

## Supplementary material

Python Script constructed for data analysis for section 4.7 in methodology.

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1. import pandas as pd
2. from pandas import read_excel
3. import openpyxl as xl
4. import xlsxwriter
5. from xlrd import open_workbook
6. import pandas
7. from openpyxl import load_workbook
8. import re
9. import numpy as np
10.
11. global content9
12. global path1
13. global column_letter_protein_names
14. protein_names = "Protein names"
15. gene_ontology = "Gene ontology (biological process)"
16. sheet_0 = 'Sheet0'
17.
18.
19.
20. def make_list_files():
21.     fname = 'excelfilelist.txt'
22.     #list of excel files to process, listed as filename.xlsx, each
on a new line
23.     with open(fname) as f:
24.         global content9
25.         content9 = f.readlines() #for every new line in text file,
make an item in a list
26.         content9 = [j.strip() for j in content9] #then strip extra
spaces for that item
27.
28. def make_list():
29.     fname = 'inputwordlist.txt' #list of words you want to search
for, each on a new line
30.     with open(fname) as f:
31.         global content
32.         content = f.readlines() #for every new line in text file,
make an item in a list
33.         content = [j.strip() for j in content] #then strip extra spaces
for that item
34.
35.
36. def get_column_letter_protein_names():
37.     row = sheet.row(0)
38.     for col_id, cell in enumerate(row): #for every item in the
first row
39.         if cell.value == protein_names :
40.             #check the column label matches "Protein names"
41.             global column_letter_protein_names
42.             column_letter_protein_names =
xlsxwriter.utility.xls_col_to_name(col_id)
43.             #if it does, find the excel column letter
44.             print ('Printing ' + protein_names + ' from column: ' +
column_letter_protein_names)
45.
46. def get_column_letter_gene_ontology():
47.     row = sheet.row(0)
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48.     for col_id, cell in enumerate(row): #for every item in the
   first row
49.         if cell.value == gene_ontology : #check the column label
   matches "Gene ontology (biological process)"
50.             global column_letter_gene_ontology
51.             column_letter_gene_ontology =
   xlsxwriter.utility.xls_col_to_name(col_id)
52.             #if it does, find the excel column letter
53.             print ('Printing ' + gene_ontology + ' from column: ' +
   column_letter_gene_ontology)
54.
55.
56.
57. def copy_proteins():
58.     for i in ws1[column_letter_protein_names + ':' +
   column_letter_protein_names]:
59.         print('printing from ' + str(i.column) + str(i.row))
60.         ws2.cell(row=i.row, column=1, value=i.value)
61.         #basically copy names of proteins to first column
62.
63. def copy_matched_processes():
64.     for i in ws1[column_letter_gene_ontology + ':' +
   column_letter_gene_ontology]:
65.         print('printing from ' + str(i.column) + str(i.row))
66.         my_regex = r"([^\;]*)(\w*"+re.escape(word_type)+
   r"\w*)([^[\;]*])"
67.         pattern = re.compile(my_regex)
68.         temp1=str(i.value)
69.         temp2 = pattern.findall(temp1)
70.         temp3 = (",".join(map("".join,temp2)))
71.         temp4 = temp3.strip()
72.         ws2.cell(row=i.row, column=2, value=temp4)
73.         print(temp3)
74.         #copy biological processes that match search term for each
   protein
75.
76. def copy_matched_processes_all():
77.     for i in ws1[column_letter_gene_ontology + ':' +
   column_letter_gene_ontology]:
78.         print('printing from ' + str(i.column) + str(i.row))
79.         my_regex = r"([^\;]*)(\w*\w*)([^[\;]*])"
80.         pattern = re.compile(my_regex)
81.         temp1=str(i.value)
82.         temp2 = pattern.findall(temp1)
83.         temp3 = (",".join(map("".join,temp2)))
84.         temp4 = temp3.strip()
85.         ws2.cell(row=i.row, column=2, value=temp4)
86.         print(temp3)
87.         #special case where we copy all biological processes
   instead of ones that match searched words
88.
89. def save_first_sheet():
90.     ws2.cell(row=1, column=1).value = 'protein_names'
91.     ws2.cell(row=1, column=2).value = 'gene_ontology'
92.     wb1.save(path1)
93.     print('Word: \'' + word_type + '\' filtered list of Biological
   Processes saved.')
94.     #saves the sheet with protein names and biological processes
95.
96. def split_by_comma():
97.     global df1

