

Αρχεία

```
In [1]: !ls -l mim2gene.txt
```

```
-rw-r--r--@ 1 admin  staff  904816 Mar 17 17:12 mim2gene.txt
```

```
In [2]: !pwd
```

```
/Users/admin/Downloads
```

```
In [237... # https://www.omim.org/static/omim/data/mim2gene.txt
with open('mim2gene.txt') as f:
    d = f.read()
```

```
In [239... print(d[:1000])
```

```
# Copyright (c) 1966–2021 Johns Hopkins University. Use of this file adheres to
# the terms specified at https://omim.org/help/agreement.
# Generated: 2021-03-18
# This file provides links between the genes in OMIM and other gene identifier
# s.
# THIS IS NOT A TABLE OF GENE-PHENOTYPE RELATIONSHIPS.
# MIM Number      MIM Entry Type (see FAQ 1.3 at https://omim.org/help/faq)
#      Entrez Gene ID (NCBI)   Approved Gene Symbol (HGNC)   Ensembl Gene ID (Ensembl)
100050  predominantly phenotypes
100070  phenotype              100329167
100100  phenotype
100200  predominantly phenotypes
100300  phenotype
100500  moved/removed
100600  phenotype
100640  gene      216      ALDH1A1  ENSG00000165092
100650  gene/phenotype  217      ALDH2    ENSG00000111275
100660  gene      218      ALDH3A1  ENSG00000108602
100670  gene      219      ALDH1B1  ENSG00000137124
100675  predominantly phenotypes
100678  gene      39      ACAT2    ENSG00000120437
100680  moved/removed
100690  gene      1134     CHRNA1   ENSG00000138435
100700  predominantly phenotypes
100710  gene      1140     CHRN1B   ENSG0000017
```

```
In [6]: len(d)
```

```
Out[6]: 904816
```

```
In [7]: f = open('mim2gene.txt')
```

```
In [8]: d = f.read()
```

```
In [9]: f.close()
```

```
In [13]: with open('mim2gene.txt') as f:
          for line in f:
              #print (line)
          break
```

```
In [ ]: with open('mim2gene.txt') as f:
        for line in f:
            print (line.strip())
        #break
```

```
In [15]: with open('mim2gene.txt') as f:
        for line_number, line in enumerate(f):
            print (line.strip())
            if line_number > 10:
                break
```

```
# Copyright (c) 1966-2021 Johns Hopkins University. Use of this file adheres to
# the terms specified at https://omim.org/help/agreement.
# Generated: 2021-03-17
# This file provides links between the genes in OMIM and other gene identifiers.
# THIS IS NOT A TABLE OF GENE-PHENOTYPE RELATIONSHIPS.
# MIM Number      MIM Entry Type (see FAQ 1.3 at https://omim.org/help/faq)
#   Entrez Gene ID (NCBI)   Approved Gene Symbol (HGNC)   Ensembl Gene ID (Ensembl)
100050  predominantly phenotypes
100070  phenotype           100329167
100100  phenotype
100200  predominantly phenotypes
100300  phenotype
100500  moved/removed
100600  phenotype
```

```
In [16]: with open('mim2gene.txt') as f:
        first_line = f.readline()
        print (first_line)
```

```
# Copyright (c) 1966-2021 Johns Hopkins University. Use of this file adheres to
# the terms specified at https://omim.org/help/agreement.
```

```
In [17]: with open('mim2gene.txt') as f:
        first_line = f.readline()
        print (first_line)
        second_line = f.readline()
        print (second_line)
```

```
# Copyright (c) 1966-2021 Johns Hopkins University. Use of this file adheres to
# the terms specified at https://omim.org/help/agreement.
```

```
# Generated: 2021-03-17
```

```
In [18]: with open('mim2gene.txt') as f:
        for i in range(10):
            line = f.readline()
            print (line.strip())
```

```
# Copyright (c) 1966-2021 Johns Hopkins University. Use of this file adheres to
# the terms specified at https://omim.org/help/agreement.
```

```
# Generated: 2021-03-17
```

```
# This file provides links between the genes in OMIM and other gene identifiers.
# THIS IS NOT A TABLE OF GENE-PHENOTYPE RELATIONSHIPS.
```

```
# MIM Number      MIM Entry Type (see FAQ 1.3 at https://omim.org/help/faq)
#   Entrez Gene ID (NCBI)   Approved Gene Symbol (HGNC)   Ensembl Gene ID (Ensembl)
```

```
100050  predominantly phenotypes
100070  phenotype           100329167
100100  phenotype
100200  predominantly phenotypes
```

```
100300    phenotype
```

```
In [19]: with open('mim2gene.txt') as f:
          lines = f.readlines()
```

```
In [20]: len(lines)
```

```
Out[20]: 27097
```

```
In [21]: print (lines[100])
```

```
102800    phenotype
```

```
In [22]: f = open('mim2gene.txt')
          l_1 = f.readline()
```

```
In [23]: print (l_1)
```

```
# Copyright (c) 1966-2021 Johns Hopkins University. Use of this file adheres to
the terms specified at https://omim.org/help/agreement.
```

```
In [24]: f.readline()
```

```
Out[24]: '# Generated: 2021-03-17\n'
```

```
In [25]: f.readline()
```

```
Out[25]: '# This file provides links between the genes in OMIM and other gene identifiers.\n'
```

```
In [26]: f.close()
```

```
In [27]: f = open('mim2gene.txt')
```

```
In [28]: f.readline()
```

```
Out[28]: '# Copyright (c) 1966-2021 Johns Hopkins University. Use of this file adheres
to the terms specified at https://omim.org/help/agreement.\n'
```

```
In [29]: f = open('mim2gene.txt')
          for l in f:
              #print ()
              pass
```

```
In [30]: f.readline()
```

```
Out[30]: ''
```

```
In [31]: f = open('mim2gene.txt')

          while True:
              line = f.readline()
              #if line == ''
              if not line:
                  break
          f.close()
```

```
In [36]: s = 'Mitsos'
        k = 'Kwstas'
```

```
In [34]: if '':
        print ('1')
        else:
        print ('2')
```

