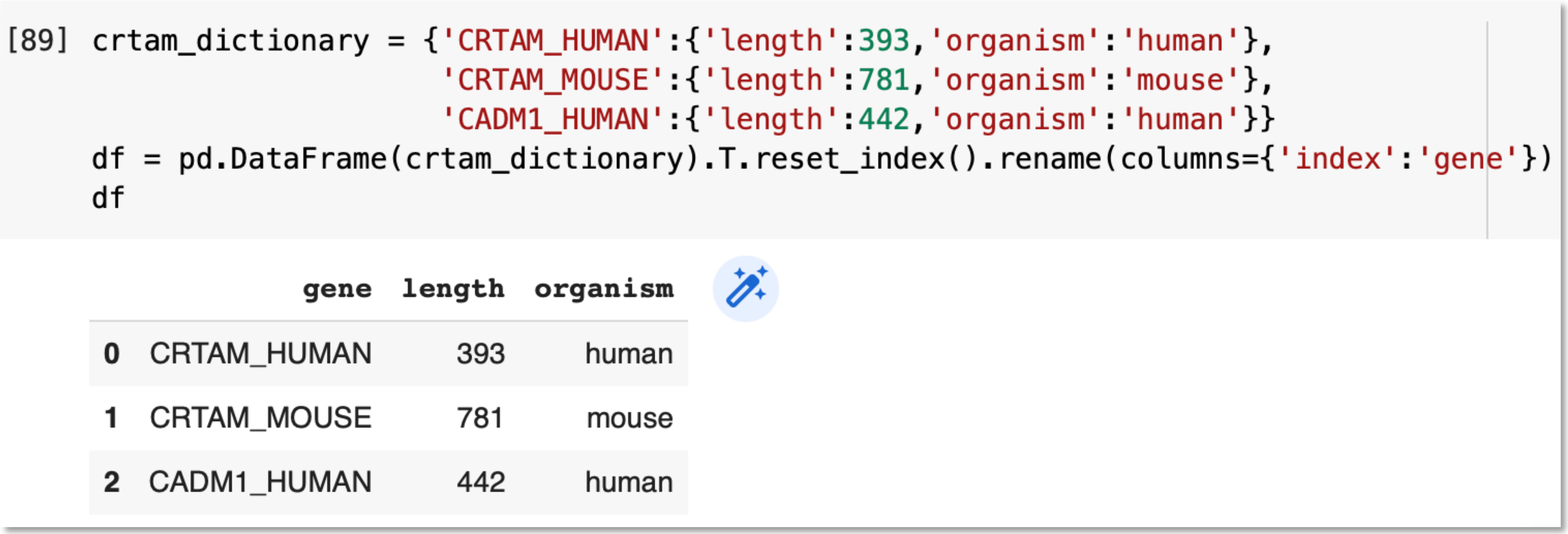
	index	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

Convert a nested dictionary into a Panda DataFrame



```
[89] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T.reset_index().rename(columns={'index':'gene'})
```