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98.      df = read_excel(path1, sheet_name = word_type)
99.      j = df['gene_ontology'].astype(str)
100.     s = j.str.split(',').apply(pd.Series, 1).stack()
101.     s.index = s.index.droplevel(-1)
102.     s.name = 'gene_ontology'
103.     del df['gene_ontology']
104.     df = df.drop(df.index[0], inplace=False)
105.     df4 = df.join(s)
106.     df5 = df4.replace(['None', 'nan', 'None', np.nan], 'NaN',
107.                        inplace=False)
108.     df6 = df5.astype(str)
109.     df1 = df6[df6.gene_ontology != 'NaN']
110.     df1 = df1.drop_duplicates()
111.     print(df1)
112.     print('Word: \'' + word_type + '\' separated into new rows by
113.           comma.')
114.     #separates biological processes each into their own row, each
115.     #next to its originating protein
116.     # then removes duplicates
117.     def split_by_semicolon():
118.         global df9
119.         df = read_excel(path1, sheet_name = 'all')
120.         s = df['gene_ontology'].str.split(';').apply(pd.Series,
121.             1).stack()
122.         s.index = s.index.droplevel(-1)
123.         s.name = 'gene_ontology'
124.         dfa = df.join(s)
125.         dfb = dfa.replace(['None', 'nan', 'None', np.nan], 'NaN',
126.                           inplace=False)
127.         dfc = dfb.astype(str)
128.         df9 = dfc[dfc.gene_ontology != 'NaN']
129.         df9 = df9.drop_duplicates()
130.         print(df9)
131.         print('Word: \'' + word_type + '\' separated into new rows by
132.               comma.')
133.         #special case for the sheet that has all biological processes
134.         #and not just by search term
135.         #separates biological processes each into their own row, each
136.         #next to its originating protein
137.         # then removes duplicates
138.         def save_second_sheet():
139.             book = load_workbook(path1)
140.             writer = pandas.ExcelWriter(path1, engine='openpyxl')
141.             writer.book = book
142.             writer.sheets = dict((ws.title, ws) for ws in book.worksheets)
143.             df1.to_excel(excel_writer = writer, sheet_name = word_type +
144.                         '_a", index=False, columns=['protein_names', 'gene_ontology'])
145.             writer.save()
146.             print('Word: \'' + word_type + '\' table saved.')
147.             #saves these sheets
148.             def save_second_sheet_all():
149.                 book = load_workbook(path1)
150.                 writer = pandas.ExcelWriter(path1, engine='openpyxl')
151.                 writer.book = book
152.                 writer.sheets = dict((ws.title, ws) for ws in book.worksheets)
153.                 df9.to_excel(excel_writer = writer, sheet_name = "all_a",
154.                             index=False, columns=['protein_names', 'gene_ontology'])

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149.     writer.save()
150.     print('Word: \'' + word_type + '\' table saved.')
151.     #special case to save sheet for all biological processes
152.
153. def count_proteins():
154.     global df2
155.     k = pd.read_excel(path1,sheet_name = word_type
156.                         +'_'+a)['protein_names']
157.     df2 = k.value_counts()
158.     print(df2)
159.     book = load_workbook(path1)
160.     writer = pandas.ExcelWriter(path1, engine='openpyxl')
161.     writer.book = book
162.     writer.sheets = dict((ws.title, ws) for ws in book.worksheets)
163.     df2.to_excel(writer,word_type + "_b")
164.     writer.save()
165.     #counts how many rows we have in the second sheet,
166.     #enumerating how many proteins we have per search term
167.
168. def count_processes():
169.     global df3
170.     j = pd.read_excel(path1,sheet_name = word_type
171.                         +'_'+a)['gene_ontology']
172.     df3 = j.value_counts()
173.     print(df3)
174.     book = load_workbook(path1)
175.     writer = pandas.ExcelWriter(path1, engine='openpyxl')
176.     writer.book = book
177.     writer.sheets = dict((ws.title, ws) for ws in book.worksheets)
178.     df3.to_excel(writer,word_type + "_c")
179.     writer.save()
180.     #counts how many rows we have in the second sheet,
181.     #enumerating how many biological processes we have per search
182.     #term
183.     #order we run the functions
184.     make_list_files()
185.     for i in (range(len(content9))):
186.         path1 = (content9[i])
187.         wb1 = xl.load_workbook(filename=path1)
188.         ws1 = wb1.worksheets[0]
189.         book = open_workbook(path1)
190.         sheet = book.sheet_by_name(sheet_0)
191.         make_list()
192.         word_type = ('all')
193.         ws2 = wb1.create_sheet(word_type)
194.         get_column_letter_protein_names()
195.         copy_proteins()
196.         get_column_letter_gene_ontology()
197.         copy_matched_processes_all()
198.         save_first_sheet()
199.         for y in (range(len(content))):
200.             word_type = (content[y])
201.             ws2 = wb1.create_sheet(word_type)
202.             get_column_letter_protein_names()
203.             copy_proteins()
204.             get_column_letter_gene_ontology()
205.             copy_matched_processes()
206.             save_first_sheet()
207.             for z in (range(len(content))):
208.                 word_type = (content[z])