2

```
In [41]: with open('my_precious.txt', 'w') as f:
        f.write(s)
        f.write(k)
```

```
In [42]: !cat my_precious.txt
```

MitsosKwstas

¶a windows:

!type my_precious.txt

```
In [43]: with open('my_precious.txt', 'w') as f:
        f.write(s + '\n')
        f.write(k + '\n')
```

```
In [44]: !cat my_precious.txt
```

Mitsos

Kwstas

```
In [48]: a = [1,2,3,4,5,6]

        with open('my_precious.txt', 'w') as f:
            for i in a:
                f.write(str(i) + '\n')
```

```
In [49]: !cat my_precious.txt
```

1

2

3

4

5

6

```
In [50]: with open('my_precious.txt', 'w') as f:
        f.write(s + ' ' + k + '\n')
```

```
In [51]: !cat my_precious.txt
```

Mitsos Kwstas

```
In [53]: a = ['kwstas', 'mitsos', 'maria', 'sadfzsdfsadc']

        with open('my_precious.txt', 'w') as f:
            f.write(' '.join(a) + '\n')
```

```
In [54]: !cat my_precious.txt
```

```
kwstas mitsos maria sadfzsdfsadc
```

```
In [55]: with open('my_precious.txt', 'a') as f:
         f.write('hello world\n')
```

```
In [56]: !cat my_precious.txt
```

```
kwstas mitsos maria sadfzsdfsadc
hello world
```

```
In [57]: with open('my_precious.txt', 'r') as f:
         d = f.read()
         print (d)
```

```
kwstas mitsos maria sadfzsdfsadc
hello world
```

```
In [58]: a = [1,2,3,4,5,6]
```

```
In [61]: with open('double.txt', 'w') as f:
         for i in a:
             f.write(str(i*2) + '\n')

         with open('half.txt', 'w') as f:
             for i in a:
                 f.write(str(i/2) + '\n')
```

```
In [60]: !cat double.txt
```

```
2
4
6
8
10
12
```

```
In [62]: !cat half.txt
```

```
0.5
1.0
1.5
2.0
2.5
3.0
```

```
In [63]: with open('double.txt', 'w') as f1, open('half.txt', 'w') as f2:
         for i in a:
             f1.write(str(i*2)+'\n')
             f2.write(str(i/1)+'\n')
```

```
In [64]: with open('half2.txt', 'a') as f:
         f.write('asdf')
```

```
In [65]: !cat half2.txt
```

```
asdf
```

```
In [67]: with open('mim2gene.txt') as f:
         for l in f:
             if l[0] == '#':
                 continue

             print (l)
             break
```