Convert a nested dictionary into a Panda DataFrame



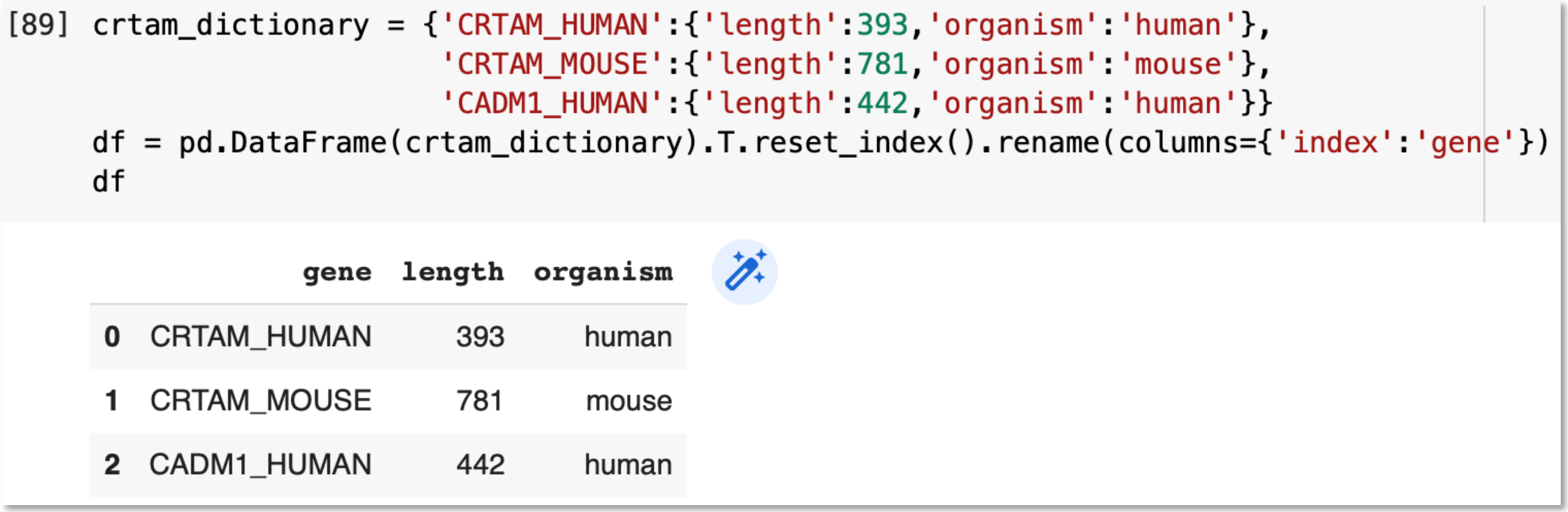
```
[89] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T.reset_index().rename(columns={'index':'gene'})
     df
```

	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

Lesson 3.2.4

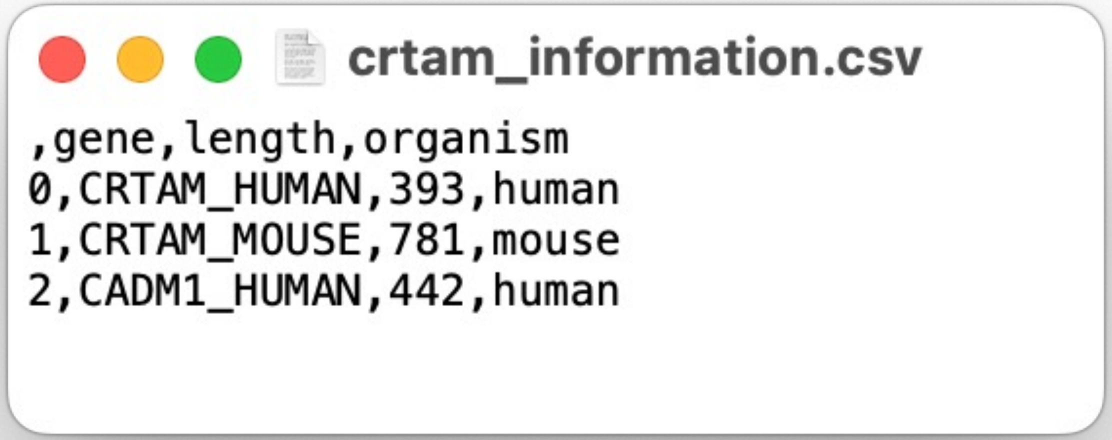
Export a Panda DataFrame as a CSV File

Export a nested dictionary to a CSV file



```
[89] crtam_dictionary = {'CRTAM_HUMAN':{'length':393,'organism':'human'},
                         'CRTAM_MOUSE':{'length':781,'organism':'mouse'},
                         'CADM1_HUMAN':{'length':442,'organism':'human'}}
     df = pd.DataFrame(crtam_dictionary).T.reset_index().rename(columns={'index':'gene'})
     df
```