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207.         split_by_comma()
208.         save_second_sheet()
209.     split_by_semicolon()
210.     save_second_sheet_all()
211.     content.insert(0, 'all')
212.     for v in (range(len(content))):
213.         word_type = (content[v])
214.         count_proteins()
215.     for u in (range(len(content))):
216.         word_type = (content[u])
217.         count_processes()
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**Supplementary Table 1** The gene ontology of proteins identified in biological processes with neural associations across dataset.

GO Term	GO:ID	Percentage Associated Proteins Found	Number of Proteins	Term P-Value
<i>neurogenesis</i>	GO:0022008	10.41	214	8.18E-06
<i>generation of neurons</i>	GO:0048699	10.46	202	1.07E-05
<i>positive regulation of cell differentiation</i>	GO:0045597	11.88	152	1.39E-07
<i>neuron differentiation</i>	GO:0030182	10.54	135	2.91E-04
<i>neuron development</i>	GO:0048666	11.40	121	2.06E-05
<i>regulation of neurogenesis</i>	GO:0050767	10.79	116	3.40E-04
<i>neuron projection development</i>	GO:0031175	12.43	109	1.13E-06
<i>regulation of neuron differentiation</i>	GO:0045664	11.14	97	3.59E-04
<i>regulation of neuron projection development</i>	GO:0010975	12.63	84	1.22E-05
<i>positive regulation of neurogenesis</i>	GO:0050769	12.62	82	1.42E-05
<i>neuron projection morphogenesis</i>	GO:0048812	12.52	81	2.59E-05
<i>positive regulation of MAPK cascade</i>	GO:0043410	9.66	71	0.067723119
<i>axon development</i>	GO:0061564	13.16	70	1.70E-05
<i>positive regulation of neuron differentiation</i>	GO:0045666	12.84	67	6.22E-05
<i>cell morphogenesis involved in neuron differentiation</i>	GO:0048667	11.78	67	8.05E-04
<i>MAPK cascade</i>	GO:0000165	13.09	64	5.11E-05
<i>regulation of neuron death</i>	GO:1901214	14.96	63	5.15E-07
<i>axonogenesis</i>	GO:0007409	12.78	62	1.43E-04
<i>positive regulation of neuron projection development</i>	GO:0010976	15.02	61	7.86E-07
<i>regulation of synapse structure or activity</i>	GO:0050803	15.99	51	8.56E-07
<i>regulation of synapse organization</i>	GO:0050807	16.61	51	2.61E-07
<i>regulation of neuron apoptotic process</i>	GO:0043523	17.69	49	5.59E-08
<i>regulation of neurotransmitter levels</i>	GO:0001505	10.31	46	0.049550793
<i>axon guidance</i>	GO:0007411	13.64	45	2.52E-04
<i>neuron projection guidance</i>	GO:0097485	13.47	45	4.07E-04
<i>negative regulation of neuron death</i>	GO:1901215	15.60	44	9.48E-06
<i>negative regulation of neurogenesis</i>	GO:0050768	10.96	41	0.031487044

<i>positive regulation of MAP kinase activity</i>	GO:0043406	10.43	39	0.063876255
<i>negative regulation of neuron apoptotic process</i>	GO:0043524	18.00	36	2.05E-06
<i>regulation of axonogenesis</i>	GO:0050770	14.63	36	2.71E-04
<i>positive regulation of ERK1 and ERK2 cascade</i>	GO:0070374	11.54	33	0.025505733
<i>negative regulation of neuron differentiation</i>	GO:0045665	10.85	32	0.061859457
<i>regulation of synaptic plasticity</i>	GO:0048167	11.65	29	0.031369787
<i>glial cell differentiation</i>	GO:0010001	10.64	25	0.110965306
<i>negative regulation of neuron projection development</i>	GO:0010977	12.76	25	0.015134848
<i>regulation of axon extension</i>	GO:0030516	20.66	25	5.96E-06
<i>positive regulation of axonogenesis</i>	GO:0050772	20.83	25	5.10E-06
<i>neuron migration</i>	GO:0001764	14.65	23	0.003883542
<i>central nervous system neuron differentiation</i>	GO:0021953	8.33	21	0.722944115
<i>neuron projection extension</i>	GO:1990138	23.60	21	3.66E-06
<i>positive regulation of neuron death</i>	GO:1901216	16.26	20	0.001844229
<i>positive regulation of axon extension</i>	GO:0045773	28.36	19	5.27E-07
<i>neurotransmitter transport</i>	GO:0006836	8.00	18	0.900360041
<i>glial cell development</i>	GO:0021782	11.46	18	0.098474084
<i>response to axon injury</i>	GO:0048678	25.00	17	1.34E-05
<i>neuromuscular process</i>	GO:0050905	10.69	17	0.1800346
<i>axon extension</i>	GO:0048675	30.19	16	1.65E-06
<i>neuron recognition</i>	GO:0008038	20.00	14	9.07E-04
<i>positive regulation of neuron apoptotic process</i>	GO:0043525	19.72	14	0.001049444
<i>astrocyte differentiation</i>	GO:0048708	17.28	14	0.005175463
<i>regulation of synapse assembly</i>	GO:0051963	10.77	14	0.191534506
<i>axonal transport</i>	GO:0098930	16.87	14	0.005944255
<i>neuromuscular junction development</i>	GO:0007528	18.57	13	0.002743423
<i>central nervous system neuron development</i>	GO:0021954	11.50	13	0.156246699
<i>neuromuscular process controlling balance</i>	GO:0050885	14.61	13	0.02665154
<i>phosphatidylinositol metabolic process</i>	GO:0046488	5.97	12	0.426269868
<i>regulation of neurotransmitter transport</i>	GO:0051588	6.94	12	0.776348742

<i>astrocyte development</i>	GO:0014002	18.64	11	0.005479412
<i>neurotransmitter metabolic process</i>	GO:0042133	9.48	11	0.485807053
<i>negative regulation of axonogenesis</i>	GO:0050771	11.70	11	0.173288857
<i>regulation of neurotransmitter receptor activity</i>	GO:0099601	9.73	11	0.478815666
<i>neuron projection organization</i>	GO:0106027	16.92	11	0.016409561
<i>neurotransmitter secretion</i>	GO:0007269	8.00	10	0.867413349
<i>ensheathment of neurons</i>	GO:0007272	6.13	10	0.55614281
<i>anterograde axonal transport</i>	GO:0008089	15.15	10	0.036115029
<i>glial cell migration</i>	GO:0008347	16.67	10	0.024648435
<i>axon ensheathment</i>	GO:0008366	6.13	10	0.55614281
<i>forebrain generation of neurons</i>	GO:0021872	12.66	10	0.135270336
<i>regulation of synaptic transmission, glutamatergic</i>	GO:0051966	11.49	10	0.224224463
<i>neuron death</i>	GO:0070997	14.29	10	0.067924084
<i>regulation of postsynaptic membrane neurotransmitter receptor levels</i>	GO:0099072	14.49	10	0.065939583
<i>phosphatidylinositol biosynthetic process</i>	GO:0006661	6.92	9	0.86951678
<i>motor neuron axon guidance</i>	GO:0008045	19.57	9	0.008365169
<i>neuron projection regeneration</i>	GO:0031102	25.71	9	0.001164549
<i>axon regeneration</i>	GO:0031103	33.33	9	1.37E-04
<i>neurotrophin signaling pathway</i>	GO:0038179	19.15	9	0.009646455
<i>neuron apoptotic process</i>	GO:0051402	15.25	9	0.046781029
<i>neuroblast proliferation</i>	GO:0007405	19.51	8	0.012811679
<i>regulation of neurotransmitter secretion</i>	GO:0046928	6.11	8	0.622536021
<i>regulation of neuron migration</i>	GO:2001222	12.70	8	0.154017294
<i>neuropeptide signaling pathway</i>	GO:0007218	5.30	7	0.331197706
<i>retrograde axonal transport</i>	GO:0008090	23.33	7	0.007242808
<i>forebrain neuron differentiation</i>	GO:0021879	11.86	7	0.224660544
<i>forebrain neuron development</i>	GO:0021884	21.88	7	0.010445554
<i>telencephalon glial cell migration</i>	GO:0022030	17.07	7	0.037940934
<i>regulation of neuronal synaptic plasticity</i>	GO:0048168	10.14	7	0.495189522
<i>glial cell activation</i>	GO:0061900	12.50	7	0.205025062

<i>neurotransmitter receptor transport</i>	GO:0099637	14.89	7	0.092783965
<i>neuroinflammatory response</i>	GO:0150076	11.86	7	0.224660544
<i>semaphorin-plexin signaling pathway involved in neuron projection guidance</i>	GO:1902285	35.00	7	5.50E-04
<i>neuron projection maintenance</i>	GO:1990535	29.17	7	0.00185991
<i>axonal fasciculation</i>	GO:0007413	17.14	6	0.051917636
<i>negative regulation of axon extension</i>	GO:0030517	12.50	6	0.271232909
<i>regulation of glial cell differentiation</i>	GO:0045685	6.45	6	0.845542224
<i>neurotrophin TRK receptor signaling pathway</i>	GO:0048011	19.35	6	0.030644531
<i>neuroepithelial cell differentiation</i>	GO:0060563	9.68	6	0.483198865
<i>neuron cellular homeostasis</i>	GO:0070050	12.00	6	0.282756046
<i>neuron projection fasciculation</i>	GO:0106030	17.14	6	0.051917636
<i>semaphorin-plexin signaling pathway involved in axon guidance</i>	GO:1902287	33.33	6	0.001845789
<i>regulation of oxidative stress-induced neuron death</i>	GO:1903203	15.38	6	0.122041196
<i>positive regulation of neuron migration</i>	GO:2001224	21.43	6	0.019132265
<i>neuropeptide receptor activity</i>	GO:0008188	8.77	5	0.802389973
<i>cerebral cortex neuron differentiation</i>	GO:0021895	12.50	5	0.238332257
<i>retinal ganglion cell axon guidance</i>	GO:0031290	19.23	5	0.048070584
<i>neurotransmitter biosynthetic process</i>	GO:0042136	8.33	5	0.808932146
<i>astrocyte activation</i>	GO:0048143	16.13	5	0.090373018
<i>regulation of long-term neuronal synaptic plasticity</i>	GO:0048169	13.16	5	0.217679369
<i>axon extension involved in axon guidance</i>	GO:0048846	41.67	5	0.001440813
<i>regulation of synapse maturation</i>	GO:0090128	18.52	5	0.055343951
<i>motor neuron migration</i>	GO:0097475	41.67	5	0.001440813
<i>neurotransmitter receptor transport to plasma membrane</i>	GO:0098877	18.52	5	0.055343951
<i>neurotransmitter receptor transport, endosome to postsynaptic membrane</i>	GO:0098887	27.78	5	0.010503591
<i>neurotransmitter receptor transport to postsynaptic membrane</i>	GO:0098969	18.52	5	0.055343951
<i>neurotransmitter receptor transport, endosome to plasma membrane</i>	GO:0099639	27.78	5	0.010503591
<i>neuron projection extension involved in neuron projection guidance</i>	GO:1902284	41.67	5	0.001440813
<i>negative regulation of oxidative stress-induced neuron death</i>	GO:1903204	16.67	5	0.080739391
<i>neurotransmitter uptake</i>	GO:0001504	8.89	4	0.777762825

<i>microglial cell activation</i>	GO:0001774	9.52	4	0.567656276
<i>astrocyte activation involved in immune response</i>	GO:0002265	33.33	4	0.011062181
<i>neuropeptide hormone activity</i>	GO:0005184	10.00	4	0.551274934
<i>peripheral nervous system axon regeneration</i>	GO:0014012	57.14	4	0.001074355
<i>cerebral cortex tangential migration using cell-axon interactions</i>	GO:0021824	57.14	4	0.001074355
<i>gonadotrophin-releasing hormone neuronal migration to the hypothalamus</i>	GO:0021828	57.14	4	0.001074355
<i>hypothalamic tangential migration using cell-axon interactions</i>	GO:0021856	57.14	4	0.001074355
<i>hypothalamus gonadotrophin-releasing hormone neuron differentiation</i>	GO:0021886	50.00	4	0.002015776
<i>hypothalamus gonadotrophin-releasing hormone neuron development</i>	GO:0021888	50.00	4	0.002015776
<i>central nervous system neuron axonogenesis</i>	GO:0021955	7.55	4	1
<i>neuronal stem cell division</i>	GO:0036445	25.00	4	0.03166553
<i>neuron maturation</i>	GO:0042551	7.02	4	1
<i>regulation of axon extension involved in axon guidance</i>	GO:0048841	11.43	4	0.349042389
<i>negative regulation of axon extension involved in axon guidance</i>	GO:0048843	13.79	4	0.281813477
<i>regulation of neurotransmitter uptake</i>	GO:0051580	16.00	4	0.126897094
<i>neuroblast division</i>	GO:0055057	25.00	4	0.03166553
<i>axonogenesis involved in innervation</i>	GO:0060385	36.36	4	0.007855058
<i>regulation of neuron projection regeneration</i>	GO:0070570	9.52	4	0.567656276
<i>commissural neuron axon guidance</i>	GO:0071679	22.22	4	0.047034962
<i>neuroligin clustering involved in postsynaptic membrane assembly</i>	GO:0097118	36.36	4	0.007855058
<i>sensory neuron axon guidance</i>	GO:0097374	57.14	4	0.001074355
<i>sympathetic neuron projection extension</i>	GO:0097490	50.00	4	0.002015776
<i>sympathetic neuron projection guidance</i>	GO:0097491	50.00	4	0.002015776
<i>regulation of neuroinflammatory response</i>	GO:0150077	8.33	4	0.787838259
<i>regulation of axon guidance</i>	GO:1902667	8.16	4	0.791680328
<i>negative regulation of axon guidance</i>	GO:1902668	12.50	4	0.311872855
<i>phosphatidylinositol 3-kinase signaling</i>	GO:0014065	6.98	3	1
<i>phosphatidylinositol phosphate kinase activity</i>	GO:0016307	17.65	3	0.142872959
<i>axonal transport of mitochondrion</i>	GO:0019896	12.00	3	0.440814094
<i>spinal cord association neuron differentiation</i>	GO:0021527	15.00	3	0.202403131

<i>branchiomotor neuron axon guidance</i>	GO:0021785	30.00	3	0.037733139
<i>regulation of synaptic transmission, GABAergic</i>	GO:0032228	6.82	3	1
<i>peripheral nervous system axon ensheathment</i>	GO:0032292	8.33	3	0.758070158
<i>neuropilin signaling pathway</i>	GO:0038189	37.50	3	0.019808704
<i>VEGF-activated neuropilin signaling pathway</i>	GO:0038190	60.00	3	0.00422891
<i>neurotransmitter catabolic process</i>	GO:0042135	13.64	3	0.244763095
<i>positive regulation of glial cell differentiation</i>	GO:0045687	5.17	3	0.62507609
<i>phosphatidylinositol phosphorylation</i>	GO:0046854	5.26	3	0.62468046
<i>axon extension involved in regeneration</i>	GO:0048677	100.00	3	4.77E-04
<i>regulation of axon regeneration</i>	GO:0048679	8.11	3	0.764252827
<i>sprouting of injured axon</i>	GO:0048682	100.00	3	4.77E-04
<i>positive regulation of axon extension involved in axon guidance</i>	GO:0048842	27.27	3	0.04893742
<i>positive regulation of neurotransmitter transport</i>	GO:0051590	5.66	3	0.797111188
<i>Bergmann glial cell differentiation</i>	GO:0060020	30.00	3	0.037733139
<i>regulation of glial cell proliferation</i>	GO:0060251	7.89	3	1
<i>dopaminergic neuron differentiation</i>	GO:0071542	7.50	3	1
<i>regulation of retinal ganglion cell axon guidance</i>	GO:0090259	33.33	3	0.028010774
<i>neurotransmitter receptor transport postsynaptic membrane to endosome</i>	GO:0098968	37.50	3	0.019808704
<i>protein localization to axon</i>	GO:0099612	25.00	3	0.0615625
<i>anterograde axonal protein transport</i>	GO:0099641	23.08	3	0.075529828
<i>neuron projection arborization</i>	GO:0140058	16.67	3	0.162040558
<i>positive regulation of retinal ganglion cell axon guidance</i>	GO:1902336	60.00	3	0.00422891
<i>VEGF-activated neuropilin signaling pathway involved in axon guidance</i>	GO:1902378	75.00	3	0.001796256
<i>positive regulation of axon guidance</i>	GO:1902669	25.00	3	0.0615625
<i>regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway</i>	GO:1903376	33.33	3	0.028010774