100050 predominantly phenotypes

```
In [72]: l.strip('\n').split('\t')
```

```
Out[72]: ['100050', 'predominantly phenotypes', '', '', '']
```

```
In [77]: l
```

```
Out[77]: '100050\tpredominantly phenotypes\t\t\t\t\n'
```

```
In [78]: l.strip('\n')
```

```
Out[78]: '100050\tpredominantly phenotypes\t\t\t\t'
```

```
In [79]: l.strip('\n').split('\t')
```

```
Out[79]: ['100050', 'predominantly phenotypes', '', '', '']
```

```
In [80]: 'ababa'.split('a')
```

```
Out[80]: ['', 'b', 'b', '']
```

```
In [81]: a = [[1,2,3], [4,5,6], [7,8,9]]
```

String formatting

```
In [82]: name = 'Mitsos'
         age  = 40
```

```
In [84]: 'my name is ' + name + ' and my age is: ' + str(age)
```

```
Out[84]: 'my name is Mitsos and my age is: 40'
```

```
In [85]: 'my name is {} and my age is: {}'.format(name, age)
```

```
Out[85]: 'my name is Mitsos and my age is: 40'
```

```
In [86]: 'my name is {onoma} and my age is: {hlikia}'.format(onoma=name, hlikia=age)
```

```
Out[86]: 'my name is Mitsos and my age is: 40'
```

```
In [87]: f'my name is {name} and my age is: {age}'
```

```
Out[87]: 'my name is Mitsos and my age is: 40'
```

```
In [89]: 'my name is %s and my age is: %s' % (name, age)
```

```
Out[89]: 'my name is Mitsos and my age is: 40'
```

```
In [94]: a=234/1345
a
```

```
Out[94]: 0.17397769516728626
```

```
In [95]: 'the result is {} {}'.format(a)
```

```
Out[95]: 'the result is 0.17397769516728626 '
```

```
In [99]: 'the result is {0:.3f} {}'.format(a)
```

```
Out[99]: 'the result is 0.174 '
```

pass

```
In [102... a = 1

if a == 1:
    print ('1')
else:
    #print ('not 1')
    pass
```

```
1
```

```
In [103... for i in [1,2,3,5]:
    pass
```

```
In [104... pass
```

```
In [105... print (1)
pass
print (2)
```

```
1
2
```

```
In [106... if a==1: # too complicated
    pass
else:
    ....
```

```
File "<ipython-input-106-9a1fdd3b174b>", line 4
```

```
....
^
```

```
SyntaxError: invalid syntax
```

ternary operator

```
In [109... age = 10
if age >= 18:
    state = 'adult'
else:
    state = 'not adult'
```

```
In [110... state
```

```
Out[110... 'not adult'
```

```
In [112... state = 'adult' if age >= 18 else 'not adult'
```

is operator

```
In [113... a=10
```

```
In [114... type(a) is int
```

```
Out[114... True
```

```
In [120... a=10
b=10
a is b
```

```
Out[120... True
```

```
In [116... a==b
```

```
Out[116... True
```

```
In [119...
```

```
Out[119... True
```

```
In [121... a=1000
b=1000
a is b
```

```
Out[121... False
```

```
In [122... a = "mitsos"
b = "mitsos"
a==b
```

```
Out[122... True
```

```
In [123... a is b
```

```
Out[123... True
```



```
In [124... a = 1000  
b = 1000  
  
a == b
```

```
Out[124... True
```

```
In [126... a is b
```

```
Out[126... False
```

```
In [127... a=b
```

```
In [128... a is b
```

```
Out[128... True
```

```
In [129... b += 1
```

```
In [130... a
```

```
Out[130... 1000
```

```
In [131... b
```

```
Out[131... 1001
```

```
In [132... a = 1000  
b = 1000  
a=b  
  
a+=1  
print(b)
```

```
1000
```

```
In [133... a = [1,2,3]  
b = [1,2,3]  
  
a=b  
  
b.append(4)  
print (a)
```

```
[1, 2, 3, 4]
```

```
In [134... a = [1,2,3]  
b = [1,2,3]  
  
b.append(4)  
print (a)
```

```
[1, 2, 3]
```

```
In [135... a = [1,2,3]
b = [1,2,3]

a==b
```