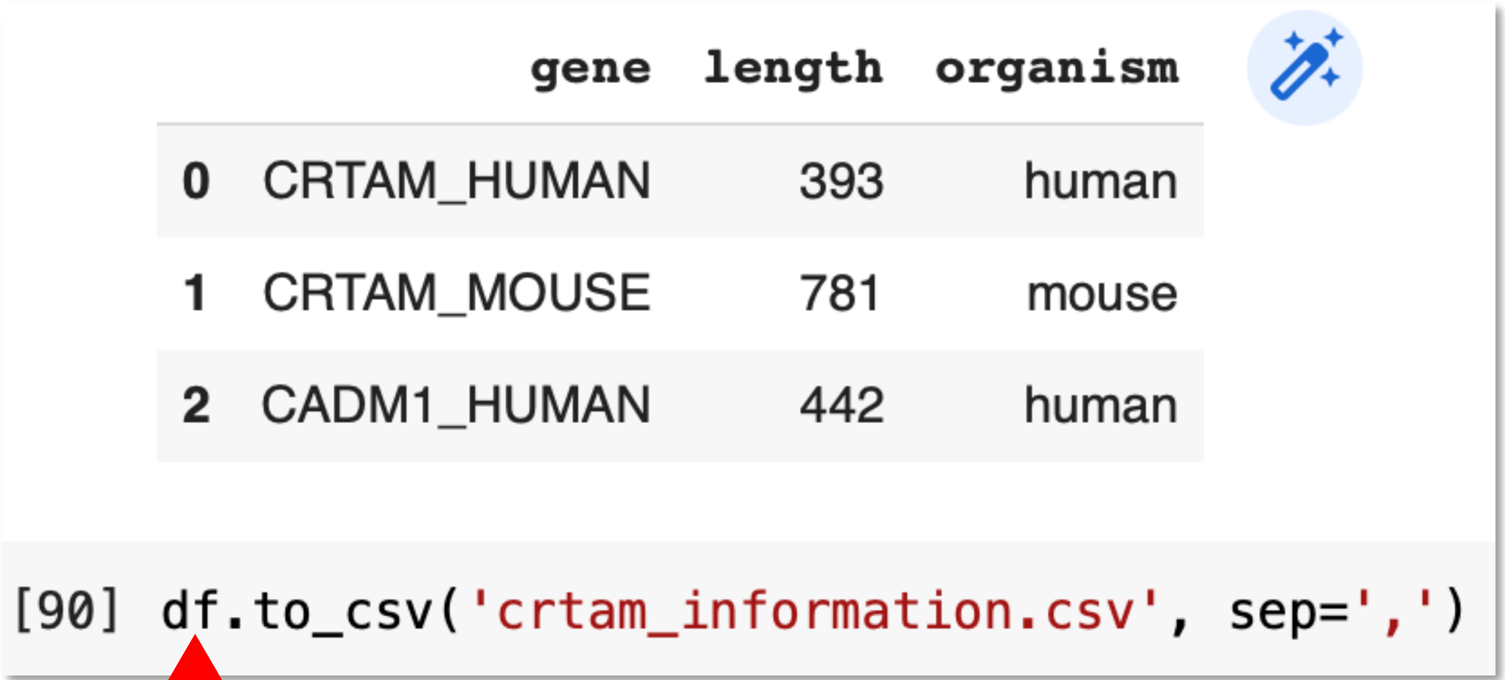
	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human



crtam_information.csv

```
,gene,length,organism
0,CRTAM_HUMAN,393,human
1,CRTAM_MOUSE,781,mouse
2,CADM1_HUMAN,442,human
```

Export a nested dictionary to a CSV file

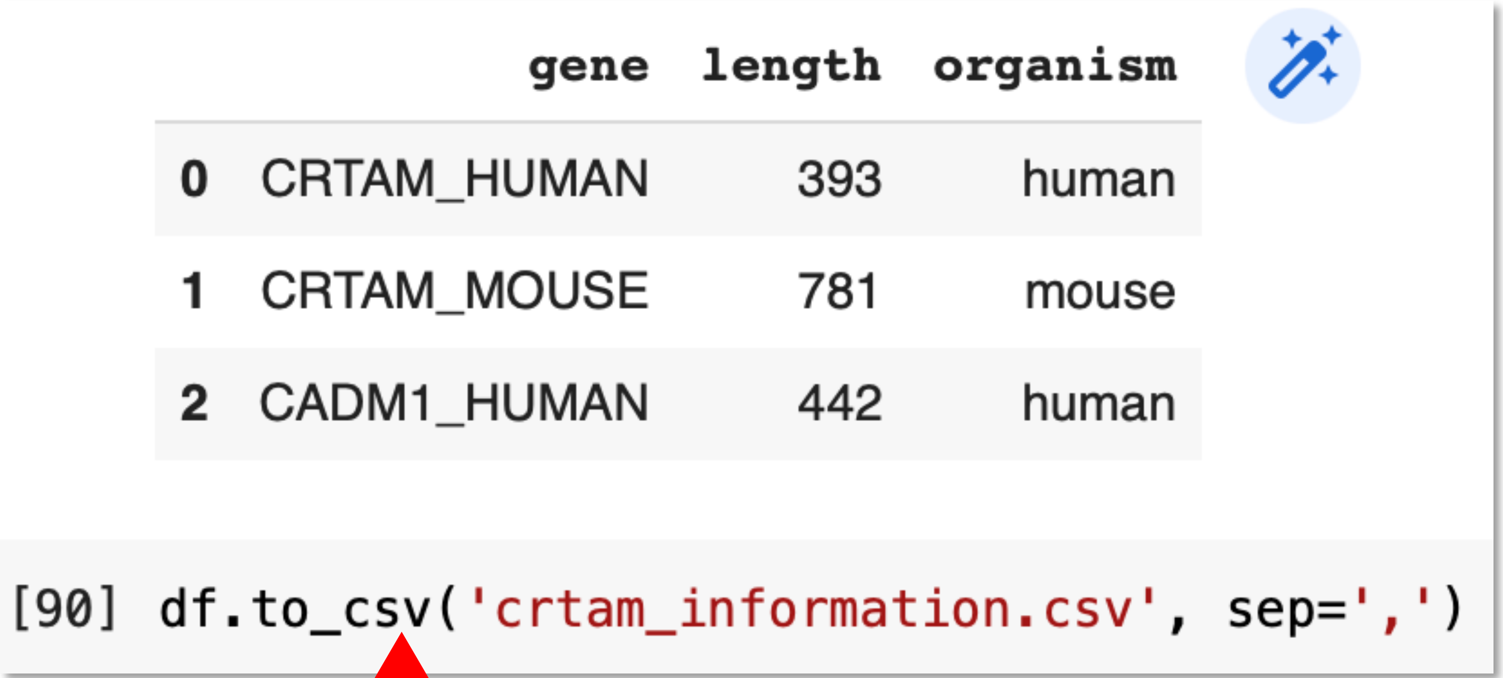


	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

```
[90] df.to_csv('crtam_information.csv', sep=',')
```

Call variable of your dataframe

Export a nested dictionary to a CSV file

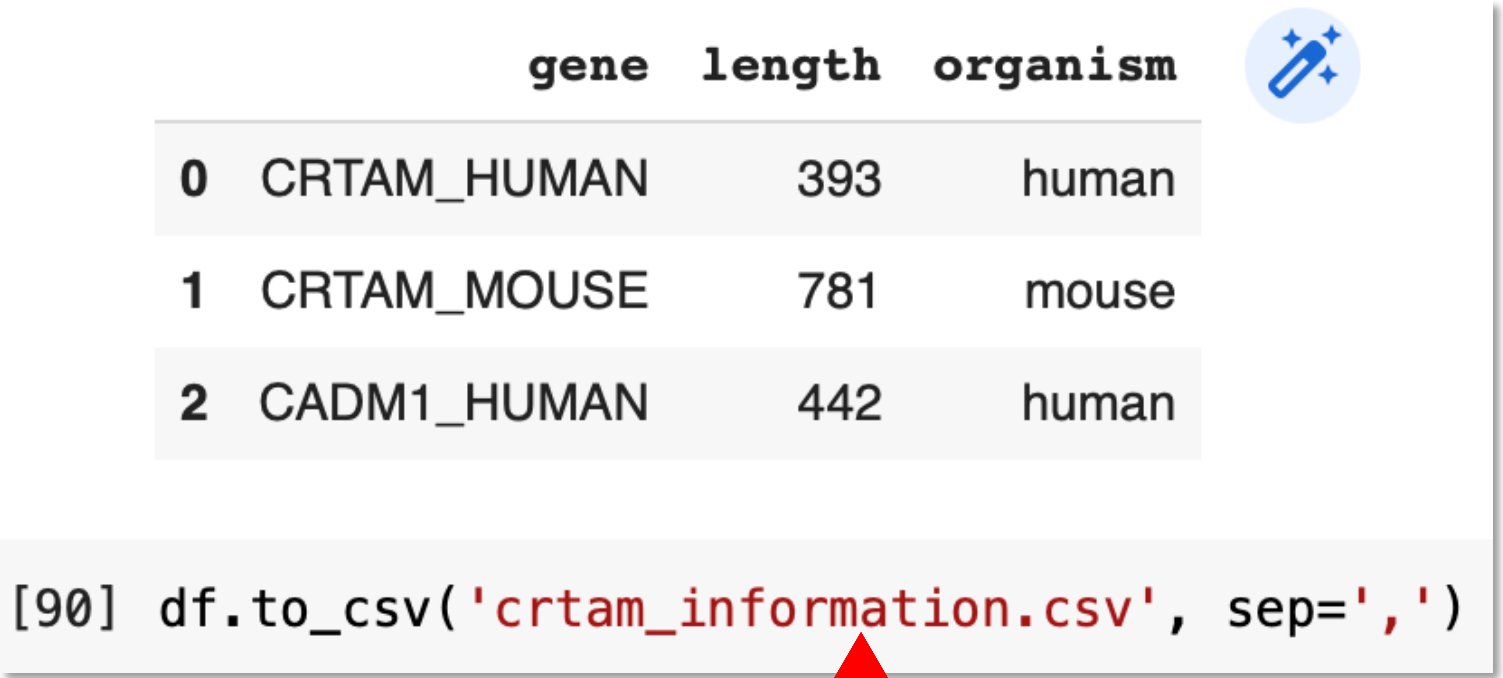


	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

```
[90] df.to_csv('crtam_information.csv', sep=',')
```

Call to_csv() function to start a Pandas Dataframe

Export a nested dictionary to a CSV file

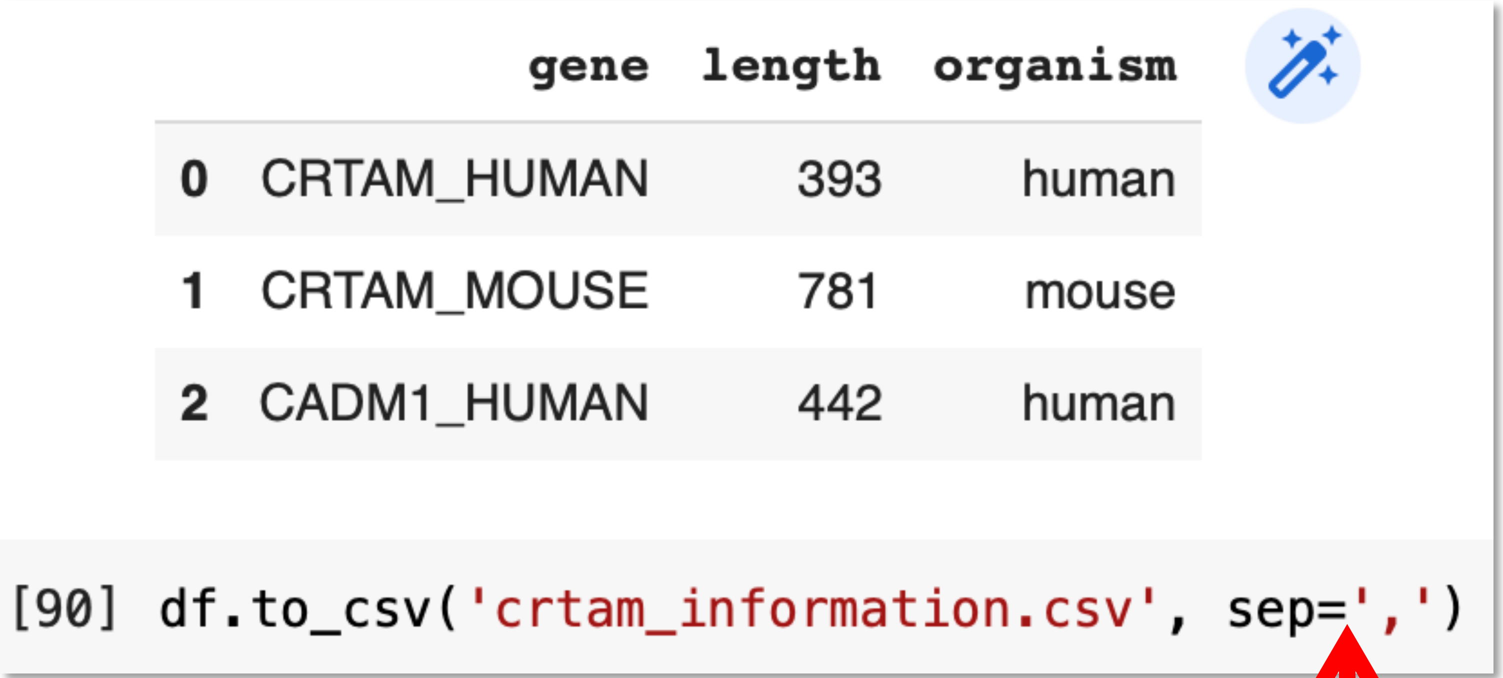


	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

```
[90] df.to_csv('crtam_information.csv', sep=',')
```

Name your file of interest

Export a nested dictionary to a CSV file

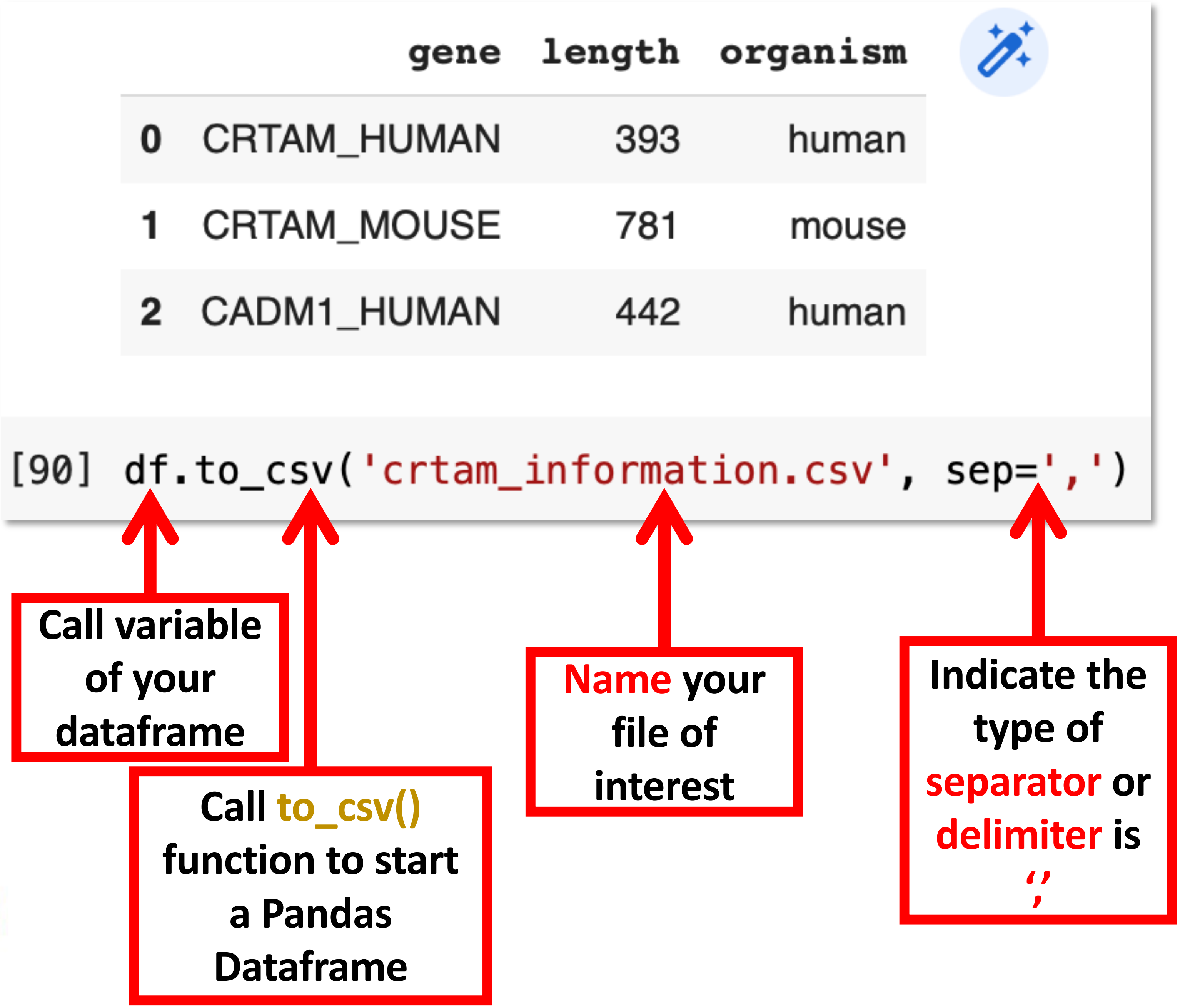


	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

```
[90] df.to_csv('crtam_information.csv', sep=',')
```

Indicate the type of **separator** or **delimiter** is **‘,’**

Export a nested dictionary to a CSV file



	gene	length	organism
0	CRTAM_HUMAN	393	human
1	CRTAM_MOUSE	781	mouse
2	CADM1_HUMAN	442	human

```
[90] df.to_csv('crtam_information.csv', sep=',')
```

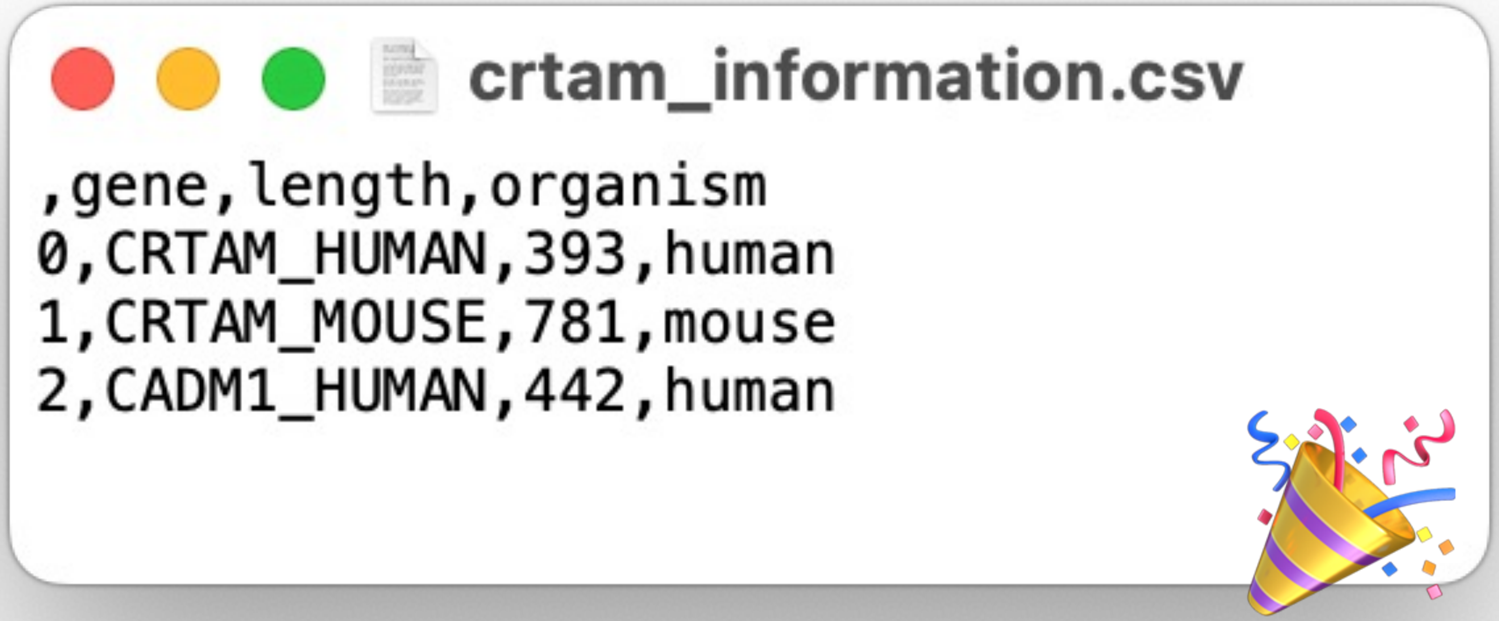
Call variable of your dataframe

Call to_csv() function to start a Pandas Dataframe

Name your file of interest

Indicate the type of separator or delimiter is ‘,’

Check out your new CSV file!



```
,gene,length,organism
0,CRTAM_HUMAN,393,human
1,CRTAM_MOUSE,781,mouse
2,CADM1_HUMAN,442,human
```

Proficiency assessment

Show off your new skills!

1. Read in the Fasta File called crtam.faa

2. Choose at least 3 of the following options below to create a dataframe with your columns of interest.
   - Gene_names
   - Length in amino acid
   - Length in it's DNA sequence
   - Total RSNNEETS
   - Total KAH
   - Total PGLRLRLLLL

3. Export a file to import into Excel