

Analysis Type:	PANTHEF
Annotation Version and Release Date:	GO Ontol
Analyzed List:	Client Tex
Reference List:	Rattus no
Bonferroni correction:	TRUE
Bonferroni count:	10689

GO of NGF identified top 100 genes

<b>GO biological process complete</b>	<b>Rattus no</b>
positive regulation of p38MAPK cascade (GO:1900745)	21
regulation of p38MAPK cascade (GO:1900744)	32
response to heat (GO:0009408)	123
positive regulation of stress-activated MAPK cascade (GO:0032874)	147
positive regulation of stress-activated protein kinase signaling cascade (GO:0070304)	148
response to hydrogen peroxide (GO:0042542)	155
regulation of reactive oxygen species metabolic process (GO:2000377)	181
response to ionizing radiation (GO:0010212)	189
response to estradiol (GO:0032355)	245
response to reactive oxygen species (GO:0000302)	245
response to hypoxia (GO:0001666)	397
response to decreased oxygen levels (GO:0036293)	409
response to oxidative stress (GO:0006979)	436
response to wounding (GO:0009611)	478
response to oxygen levels (GO:0070482)	447
positive regulation of MAPK cascade (GO:0043410)	488
aging (GO:0007568)	415
regulation of mitotic cell cycle (GO:0007346)	493
response to molecule of bacterial origin (GO:0002237)	418
response to peptide (GO:1901652)	546
response to radiation (GO:0009314)	491
response to cytokine (GO:0034097)	833
response to drug (GO:0042493)	627
response to inorganic substance (GO:0010035)	672
regulation of MAPK cascade (GO:0043408)	697
response to biotic stimulus (GO:0009607)	853
positive regulation of cell death (GO:0010942)	674
response to other organism (GO:0051707)	827
response to external biotic stimulus (GO:0043207)	831
cellular response to cytokine stimulus (GO:0071345)	696
response to organonitrogen compound (GO:0010243)	1124
regulation of cell cycle (GO:0051726)	923
response to nitrogen compound (GO:1901698)	1234
response to abiotic stimulus (GO:0009628)	1305

regulation of programmed cell death (GO:0043067)	1519
negative regulation of apoptotic process (GO:0043066)	905
regulation of apoptotic process (GO:0042981)	1500
negative regulation of programmed cell death (GO:0043069)	921
response to organic cyclic compound (GO:0014070)	1260
response to hormone (GO:0009725)	993
regulation of cell death (GO:0010941)	1662
defense response (GO:0006952)	942
positive regulation of protein modification process (GO:0031401)	1131
negative regulation of cell death (GO:0060548)	1020
positive regulation of phosphorylation (GO:0042327)	969
response to lipid (GO:0033993)	1167
intracellular signal transduction (GO:0035556)	1308
regulation of cell proliferation (GO:0042127)	1631
positive regulation of phosphorus metabolic process (GO:0010562)	1094
positive regulation of phosphate metabolic process (GO:0045937)	1094
positive regulation of cellular protein metabolic process (GO:0032270)	1445
positive regulation of protein metabolic process (GO:0051247)	1538
positive regulation of catalytic activity (GO:0043085)	1345
reproductive process (GO:0022414)	1435
reproduction (GO:0000003)	1437
response to stress (GO:0006950)	2955
response to external stimulus (GO:0009605)	1935
multi-organism process (GO:0051704)	1894
response to endogenous stimulus (GO:0009719)	1477
tissue development (GO:0009888)	1620
response to oxygen-containing compound (GO:1901700)	1817
regulation of protein modification process (GO:0031399)	1677
positive regulation of molecular function (GO:0044093)	1681
positive regulation of response to stimulus (GO:0048584)	1842
regulation of catalytic activity (GO:0050790)	2150
positive regulation of cellular metabolic process (GO:0031325)	2994
regulation of cellular protein metabolic process (GO:0032268)	2406
positive regulation of metabolic process (GO:0009893)	3195
regulation of protein metabolic process (GO:0051246)	2572
cellular response to chemical stimulus (GO:0070887)	2421
response to organic substance (GO:0010033)	3012
positive regulation of macromolecule metabolic process (GO:0010604)	2953
positive regulation of nitrogen compound metabolic process (GO:0051173)	2876
regulation of developmental process (GO:0050793)	2419
regulation of molecular function (GO:0065009)	2778
regulation of multicellular organismal process (GO:0051239)	2798
cell differentiation (GO:0030154)	3370
negative regulation of cellular process (GO:0048523)	4337
negative regulation of biological process (GO:0048519)	4748
cellular developmental process (GO:0048869)	3445
positive regulation of cellular process (GO:0048522)	4867

positive regulation of biological process (GO:0048518)	5369
response to chemical (GO:0042221)	5055
anatomical structure development (GO:0048856)	4991
developmental process (GO:0032502)	5312
system development (GO:0048731)	4282
multicellular organism development (GO:0007275)	4662
regulation of cellular metabolic process (GO:0031323)	5370
regulation of primary metabolic process (GO:0080090)	5220
regulation of macromolecule metabolic process (GO:0060255)	5236
regulation of metabolic process (GO:0019222)	5686
regulation of nitrogen compound metabolic process (GO:0051171)	5097
response to stimulus (GO:0050896)	7990
biological regulation (GO:0065007)	11575
biological_process (GO:0008150)	16507

R Overrepresentation Test (release 20170413)  
 ogy database Released 2017-09-26  
 t Box Input (Rattus norvegicus)  
 rvegicus (all genes in database)

**Client Te Client Te Client Te Client Te Client Text Box Input (P-value)**

5	0.1 +	51.35	0.00065
5	0.15 +	33.7	0.00515
7	0.57 +	12.27	0.0212
8	0.68 +	11.74	0.00532
8	0.69 +	11.66	0.0056
8	0.72 +	11.13	0.00789
8	0.84 +	9.53	0.0247
8	0.88 +	9.13	0.0339
10	1.14 +	8.8	0.00262
10	1.14 +	8.8	0.00262
12	1.84 +	6.52	0.00381
12	1.9 +	6.33	0.00521
12	2.02 +	5.94	0.0101
13	2.22 +	5.87	0.00394
12	2.07 +	5.79	0.0131
13	2.26 +	5.74	0.00496
11	1.92 +	5.72	0.0422
13	2.29 +	5.69	0.00556
11	1.94 +	5.68	0.0452
14	2.53 +	5.53	0.00273
12	2.28 +	5.27	0.0342
19	3.86 +	4.92	9.9E-05
14	2.91 +	4.82	0.014
15	3.12 +	4.81	0.00564
15	3.23 +	4.64	0.00889
18	3.96 +	4.55	0.00083
14	3.13 +	4.48	0.0321
17	3.83 +	4.43	0.00286
17	3.85 +	4.41	0.00306
14	3.23 +	4.34	0.0463
22	5.21 +	4.22	8.9E-05
18	4.28 +	4.21	0.00263
24	5.72 +	4.19	1.8E-05
25	6.05 +	4.13	1.1E-05

29	7.04 +	4.12	3.6E-07
17	4.2 +	4.05	0.0099
28	6.96 +	4.03	1.4E-06
17	4.27 +	3.98	0.0126
23	5.84 +	3.94	0.00014
18	4.6 +	3.91	0.00756
30	7.71 +	3.89	5.9E-07
17	4.37 +	3.89	0.017
20	5.24 +	3.81	0.00244
18	4.73 +	3.81	0.0111
17	4.49 +	3.78	0.0249
20	5.41 +	3.7	0.004
22	6.07 +	3.63	0.00129
27	7.56 +	3.57	4.5E-05
18	5.07 +	3.55	0.0296
18	5.07 +	3.55	0.0296
23	6.7 +	3.43	0.00168
23	7.13 +	3.22	0.00503
20	6.24 +	3.21	0.0354
21	6.65 +	3.16	0.0247
21	6.66 +	3.15	0.0252
43	13.7 +	3.14	9.4E-09
28	8.97 +	3.12	0.0004
27	8.78 +	3.07	0.00102
21	6.85 +	3.07	0.0388
23	7.51 +	3.06	0.0123
25	8.43 +	2.97	0.00669
23	7.78 +	2.96	0.0222
23	7.79 +	2.95	0.0231
25	8.54 +	2.93	0.00861
29	9.97 +	2.91	0.00097
40	13.88 +	2.88	1.3E-06
31	11.16 +	2.78	0.00084
40	14.82 +	2.7	9.2E-06
32	11.93 +	2.68	0.00108
30	11.23 +	2.67	0.00345
37	13.97 +	2.65	9.3E-05
36	13.69 +	2.63	0.0002
35	13.34 +	2.62	0.00036
28	11.22 +	2.5	0.0373
31	12.88 +	2.41	0.02
31	12.97 +	2.39	0.0233
36	15.63 +	2.3	0.00575
46	20.11 +	2.29	5.8E-05
50	22.02 +	2.27	8.8E-06
36	15.97 +	2.25	0.00987
49	22.57 +	2.17	7.3E-05

53	24.9 +	2.13	2E-05
48	23.44 +	2.05	0.00083
47	23.14 +	2.03	0.00167
50	24.63 +	2.03	0.00046
40	19.86 +	2.01	0.0332
43	21.62 +	1.99	0.0153
49	24.9 +	1.97	0.00199
47	24.21 +	1.94	0.00673
47	24.28 +	1.94	0.00739
51	26.37 +	1.93	0.00155
45	23.64 +	1.9	0.0253
67	37.05 +	1.81	1.5E-05
78	53.67 +	1.45	0.00522
95	76.54 +	1.24	0.0122

Analysis Type:	PANTHER Overrepresentation Test (
Annotation Version and Release Date:	GO Ontology database Released 20
Analyzed List:	Client Text Box Input (Rattus norvegic
Reference List:	Rattus norvegicus (all genes in datab
Bonferroni correction:	TRUE
Bonferroni count:	10689

GO of top 100 genes by fold changes

<b>GO biological process complete</b>	<b>Rattus n</b>	<b>Client Tε</b>	<b>Client Tε</b>	<b>Client Tε</b>
positive regulation of adenylate cyclase activity (GO:00	32	5	0.15	+
positive regulation of lyase activity (GO:0051349)	44	5	0.21	+
positive regulation of cyclase activity (GO:0031281)	44	5	0.21	+
positive regulation of cAMP metabolic process (GO:003	79	7	0.37	+
positive regulation of cAMP biosynthetic process (GO:C	70	6	0.33	+
positive regulation of endothelial cell proliferation (GO:(	72	6	0.34	+
cAMP-mediated signaling (GO:0019933)	83	6	0.39	+
positive regulation of cyclic nucleotide metabolic proces	97	7	0.45	+
positive regulation of cyclic nucleotide biosynthetic proc	86	6	0.4	+
regulation of cAMP metabolic process (GO:0030814)	129	7	0.6	+
positive regulation of purine nucleotide metabolic proce	130	7	0.61	+
positive regulation of nucleotide metabolic process (GC	130	7	0.61	+
positive regulation of epithelial cell proliferation (GO:00	181	9	0.85	+
defense response (GO:0006952)	942	17	4.41	+
response to stress (GO:0006950)	2955	35	13.84	+
response to stimulus (GO:0050896)	7990	62	37.42	+

release 20170413)  
17-09-26  
cus)  
ase)

**Client Text Box Input (P-value)**

33.37	0.00541
24.27	0.0254
24.27	0.0254
18.92	0.00121
18.3	0.0122
17.79	0.0143
15.44	0.0322
15.41	0.00474
14.9	0.0394
11.59	0.0309
11.5	0.0325
11.5	0.0325
10.62	0.00231
3.85	0.0196
2.53	0.00095
1.66	0.00714

<b>Gene Name</b>	<b>Key Word</b>	<b>Associated Publications</b>
Bdnf	nerve injury	1267
Cntf	nerve injury	404
Cp	nerve injury	144
Ttr	nerve injury	17
Manf	nerve injury	9
Comt	nerve injury	5
Serping1	nerve injury	5
Cst3	nerve injury	4
Gabra5	nerve injury	3
C1s	nerve injury	3
Snph	neuronal regeneration	2
Ncdn	neuronal regeneration	2
Cryba1	nerve injury	2
Cryab	nerve injury	2
Aak1	nerve injury	1
Fxyd5	axonal regeneration	1
Dgat1	nerve injury	1
Gprc5b	neuronal regeneration	1
Tirap	nerve injury	1
Plxnd1	neuronal regeneration	1
Plin2	nerve injury	1
Arf2	neuronal regeneration	1
Bcl10	nerve injury	1
Tmem60	None	0
Ifitm2	None	0
Ptk7	None	0
Kcnh5	None	0
Xdh	None	0
Impg2	None	0
Hpcal4	None	0
RGD1309748	None	0
Ifnlr1	None	0
Prr36	None	0
Gabrg2	None	0
Tmed6	None	0
Emp3	None	0
Gpr83	None	0
Irak3	None	0
Gpr75	None	0
Rbp4	None	0
Kctd20	None	0
Coq9	None	0
Wdr37	None	0
Plp2	None	0
Slc46a1	None	0

LOC100910275	None	0
Kctd14	None	0
Kcnab2	None	0
Tulp2	None	0
Nxph3	None	0
Sema4g	None	0
Coq8b	None	0
Ostc	None	0
Fbxo4	None	0
Cpped1	None	0
Coq10b	None	0
Slc6a13	None	0
Pi4kb	None	0
Clic1	None	0
43160	None	0
Ap5b1	None	0
Slc40a1	None	0
Ifitm3	None	0
Abhd5	None	0
Gpr85	None	0