Out[135... True

```
In [136... a is b
```

Out[136... False

```
In [137... a = [1,2,3]
b = [1,2,3]

a=b

a is b
```

Out[137... True

```
In [139... a = 3
def f(x):
    a=4

f(10)
print(a)
```

3

```
In [141... a=[1,2,3]
def f(x):
    a.append(5)

f(10)
print (a)
```

[1, 2, 3, 5]

```
In [142... def f(a):
    a=4

a=2
f(a)
print (a)
```

2

```
In [143... def f(a):
    a.append(4)

a=[1,2,3]
f(a)
print (a)
```

[1, 2, 3, 4]

In []:

```
In [146... int(4).__add__(6)
```

```
Out[146... 10
```

lambda functions

```
In [147... a = [1,2,3,4,5,6,7,8,9,10]
```

```
def f(x):  
    return x%2 == 1  
  
list(filter(f, a))
```

```
Out[147... [1, 3, 5, 7, 9]
```

```
In [148... def g(x):  
    return x*2  
  
list(map(g, a))
```

```
Out[148... [2, 4, 6, 8, 10, 12, 14, 16, 18, 20]
```

```
In [149... def g(x):  
    return x*2
```

```
In [150... g(10)
```

```
Out[150... 20
```

```
In [156... g = lambda x : (x*2, x/2)
```

```
In [160... a,b = g(10)  
print(a)  
print (b)  
  
20  
5.0
```

```
In [162... add = lambda a,b: a+b
```

```
In [163... add(5,4)
```

```
Out[163... 9
```

```
In [154... def g(x):  
    print ("hello")  
    return x*2
```

```
In [164... a = [1,2,3,4,5,6,7,8,9,10]
```

```
In [167... list(map(lambda x:x*2, a))
```

```
Out[167... [2, 4, 6, 8, 10, 12, 14, 16, 18, 20]
```

```
In [168... list(filter(lambda x:x%2==1, a))
```

```
Out[168... [1, 3, 5, 7, 9]
```

```
In [171... a = ['edessa', 'Bethleem', 'Thessaloniki']
```

```
In [172... def f(x):  
    return x.count('e')  
  
sorted(a, key=f)
```

```
Out[172... ['Thessaloniki', 'edessa', 'Bethleem']
```

```
In [173... sorted(a, key= lambda x:x.count('e') )
```

```
Out[173... ['Thessaloniki', 'edessa', 'Bethleem']
```

```
In [174... min(a, key=lambda x:x.count('e') )
```

```
Out[174... 'Thessaloniki'
```

```
In [175... max(a, key=lambda x:x.count('e') )
```

```
Out[175... 'Bethleem'
```

```
In [176... def f(x):  
  
    b = lambda y : y*2  
    return b(x)
```

```
In [177... f(10)
```

```
Out[177... 20
```

```
In [178... a = [lambda x:x*2, lambda x:x/2]
```

```
In [179... a[0](10)
```

```
Out[179... 20
```

```
In [180... a[1](10)
```

```
Out[180... 5.0
```

```
In [181... a = {}
```

```
In [222... a[lambda x:x*2] = 4
```

```
In [193... hash(lambda x:x*2)
```

```
Out[193... 8781085966026
```


Out[232...] `[[2, 3], [1, 2]]`

In [233...] `[sum(x) for x in a]`

Out[233...] `[3, 5]`

In [234...] `[sum(x) for x in b]`

Out[234...] `[3, 5]`

In []: