Table 1-6 - Biological processes associated with mRNAs co-immunoprecipitated with hnRNP K and regulated by BDNF as assessed by Gene Ontology

GO biological process	Rattus norvegicus (reference list)	uploaded list	(expected)	(over/under)	(fold enrichment)	(P-value)
organelle transport along microtubule (GO:0072384)	55	35	14.20	+	2.47	1.81E-02
central nervous system neuron development (GO:0021954)	85	53	21.94	+	2.42	1.07E-04
negative regulation of protein depolymerization (GO:1901880)	55	34	14.20	+	2.40	4.55E-02
dendrite development (GO:0016358)	106	65	27.36	+	2.38	5.08E-06
membrane docking (GO:0022406)	64	38	16.52	+	2.30	3.32E-02
regulation of protein depolymerization (GO:1901879)	75	44	19.36	+	2.27	8.34E-03
regulation of dendrite morphogenesis (GO:0048814)	94	55	24.26	+	2.27	4.49E-04
neurotransmitter secretion (GO:0007269)	102	59	26.33	+	2.24	2.24E-04
signal release from synapse (GO:0099643)	102	59	26.33	+	2.24	2.24E-04
presynaptic process involved in chemical synaptic transmission (GO:0099531)	106	61	27.36	+	2.23	1.58E-04
regulation of protein complex disassembly (GO:0043244)	87	50	22.46	+	2.23	2.91E-03
regulation of neurotransmitter transport (GO:0051588)	70	40	18.07	+	2.21	4.57E-02
positive regulation of dendrite development (GO:1900006)	91	52	23.49	+	2.21	2.04E-03
establishment of vesicle localization (GO:0051650)	160	91	41.30	+	2.20	1.16E-07
vesicle localization (GO:0051648)	169	96	43.62	+	2.20	3.48E-08
synaptic vesicle localization (GO:0097479)	110	62	28.39	+	2.18	2.50E-04
regulation of protein dephosphorylation (GO:0035304)	88	49	22.71	+	2.16	9.02E-03
amino acid transport (GO:0006865)	90	50	23.23	+	2.15	7.53E-03
Golgi organization (GO:0007030)	90	50	23.23	+	2.15	7.53E-03
synaptic vesicle transport (GO:0048489)	108	60	27.88	+	2.15	6.67E-04
establishment of synaptic vesicle localization (GO:0097480)	108	60	27.88	+	2.15	6.67E-04
positive regulation of exocytosis (GO:0045921)	83	46	21.42	+	2.15	2.12E-02
regulation of axonogenesis (GO:0050770)	181	100	46.72	+	2.14	5.85E-08
protein dephosphorylation (GO:0006470)	176	97	45.43	+	2.14	1.36E-07
regulation of synapse organization (GO:0050807)	120	66	30.97	+	2.13	2.25E-04
negative regulation of protein serine/threonine kinase activity (GO:0071901)	122	67	31.49	+	2.13	1.87E-04
hippocampus development (GO:0021766)	106	58	27.36	+	2.12	1.75E-03
regulation of potassium ion transport (GO:0043266)	86	47	22.20	+	2.12	2.39E-02
regulation of proteasomal ubiquitin-dependent protein catabolic process (GO:0032434)	105	57	27.10	+	2.10	2.83E-03
synaptic vesicle cycle (GO:0099504)	94	51	24.26	+	2.10	1.14E-02
regulation of extent of cell growth (GO:0061387)	115	62	29.68	+	2.09	1.13E-03
regulation of cell morphogenesis involved in differentiation (GO:0010769)	366	197	94.47	+	2.09	8.25E-17
regulation of neuron projection development (GO:0010975)	498	268	128.54	+	2.09	8.31E-24
negative regulation of neuron projection development (GO:0010977)	147	79	37.94	+	2.08	2.81E-05

negative regulation of neuron differentiation (GO:0045665)	222	119	57.30	+	2.08	4.41E-09
regulation of dendrite development (GO:0050773)	157	84	40.52	+	2.07	1.12E-05
negative regulation of neurogenesis (GO:0050768)	285	152	73.56	+	2.07	4.36E-12
neuron projection development (GO:0031175)	592	315	152.80	+	2.06	1.15E-27
regulation of cell size (GO:0008361)	192	102	49.56	+	2.06	3.10E-07
neurotransmitter transport (GO:0006836)	147	78	37.94	+	2.06	5.95E-05
negative regulation of cell morphogenesis involved in differentiation (GO:0010771)	115	61	29.68	+	2.06	2.41E-03
negative regulation of cell development (GO:0010721)	340	180	87.76	+	2.05	1.85E-14
regulation of synapse structure or activity (GO:0050803)	280	148	72.27	+	2.05	2.11E-11
regulation of proteasomal protein catabolic process (GO:0061136)	140	74	36.13	+	2.05	1.65E-04
negative regulation of nervous system development (GO:0051961)	307	162	79.24	+	2.04	1.20E-12
regulation of neurotransmitter levels (GO:0001505)	199	105	51.36	+	2.04	2.36E-07
neuron projection morphogenesis (GO:0048812)	425	224	109.69	+	2.04	2.20E-18
positive regulation of neuron projection development (GO:0010976)	293	154	75.62	+	2.04	9.15E-12
positive regulation of proteolysis involved in cellular protein catabolic process (GO:1903052)	99	52	25.55	+	2.04	2.24E-02
synapse organization (GO:0050808)	139	73	35.88	+	2.03	2.61E-04
regulation of synaptic plasticity (GO:0048167)	181	95	46.72	+	2.03	2.59E-06
regulation of axon extension (GO:0030516)	101	53	26.07	+	2.03	1.86E-02
Golgi vesicle transport (GO:0048193)	180	94	46.46	+	2.02	4.08E-06
regulation of Rho protein signal transduction (GO:0035023)	115	60	29.68	+	2.02	5.04E-03
regulation of proteolysis involved in cellular protein catabolic process (GO:1903050)	163	85	42.07	+	2.02	2.83E-05
axon development (GO:0061564)	359	187	92.66	+	2.02	1.97E-14
mitotic cell cycle phase transition (GO:0044772)	121	63	31.23	+	2.02	2.89E-03
negative regulation of cell projection organization (GO:0031345)	173	90	44.65	+	2.02	1.12E-05
axonogenesis (GO:0007409)	325	169	83.88	+	2.01	9.69E-13
regulation of neuron apoptotic process (GO:0043523)	243	126	62.72	+	2.01	8.33E-09
learning (GO:0007612)	159	82	41.04	+	2.00	8.45E-05
cell cycle phase transition (GO:0044770)	128	66	33.04	+	2.00	2.16E-03
regulation of exocytosis (GO:0017157)	183	94	47.23	+	1.99	9.10E-06
positive regulation of cellular protein catabolic process (GO:1903364)	113	58	29.17	+	1.99	1.25E-02
neuron projection guidance (GO:0097485)	195	100	50.33	+	1.99	2.99E-06
negative regulation of neuron apoptotic process (GO:0043524)	160	82	41.30	+	1.99	1.10E-04
protein polyubiquitination (GO:0000209)	162	83	41.81	+	1.99	9.13E-05
positive regulation of cell growth (GO:0030307)	162	83	41.81	+	1.99	9.13E-05
phospholipid biosynthetic process (GO:0008654)	123	63	31.75	+	1.98	4.92E-03
cell morphogenesis involved in neuron differentiation (GO:0048667)	389	199	100.40	+	1.98	1.02E-14
dephosphorylation (GO:0016311)	270	138	69.69	+	1.98	1.97E-09
negative regulation of MAPK cascade (GO:0043409)	155	79	40.01	+	1.97	2.49E-04

regulation of neuron differentiation (GO:0045664)	662	337	170.87	+	1.97	1.93E-26
regulation of cellular protein catabolic process (GO:1903362)	183	93	47.23	+	1.97	1.84E-05
developmental growth involved in morphogenesis (GO:0060560)	122	62	31.49	+	1.97	7.71E-03
cerebellum development (GO:0021549)	126	64	32.52	+	1.97	5.30E-03
axon guidance (GO:0007411)	193	98	49.81	+	1.97	7.27E-06
pallium development (GO:0021543)	203	103	52.40	+	1.97	2.87E-06
modulation of synaptic transmission (GO:0050804)	340	172	87.76	+	1.96	5.81E-12
regulation of cell projection organization (GO:0031344)	657	331	169.58	+	1.95	3.70E-25
regulation of ion transmembrane transporter activity (GO:0032412)	191	96	49.30	+	1.95	1.75E-05
regulation of transmembrane transporter activity (GO:0022898)	197	99	50.85	+	1.95	1.00E-05
limbic system development (GO:0021761)	136	68	35.10	+	1.94	4.17E-03
regulation of transporter activity (GO:0032409)	210	105	54.20	+	1.94	4.22E-06
regulation of neuron death (GO:1901214)	318	159	82.08	+	1.94	1.80E-10
positive regulation of cell projection organization (GO:0031346)	372	186	96.02	+	1.94	1.15E-12
regulation of Ras protein signal transduction (GO:0046578)	200	100	51.62	+	1.94	1.07E-05
regulation of cell morphogenesis (GO:0022604)	582	289	150.22	+	1.92	1.10E-20
organelle fusion (GO:0048284)	127	63	32.78	+	1.92	1.36E-02
regulation of cellular component size (GO:0032535)	359	178	92.66	+	1.92	1.08E-11
establishment or maintenance of cell polarity (GO:0007163)	152	75	39.23	+	1.91	1.85E-03
regulation of small GTPase mediated signal transduction (GO:0051056)	223	110	57.56	+	1.91	3.47E-06
metencephalon development (GO:0022037)	138	68	35.62	+	1.91	6.84E-03
regulation of neurogenesis (GO:0050767)	802	395	207.00	+	1.91	1.06E-28
establishment of protein localization to membrane (GO:0090150)	173	85	44.65	+	1.90	3.65E-04
negative regulation of cell growth (GO:0030308)	173	85	44.65	+	1.90	3.65E-04
chemical synaptic transmission (GO:0007268)	334	164	86.21	+	1.90	3.06E-10
trans-synaptic signaling (GO:0099537)	334	164	86.21	+	1.90	3.06E-10
synaptic signaling (GO:0099536)	334	164	86.21	+	1.90	3.06E-10
anterograde trans-synaptic signaling (GO:0098916)	334	164	86.21	+	1.90	3.06E-10
establishment of organelle localization (GO:0051656)	314	154	81.05	+	1.90	1.98E-09
telencephalon development (GO:0021537)	292	143	75.37	+	1.90	1.53E-08
positive regulation of neuron differentiation (GO:0045666)	384	188	99.11	+	1.90	5.55E-12
neuron development (GO:0048666)	760	372	196.16	+	1.90	2.43E-26
regulation of nervous system development (GO:0051960)	897	439	231.52	+	1.90	1.08E-31
negative regulation of protein kinase activity (GO:0006469)	229	112	59.11	+	1.89	3.87E-06
learning or memory (GO:0007611)	272	133	70.20	+	1.89	9.87E-08
positive regulation of synaptic transmission (GO:0050806)	131	64	33.81	+	1.89	1.84E-02
Ras protein signal transduction (GO:0007265)	129	63	33.30	+	1.89	2.22E-02
organelle localization (GO:0051640)	385	188	99.37	+	1.89	7.04E-12

negative regulation of neuron death (GO:1901215)	209	102	53.94	+	1.89	2.48E-05
endosomal transport (GO:0016197)	191	93	49.30	+	1.89	1.32E-04
positive regulation of cell morphogenesis involved in differentiation (GO:0010770)	185	90	47.75	+	1.88	2.32E-04
gliogenesis (GO:0042063)	218	106	56.27	+	1.88	1.50E-05
phospholipid metabolic process (GO:0006644)	249	121	64.27	+	1.88	1.16E-06
maintenance of location (GO:0051235)	132	64	34.07	+	1.88	2.33E-02
cerebral cortex development (GO:0021987)	128	62	33.04	+	1.88	3.39E-02
negative regulation of kinase activity (GO:0033673)	246	119	63.49	+	1.87	2.13E-06
regulation of cell development (GO:0060284)	971	469	250.62	+	1.87	8.42E-33
brain development (GO:0007420)	821	396	211.90	+	1.87	5.07E-27
glycerophospholipid metabolic process (GO:0006650)	168	81	43.36	+	1.87	1.56E-03
positive regulation of cellular catabolic process (GO:0031331)	195	94	50.33	+	1.87	1.76E-04
vesicle organization (GO:0016050)	206	99	53.17	+	1.86	8.74E-05
protein localization to plasma membrane (GO:0072659)	150	72	38.72	+	1.86	8.35E-03
regulation of cellular catabolic process (GO:0031329)	311	149	80.27	+	1.86	2.56E-08
vacuolar transport (GO:0007034)	228	109	58.85	+	1.85	2.16E-05
positive regulation of protein catabolic process (GO:0045732)	182	87	46.98	+	1.85	8.10E-04
lipid modification (GO:0030258)	159	76	41.04	+	1.85	4.98E-03
head development (GO:0060322)	861	411	222.23	+	1.85	2.80E-27
forebrain development (GO:0030900)	443	211	114.34	+	1.85	1.52E-12
regulation of cell growth (GO:0001558)	395	188	101.95	+	1.84	7.06E-11
positive regulation of nervous system development (GO:0051962)	540	257	139.38	+	1.84	8.44E-16
peptidyl-tyrosine modification (GO:0018212)	143	68	36.91	+	1.84	2.21E-02
positive regulation of growth (GO:0045927)	263	125	67.88	+	1.84	2.19E-06
peptidyl-tyrosine phosphorylation (GO:0018108)	141	67	36.39	+	1.84	2.66E-02
positive regulation of developmental growth (GO:0048639)	179	85	46.20	+	1.84	1.47E-03
central nervous system development (GO:0007417)	1018	482	262.75	+	1.83	8.36E-32
exocytosis (GO:0006887)	207	98	53.43	+	1.83	2.07E-04
regulation of protein catabolic process (GO:0042176)	311	147	80.27	+	1.83	9.11E-08
peptidyl-serine phosphorylation (GO:0018105)	144	68	37.17	+	1.83	2.77E-02
hindbrain development (GO:0030902)	178	84	45.94	+	1.83	2.22E-03
protein transport (GO:0015031)	946	445	244.17	+	1.82	1.78E-28
regulation of membrane potential (GO:0042391)	375	176	96.79	+	1.82	1.59E-09
cell division (GO:0051301)	277	130	71.50	+	1.82	2.10E-06
protein localization to cell periphery (GO:1990778)	162	76	41.81	+	1.82	9.75E-03
peptidyl-serine modification (GO:0018209)	160	75	41.30	+	1.82	1.17E-02
central nervous system neuron differentiation (GO:0021953)	192	90	49.56	+	1.82	1.13E-03
positive regulation of neurogenesis (GO:0050769)	476	223	122.86	+	1.82	1.18E-12

regulation of actin filament length (GO:0030832)	158	74	40.78	+	1.81	1.41E-02
regulation of actin polymerization or depolymerization (GO:0008064)	158	74	40.78	+	1.81	1.41E-02
glial cell differentiation (GO:0010001)	171	80	44.14	+	1.81	5.79E-03
negative regulation of cellular component organization (GO:0051129)	633	296	163.38	+	1.81	1.51E-17
regulation of catabolic process (GO:0009894)	455	212	117.44	+	1.81	1.13E-11
neuron differentiation (GO:0030182)	968	451	249.85	+	1.81	5.02E-28
membrane fusion (GO:0061025)	146	68	37.68	+	1.80	4.30E-02
cellular response to insulin stimulus (GO:0032869)	159	74	41.04	+	1.80	1.76E-02
cognition (GO:0050890)	303	141	78.21	+	1.80	6.58E-07
establishment of protein localization (GO:0045184)	1072	498	276.69	+	1.80	4.80E-31
negative regulation of protein phosphorylation (GO:0001933)	399	185	102.98	+	1.80	1.09E-09
negative regulation of intracellular signal transduction (GO:1902532)	466	216	120.28	+	1.80	1.02E-11
negative regulation of transferase activity (GO:0051348)	274	127	70.72	+	1.80	6.97E-06
regulation of developmental growth (GO:0048638)	337	156	86.98	+	1.79	9.75E-08
generation of neurons (GO:0048699)	1493	691	385.35	+	1.79	2.20E-44
positive regulation of catabolic process (GO:0009896)	255	118	65.82	+	1.79	2.94E-05
secretion by cell (GO:0032940)	383	177	98.85	+	1.79	4.76E-09
positive regulation of apoptotic signaling pathway (GO:2001235)	169	78	43.62	+	1.79	1.29E-02
protein localization to membrane (GO:0072657)	297	137	76.66	+	1.79	2.09E-06
negative regulation of protein modification process (GO:0031400)	527	243	136.02	+	1.79	3.01E-13
regulation of vesicle-mediated transport (GO:0060627)	454	209	117.18	+	1.78	5.69E-11
signal release (GO:0023061)	176	81	45.43	+	1.78	9.14E-03
locomotory behavior (GO:0007626)	224	103	57.82	+	1.78	3.73E-04
nervous system development (GO:0007399)	2238	1029	577.64	+	1.78	1.49E-68
regulation of autophagy (GO:0010506)	198	91	51.10	+	1.78	2.22E-03
regulation of protein polymerization (GO:0032271)	172	79	44.39	+	1.78	1.32E-02
cell projection organization (GO:0030030)	952	437	245.72	+	1.78	9.71E-26
adult behavior (GO:0030534)	170	78	43.88	+	1.78	1.59E-02
negative regulation of phosphorylation (GO:0042326)	436	200	112.53	+	1.78	2.99E-10
cell projection morphogenesis (GO:0048858)	636	291	164.15	+	1.77	6.05E-16
single-organism behavior (GO:0044708)	470	215	121.31	+	1.77	4.32E-11
transmembrane receptor protein tyrosine kinase signaling pathway (GO:0007169)	339	155	87.50	+	1.77	2.70E-07
glycerolipid metabolic process (GO:0046486)	245	112	63.24	+	1.77	1.34E-04
neurogenesis (GO:0022008)	1608	734	415.03	+	1.77	1.91E-45
autophagy (GO:0006914)	301	137	77.69	+	1.76	4.79E-06
behavior (GO:0007610)	633	288	163.38	+	1.76	1.96E-15
plasma membrane organization (GO:0007009)	209	95	53.94	+	1.76	1.98E-03
endomembrane system organization (GO:0010256)	419	190	108.15	+	1.76	3.45E-09

modification-dependent protein catabolic process (GO:0019941)	400	181	103.24	+	1.75	1.46E-08
positive regulation of cell development (GO:0010720)	575	260	148.41	+	1.75	2.31E-13
ubiquitin-dependent protein catabolic process (GO:0006511)	392	177	101.18	+	1.75	3.02E-08
cell part morphogenesis (GO:0032990)	660	298	170.35	+	1.75	1.27E-15
single-organism membrane organization (GO:0044802)	605	273	156.15	+	1.75	4.70E-14
modification-dependent macromolecule catabolic process (GO:0043632)	408	184	105.31	+	1.75	1.26E-08
regulation of endocytosis (GO:0030100)	213	96	54.98	+	1.75	2.47E-03
intracellular protein transport (GO:0006886)	587	264	151.51	+	1.74	2.46E-13
protein autophosphorylation (GO:0046777)	198	89	51.10	+	1.74	7.23E-03
cell morphogenesis involved in differentiation (GO:0000904)	554	249	142.99	+	1.74	2.13E-12
small GTPase mediated signal transduction (GO:0007264)	336	151	86.72	+	1.74	1.53E-06
actin filament organization (GO:0007015)	185	83	47.75	+	1.74	1.76E-02
signal transduction by protein phosphorylation (GO:0023014)	214	96	55.23	+	1.74	3.02E-03
connective tissue development (GO:0061448)	212	95	54.72	+	1.74	3.62E-03
negative regulation of cell migration (GO:0030336)	217	97	56.01	+	1.73	3.07E-03
regulation of ion transmembrane transport (GO:0034765)	396	177	102.21	+	1.73	6.66E-08
cellular component disassembly (GO:0022411)	282	126	72.79	+	1.73	6.41E-05
actin cytoskeleton organization (GO:0030036)	383	171	98.85	+	1.73	1.62E-07
actin filament-based process (GO:0030029)	424	189	109.44	+	1.73	1.65E-08
negative regulation of phosphorus metabolic process (GO:0010563)	552	246	142.47	+	1.73	8.07E-12
negative regulation of phosphate metabolic process (GO:0045936)	552	246	142.47	+	1.73	8.07E-12
regulation of protein modification by small protein conjugation or removal (GO:1903320)	211	94	54.46	+	1.73	5.28E-03
regulation of transmembrane transport (GO:0034762)	411	183	106.08	+	1.73	4.03E-08
regulation of cation transmembrane transport (GO:1904062)	227	101	58.59	+	1.72	2.20E-03
intracellular transport (GO:0046907)	904	402	233.33	+	1.72	6.36E-21
single-organism carbohydrate metabolic process (GO:0044723)	470	209	121.31	+	1.72	1.42E-09
phosphorus metabolic process (GO:0006793)	1725	767	445.23	+	1.72	9.70E-44
phosphate-containing compound metabolic process (GO:0006796)	1723	766	444.72	+	1.72	1.19E-43
negative regulation of cellular component movement (GO:0051271)	259	115	66.85	+	1.72	3.83E-04
establishment of localization in cell (GO:0051649)	1170	519	301.98	+	1.72	8.78E-28
regulation of anatomical structure size (GO:0090066)	519	230	133.96	+	1.72	1.22E-10
apoptotic signaling pathway (GO:0097190)	271	120	69.95	+	1.72	2.29E-04
secretion (GO:0046903)	511	226	131.89	+	1.71	2.51E-10
striated muscle cell differentiation (GO:0051146)	197	87	50.85	+	1.71	1.86E-02
regulation of binding (GO:0051098)	315	139	81.30	+	1.71	2.38E-05
protein localization (GO:0008104)	1523	672	393.09	+	1.71	1.33E-36
regulation of protein ubiquitination (GO:0031396)	186	82	48.01	+	1.71	3.79E-02
proteasomal protein catabolic process (GO:0010498)	211	93	54.46	+	1.71	9.29E-03

regulation of cellular component biogenesis (GO:0044087)	774	341	199.77	+	1.71	1.09E-16
protein targeting (GO:0006605)	318	140	82.08	+	1.71	2.41E-05
regulation of protein binding (GO:0043393)	184	81	47.49	+	1.71	4.54E-02
negative regulation of cell differentiation (GO:0045596)	665	292	171.64	+	1.70	1.04E-13
negative regulation of growth (GO:0045926)	246	108	63.49	+	1.70	1.63E-03
single-organism cellular localization (GO:1902580)	695	305	179.38	+	1.70	2.08E-14
regulation of cellular localization (GO:0060341)	839	368	216.55	+	1.70	6.16E-18
protein homooligomerization (GO:0051260)	283	124	73.04	+	1.70	2.39E-04
regulation of cytoskeleton organization (GO:0051493)	418	183	107.89	+	1.70	1.52E-07
negative regulation of locomotion (GO:0040013)	263	115	67.88	+	1.69	8.18E-04
rhythmic process (GO:0048511)	341	149	88.01	+	1.69	1.23E-05
regulation of actin cytoskeleton organization (GO:0032956)	284	124	73.30	+	1.69	2.88E-04
carbohydrate homeostasis (GO:0033500)	213	93	54.98	+	1.69	1.35E-02
protein phosphorylation (GO:0006468)	781	341	201.58	+	1.69	4.07E-16
glucose homeostasis (GO:0042593)	213	93	54.98	+	1.69	1.35E-02
regulation of protein serine/threonine kinase activity (GO:0071900)	433	189	111.76	+	1.69	9.10E-08
cellular localization (GO:0051641)	1645	718	424.58	+	1.69	5.60E-38
glycoprotein metabolic process (GO:0009100)	282	123	72.79	+	1.69	3.44E-04
cellular macromolecule localization (GO:0070727)	1093	476	282.11	+	1.69	1.63E-23
intracellular signal transduction (GO:0035556)	1302	567	336.05	+	1.69	9.74E-29
response to insulin (GO:0032868)	246	107	63.49	+	1.69	2.82E-03
small molecule catabolic process (GO:0044282)	246	107	63.49	+	1.69	2.82E-03
establishment of protein localization to organelle (GO:0072594)	267	116	68.91	+	1.68	9.91E-04
regulation of GTPase activity (GO:0043087)	495	215	127.76	+	1.68	5.54E-09
cellular protein localization (GO:0034613)	1085	471	280.04	+	1.68	6.01E-23
mitotic cell cycle (GO:0000278)	484	210	124.92	+	1.68	1.13E-08
organic anion transport (GO:0015711)	242	105	62.46	+	1.68	4.03E-03
cellular protein catabolic process (GO:0044257)	482	209	124.41	+	1.68	1.34E-08
phosphorylation (GO:0016310)	1063	460	274.37	+	1.68	4.61E-22
mitotic cell cycle process (GO:1903047)	453	196	116.92	+	1.68	7.85E-08
mitotic nuclear division (GO:0007067)	243	105	62.72	+	1.67	4.83E-03
protein modification by small protein conjugation or removal (GO:0070647)	676	292	174.48	+	1.67	7.92E-13
regulation of growth (GO:0040008)	639	276	164.93	+	1.67	5.63E-12
regulation of actin filament-based process (GO:0032970)	322	139	83.11	+	1.67	8.69E-05
regulation of apoptotic signaling pathway (GO:2001233)	380	164	98.08	+	1.67	4.45E-06
carboxylic acid transport (GO:0046942)	211	91	54.46	+	1.67	2.79E-02
protein ubiquitination (GO:0016567)	515	222	132.92	+	1.67	4.73E-09
protein modification by small protein conjugation (GO:0032446)	555	239	143.25	+	1.67	6.80E-10

negative regulation of cell motility (GO:2000146)	230	99	59.36	+	1.67	1.16E-02
response to light stimulus (GO:0009416)	300	129	77.43	+	1.67	3.54E-04
regulation of cellular component organization (GO:0051128)	2292	985	591.58	+	1.67	9.07E-52
regulation of cellular protein localization (GO:1903827)	545	234	140.67	+	1.66	1.65E-09
regulation of MAP kinase activity (GO:0043405)	301	129	77.69	+	1.66	4.23E-04
positive regulation of proteolysis (GO:0045862)	294	126	75.88	+	1.66	5.99E-04
cellular response to peptide hormone stimulus (GO:0071375)	259	111	66.85	+	1.66	3.44E-03
glycoprotein biosynthetic process (GO:0009101)	245	105	63.24	+	1.66	6.92E-03
proteolysis involved in cellular protein catabolic process (GO:0051603)	467	200	120.54	+	1.66	1.13E-07
organic substance transport (GO:0071702)	1547	662	399.29	+	1.66	3.83E-32
negative regulation of organelle organization (GO:0010639)	300	128	77.43	+	1.65	6.01E-04
cellular response to peptide (GO:1901653)	286	122	73.82	+	1.65	1.21E-03
macromolecule localization (GO:0033036)	1795	764	463.30	+	1.65	3.75E-37
response to drug (GO:0042493)	614	261	158.48	+	1.65	1.96E-10
positive regulation of apoptotic process (GO:0043065)	584	248	150.73	+	1.65	9.64E-10
regulation of mitotic cell cycle (GO:0007346)	391	166	100.92	+	1.64	1.08E-05
organophosphate metabolic process (GO:0019637)	703	298	181.45	+	1.64	3.87E-12
cell morphogenesis (GO:0000902)	880	373	227.13	+	1.64	6.83E-16
protein localization to organelle (GO:0033365)	477	202	123.12	+	1.64	2.27E-07
positive regulation of programmed cell death (GO:0043068)	588	249	151.77	+	1.64	1.14E-09
enzyme linked receptor protein signaling pathway (GO:0007167)	520	220	134.21	+	1.64	3.27E-08
regulation of metal ion transport (GO:0010959)	360	152	92.92	+	1.64	7.34E-05
response to hypoxia (GO:0001666)	375	158	96.79	+	1.63	4.32E-05
positive regulation of cell death (GO:0010942)	629	265	162.35	+	1.63	3.24E-10
protein catabolic process (GO:0030163)	513	216	132.41	+	1.63	7.77E-08
vesicle-mediated transport (GO:0016192)	960	404	247.78	+	1.63	6.01E-17
cellular response to hormone stimulus (GO:0032870)	561	236	144.80	+	1.63	9.32E-09
positive regulation of cellular component organization (GO:0051130)	1203	506	310.50	+	1.63	5.19E-22
regulation of kinase activity (GO:0043549)	718	302	185.32	+	1.63	6.35E-12
cellular protein modification process (GO:0006464)	2383	1002	615.06	+	1.63	1.15E-48
protein modification process (GO:0036211)	2383	1002	615.06	+	1.63	1.15E-48
regulation of cell differentiation (GO:0045595)	1651	694	426.13	+	1.63	1.15E-31
regulation of protein kinase activity (GO:0045859)	659	277	170.09	+	1.63	1.10E-10
muscle cell differentiation (GO:0042692)	269	113	69.43	+	1.63	6.87E-03
aging (GO:0007568)	398	167	102.73	+	1.63	2.12E-05
angiogenesis (GO:0001525)	258	108	66.59	+	1.62	1.38E-02
macromolecule modification (GO:0043412)	2576	1077	664.88	+	1.62	7.42E-52
cellular macromolecule catabolic process (GO:0044265)	627	262	161.83	+	1.62	1.07E-09

single-organism intracellular transport (GO:1902582)	371	155	95.76	+	1.62	1.01E-04
regulation of ion transport (GO:0043269)	596	249	153.83	+	1.62	4.42E-09
positive regulation of GTPase activity (GO:0043547)	443	185	114.34	+	1.62	4.31E-06
response to decreased oxygen levels (GO:0036293)	386	161	99.63	+	1.62	5.96E-05
carbohydrate metabolic process (GO:0005975)	559	233	144.28	+	1.61	3.06E-08
anion transport (GO:0006820)	360	150	92.92	+	1.61	2.03E-04
epithelial tube morphogenesis (GO:0060562)	348	145	89.82	+	1.61	3.43E-04
apoptotic process (GO:0006915)	675	281	174.22	+	1.61	2.09E-10
response to oxygen levels (GO:0070482)	418	174	107.89	+	1.61	1.73E-05
cellular component morphogenesis (GO:0032989)	966	402	249.33	+	1.61	4.63E-16
programmed cell death (GO:0012501)	702	292	181.19	+	1.61	7.09E-11
peptidyl-amino acid modification (GO:0018193)	703	292	181.45	+	1.61	8.36E-11
lipid biosynthetic process (GO:0008610)	383	159	98.85	+	1.61	9.90E-05
chemotaxis (GO:0006935)	410	170	105.82	+	1.61	3.43E-05
response to peptide hormone (GO:0043434)	454	188	117.18	+	1.60	5.85E-06
negative regulation of developmental process (GO:0051093)	884	366	228.17	+	1.60	4.91E-14
regulation of protein complex assembly (GO:0043254)	343	142	88.53	+	1.60	6.74E-04
regulation of transport (GO:0051049)	1813	750	467.94	+	1.60	1.73E-32
membrane organization (GO:0061024)	747	309	192.80	+	1.60	2.27E-11
regulation of intracellular protein transport (GO:0033157)	370	153	95.50	+	1.60	2.34E-04
regulation of intracellular transport (GO:0032386)	467	193	120.54	+	1.60	4.06E-06
cytoskeleton organization (GO:0007010)	859	355	221.71	+	1.60	2.04E-13
morphogenesis of an epithelium (GO:0002009)	489	202	126.21	+	1.60	1.67E-06
regulation of transferase activity (GO:0051338)	809	334	208.81	+	1.60	2.12E-12
taxis (GO:0042330)	412	170	106.34	+	1.60	4.74E-05
positive regulation of hydrolase activity (GO:0051345)	732	302	188.93	+	1.60	6.45E-11
organophosphate biosynthetic process (GO:0090407)	337	139	86.98	+	1.60	1.12E-03
negative regulation of transport (GO:0051051)	490	202	126.47	+	1.60	1.97E-06
tube morphogenesis (GO:0035239)	393	162	101.44	+	1.60	1.14E-04
positive regulation of cellular protein localization (GO:1903829)	343	141	88.53	+	1.59	1.10E-03
cell death (GO:0008219)	745	306	192.29	+	1.59	7.24E-11
cell-cell signaling (GO:0007267)	704	289	181.71	+	1.59	4.34E-10
positive regulation of intracellular transport (GO:0032388)	290	119	74.85	+	1.59	1.08E-02
small molecule biosynthetic process (GO:0044283)	334	137	86.21	+	1.59	1.85E-03
regulation of lipid metabolic process (GO:0019216)	300	123	77.43	+	1.59	7.56E-03
positive regulation of cellular component biogenesis (GO:0044089)	405	166	104.53	+	1.59	1.09E-04
posttranscriptional regulation of gene expression (GO:0010608)	371	152	95.76	+	1.59	4.48E-04
urogenital system development (GO:0001655)	354	145	91.37	+	1.59	9.05E-04

response to peptide (GO:1901652)	504	206	130.09	+	1.58	2.59E-06
ribose phosphate metabolic process (GO:0019693)	311	127	80.27	+	1.58	6.19E-03
muscle structure development (GO:0061061)	458	187	118.21	+	1.58	1.81E-05
negative regulation of cell communication (GO:0010648)	1159	473	299.14	+	1.58	7.15E-18
positive regulation of cell cycle (GO:0045787)	299	122	77.17	+	1.58	1.05E-02
nitrogen compound transport (GO:0071705)	402	164	103.76	+	1.58	1.79E-04
negative regulation of signaling (GO:0023057)	1162	474	299.92	+	1.58	7.03E-18
negative regulation of cellular protein metabolic process (GO:0032269)	939	383	242.36	+	1.58	7.54E-14
negative regulation of cell death (GO:0060548)	967	394	249.59	+	1.58	2.92E-14
developmental growth (GO:0048589)	410	167	105.82	+	1.58	1.48E-04
response to hormone (GO:0009725)	965	393	249.07	+	1.58	3.47E-14
regulation of cell cycle (GO:0051726)	811	330	209.32	+	1.58	2.06E-11
regulation of localization (GO:0032879)	2487	1011	641.91	+	1.57	5.99E-43
response to mechanical stimulus (GO:0009612)	278	113	71.75	+	1.57	2.96E-02
single-organism organelle organization (GO:1902589)	1369	556	353.35	+	1.57	3.63E-21
response to organonitrogen compound (GO:0010243)	993	403	256.30	+	1.57	2.18E-14
regulation of protein localization (GO:0032880)	971	394	250.62	+	1.57	5.47E-14
regulation of cellular response to stress (GO:0080135)	530	215	136.80	+	1.57	1.99E-06
negative regulation of signal transduction (GO:0009968)	1041	422	268.69	+	1.57	3.97E-15
regulation of intracellular signal transduction (GO:1902531)	1513	613	390.51	+	1.57	1.74E-23
carbohydrate derivative biosynthetic process (GO:1901137)	469	190	121.05	+	1.57	2.37E-05
cell development (GO:0048468)	1575	638	406.52	+	1.57	1.36E-24
response to steroid hormone (GO:0048545)	457	185	117.95	+	1.57	4.02E-05
sulfur compound metabolic process (GO:0006790)	272	110	70.20	+	1.57	4.89E-02
regulation of anatomical structure morphogenesis (GO:0022603)	1017	411	262.49	+	1.57	1.92E-14
regulation of MAPK cascade (GO:0043408)	681	275	175.77	+	1.56	1.01E-08
negative regulation of cell proliferation (GO:0008285)	629	254	162.35	+	1.56	7.36E-08
positive regulation of transferase activity (GO:0051347)	503	203	129.83	+	1.56	9.27E-06
organic hydroxy compound metabolic process (GO:1901615)	300	121	77.43	+	1.56	1.97E-02
regulation of multicellular organismal development (GO:2000026)	1784	719	460.46	+	1.56	1.13E-27
regulation of organelle organization (GO:0033043)	1099	442	283.66	+	1.56	2.07E-15
regulation of cell death (GO:0010941)	1550	623	400.06	+	1.56	4.25E-23
renal system development (GO:0072001)	311	125	80.27	+	1.56	1.60E-02
regulation of signaling (GO:0023051)	2786	1118	719.08	+	1.55	7.14E-46
cellular catabolic process (GO:0044248)	1095	439	282.63	+	1.55	4.67E-15
regulation of cell communication (GO:0010646)	2764	1108	713.40	+	1.55	3.58E-45
negative regulation of protein metabolic process (GO:0051248)	998	400	257.59	+	1.55	1.96E-13
cellular response to abiotic stimulus (GO:0071214)	307	123	79.24	+	1.55	2.23E-02

negative regulation of cell cycle (GO:0045786)	327	131	84.40	+	1.55	1.09E-02
cofactor metabolic process (GO:0051186)	327	131	84.40	+	1.55	1.09E-02
microtubule cytoskeleton organization (GO:0000226)	362	145	93.43	+	1.55	3.09E-03
positive regulation of kinase activity (GO:0033674)	437	175	112.79	+	1.55	2.10E-04
macromolecule catabolic process (GO:0009057)	713	285	184.03	+	1.55	1.16E-08
regulation of developmental process (GO:0050793)	2362	944	609.64	+	1.55	8.53E-37
cellular response to growth factor stimulus (GO:0071363)	463	185	119.50	+	1.55	9.91E-05
positive regulation of protein kinase activity (GO:0045860)	403	161	104.02	+	1.55	8.55E-04
regulation of cellular amide metabolic process (GO:0034248)	343	137	88.53	+	1.55	7.36E-03
tube development (GO:0035295)	681	272	175.77	+	1.55	4.10E-08
positive regulation of catalytic activity (GO:0043085)	1252	500	323.15	+	1.55	2.81E-17
cellular lipid metabolic process (GO:0044255)	749	299	193.32	+	1.55	3.76E-09
positive regulation of transport (GO:0051050)	990	395	255.52	+	1.55	6.13E-13
negative regulation of transcription from RNA polymerase II promoter (GO:0000122)	757	302	195.39	+	1.55	3.07E-09
cellular response to organic cyclic compound (GO:0071407)	549	219	141.70	+	1.55	5.37E-06
growth (GO:0040007)	484	193	124.92	+	1.54	5.59E-05
single-organism biosynthetic process (GO:0044711)	841	335	217.07	+	1.54	1.85E-10
ribonucleotide metabolic process (GO:0009259)	299	119	77.17	+	1.54	4.29E-02
regulation of protein targeting (GO:1903533)	299	119	77.17	+	1.54	4.29E-02
regulation of molecular function (GO:0065009)	2574	1024	664.36	+	1.54	9.73E-40
tissue morphogenesis (GO:0048729)	596	237	153.83	+	1.54	1.42E-06
cellular response to organonitrogen compound (GO:0071417)	498	198	128.54	+	1.54	4.44E-05
positive regulation of molecular function (GO:0044093)	1557	619	401.87	+	1.54	8.44E-22
regulation of cell cycle process (GO:0010564)	476	189	122.86	+	1.54	1.07E-04
negative regulation of apoptotic process (GO:0043066)	864	343	223.00	+	1.54	1.38E-10
regulation of cell migration (GO:0030334)	711	282	183.51	+	1.54	3.43E-08
response to oxidative stress (GO:0006979)	411	163	106.08	+	1.54	1.11E-03
regulation of secretion by cell (GO:1903530)	694	275	179.13	+	1.54	6.98E-08
nucleotide metabolic process (GO:0009117)	409	162	105.57	+	1.53	1.30E-03
blood vessel development (GO:0001568)	452	179	116.66	+	1.53	3.05E-04
covalent chromatin modification (GO:0016569)	379	150	97.82	+	1.53	3.83E-03
positive regulation of cell differentiation (GO:0045597)	940	372	242.62	+	1.53	1.57E-11
negative regulation of programmed cell death (GO:0043069)	878	347	226.62	+	1.53	1.70E-10
regulation of catalytic activity (GO:0050790)	2047	809	528.34	+	1.53	4.01E-29
response to abiotic stimulus (GO:0009628)	1245	492	321.34	+	1.53	4.14E-16
regulation of protein modification process (GO:0031399)	1612	637	416.07	+	1.53	6.38E-22
positive regulation of secretion by cell (GO:1903532)	390	154	100.66	+	1.53	3.09E-03
positive regulation of organelle organization (GO:0010638)	580	229	149.70	+	1.53	5.21E-06

nucleoside phosphate metabolic process (GO:0006753)	418	165	107.89	+	1.53	1.24E-03
response to nitrogen compound (GO:1901698)	1092	431	281.85	+	1.53	1.23E-13
regulation of phosphorylation (GO:0042325)	1399	552	361.09	+	1.53	2.36E-18
regulation of apoptotic process (GO:0042981)	1412	557	364.44	+	1.53	1.57E-18
response to endogenous stimulus (GO:0009719)	1620	639	418.13	+	1.53	8.16E-22
response to radiation (GO:0009314)	477	188	123.12	+	1.53	1.94E-04
metal ion transport (GO:0030001)	543	214	140.15	+	1.53	2.16E-05
establishment of localization (GO:0051234)	3456	1362	892.01	+	1.53	5.41E-54
regulation of programmed cell death (GO:0043067)	1427	562	368.32	+	1.53	1.39E-18
response to growth factor (GO:0070848)	498	196	128.54	+	1.52	1.09E-04
negative regulation of cellular process (GO:0048523)	4088	1608	1055.13	+	1.52	4.73E-66
regulation of signal transduction (GO:0009966)	2441	960	630.03	+	1.52	6.38E-35
cell migration (GO:0016477)	712	280	183.77	+	1.52	9.74E-08
cellular response to endogenous stimulus (GO:0071495)	1038	408	267.91	+	1.52	1.75E-12
transport (GO:0006810)	3305	1299	853.04	+	1.52	2.65E-50
carbohydrate derivative metabolic process (GO:1901135)	828	325	213.71	+	1.52	2.63E-09
positive regulation of transcription from RNA polymerase II promoter (GO:0045944)	1050	412	271.01	+	1.52	1.60E-12
regulation of cellular component movement (GO:0051270)	813	319	209.84	+	1.52	4.55E-09
system development (GO:0048731)	4152	1629	1071.65	+	1.52	2.07E-66
multicellular organism development (GO:0007275)	4547	1783	1173.60	+	1.52	1.57E-74
protein oligomerization (GO:0051259)	482	189	124.41	+	1.52	2.53E-04
negative regulation of multicellular organismal process (GO:0051241)	1064	417	274.62	+	1.52	1.24E-12
monovalent inorganic cation transport (GO:0015672)	370	145	95.50	+	1.52	9.87E-03
locomotion (GO:0040011)	980	384	252.94	+	1.52	2.16E-11
RNA biosynthetic process (GO:0032774)	1215	476	313.60	+	1.52	7.99E-15
regulation of secretion (GO:0051046)	743	291	191.77	+	1.52	5.87E-08
negative regulation of catalytic activity (GO:0043086)	751	294	193.84	+	1.52	4.79E-08
blood vessel morphogenesis (GO:0048514)	350	137	90.34	+	1.52	2.02E-02
transcription, DNA-templated (GO:0006351)	1201	469	309.98	+	1.51	2.54E-14
single-organism localization (GO:1902578)	2021	789	521.63	+	1.51	1.09E-26
positive regulation of cellular protein metabolic process (GO:0032270)	1348	526	347.93	+	1.51	2.15E-16
nucleic acid-templated transcription (GO:0097659)	1202	469	310.24	+	1.51	2.92E-14
regulation of locomotion (GO:0040012)	787	307	203.13	+	1.51	2.39E-08
organic substance catabolic process (GO:1901575)	1264	493	326.24	+	1.51	4.01E-15
inorganic cation transmembrane transport (GO:0098662)	467	182	120.54	+	1.51	6.72E-04
regulation of phosphate metabolic process (GO:0019220)	1622	632	418.65	+	1.51	2.73E-20
localization (GO:0051179)	4363	1700	1126.11	+	1.51	4.63E-68
vasculature development (GO:0001944)	480	187	123.89	+	1.51	4.60E-04

regulation of phosphorus metabolic process (GO:0051174)	1623	632	418.90	+	1.51	3.15E-20
response to metal ion (GO:0010038)	434	169	112.02	+	1.51	2.01E-03
negative regulation of response to stimulus (GO:0048585)	1346	524	347.41	+	1.51	3.97E-16
positive regulation of secretion (GO:0051047)	419	163	108.15	+	1.51	3.43E-03
regulation of homeostatic process (GO:0032844)	473	184	122.08	+	1.51	6.45E-04
cellular response to lipid (GO:0071396)	522	203	134.73	+	1.51	1.44E-04
regulation of hydrolase activity (GO:0051336)	1184	460	305.60	+	1.51	1.28E-13
ion transport (GO:0006811)	1064	413	274.62	+	1.50	7.29E-12
regulation of biological quality (GO:0065008)	3322	1289	857.43	+	1.50	5.57E-47
regulation of protein phosphorylation (GO:0001932)	1297	503	334.76	+	1.50	4.76E-15
cation homeostasis (GO:0055080)	555	215	143.25	+	1.50	7.41E-05
negative regulation of biological process (GO:0048519)	4402	1705	1136.18	+	1.50	1.68E-66
response to acid chemical (GO:0001101)	403	156	104.02	+	1.50	7.88E-03
regulation of establishment of protein localization (GO:0070201)	819	317	211.39	+	1.50	2.51E-08
single-multicellular organism process (GO:0044707)	5153	1994	1330.02	+	1.50	1.28E-81
positive regulation of developmental process (GO:0051094)	1300	503	335.54	+	1.50	7.20E-15
regulation of cell motility (GO:2000145)	750	290	193.58	+	1.50	2.38E-07
regulation of protein transport (GO:0051223)	763	295	196.93	+	1.50	1.62E-07
cell differentiation (GO:0030154)	3267	1263	843.23	+	1.50	5.03E-45
nucleobase-containing small molecule metabolic process (GO:0055086)	471	182	121.57	+	1.50	1.16E-03
catabolic process (GO:0009056)	1326	512	342.25	+	1.50	4.97E-15
regulation of cellular protein metabolic process (GO:0032268)	2291	884	591.32	+	1.49	6.76E-29
cation transmembrane transport (GO:0098655)	529	204	136.54	+	1.49	2.43E-04
negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	1250	482	322.63	+	1.49	7.34E-14
negative regulation of molecular function (GO:0044092)	1020	393	263.27	+	1.49	1.05E-10
positive regulation of protein metabolic process (GO:0051247)	1438	554	371.16	+	1.49	2.39E-16
chemical homeostasis (GO:0048878)	927	357	239.26	+	1.49	1.92E-09
cellular response to nitrogen compound (GO:1901699)	574	221	148.15	+	1.49	7.41E-05
positive regulation of nucleic acid-templated transcription (GO:1903508)	1328	511	342.76	+	1.49	1.01E-14
positive regulation of transcription, DNA-templated (GO:0045893)	1328	511	342.76	+	1.49	1.01E-14
positive regulation of RNA biosynthetic process (GO:1902680)	1331	512	343.54	+	1.49	9.82E-15
positive regulation of cellular metabolic process (GO:0031325)	2727	1049	703.85	+	1.49	5.22E-35
positive regulation of intracellular signal transduction (GO:1902533)	884	340	228.17	+	1.49	8.48E-09
in utero embryonic development (GO:0001701)	429	165	110.73	+	1.49	5.65E-03
response to organic cyclic compound (GO:0014070)	1209	465	312.05	+	1.49	4.43E-13
divalent inorganic cation homeostasis (GO:0072507)	372	143	96.02	+	1.49	3.08E-02
positive regulation of cellular process (GO:0048522)	4627	1778	1194.25	+	1.49	9.43E-68
single-organism transport (GO:0044765)	1801	692	464.85	+	1.49	4.37E-21

cellular chemical homeostasis (GO:0055082)	617	237	159.25	+	1.49	2.63E-05
protein complex subunit organization (GO:0071822)	1034	397	266.88	+	1.49	1.24E-10
organelle organization (GO:0006996)	2821	1082	728.11	+	1.49	7.65E-36
positive regulation of signaling (GO:0023056)	1468	563	378.90	+	1.49	2.80E-16
mitochondrion organization (GO:0007005)	480	184	123.89	+	1.49	1.65E-03
negative regulation of macromolecule biosynthetic process (GO:0010558)	1315	504	339.41	+	1.48	3.58E-14
negative regulation of nitrogen compound metabolic process (GO:0051172)	1422	545	367.03	+	1.48	1.36E-15
movement of cell or subcellular component (GO:0006928)	1122	430	289.59	+	1.48	1.23E-11
cellular developmental process (GO:0048869)	3473	1331	896.40	+	1.48	4.11E-46
single-organism catabolic process (GO:0044712)	608	233	156.93	+	1.48	4.30E-05
cellular response to stress (GO:0033554)	1412	541	364.44	+	1.48	1.98E-15
regulation of protein metabolic process (GO:0051246)	2436	933	628.74	+	1.48	9.94E-30
positive regulation of macromolecule metabolic process (GO:0010604)	2718	1041	701.53	+	1.48	5.93E-34
regulation of multicellular organismal process (GO:0051239)	2658	1018	686.04	+	1.48	4.86E-33
positive regulation of biological process (GO:0048518)	5076	1944	1310.14	+	1.48	3.45E-75
positive regulation of protein modification process (GO:0031401)	1068	409	275.66	+	1.48	7.01E-11
negative regulation of biosynthetic process (GO:0009890)	1405	538	362.64	+	1.48	2.82E-15
regulation of transcription from RNA polymerase II promoter (GO:0006357)	1771	678	457.10	+	1.48	3.42E-20
negative regulation of cellular biosynthetic process (GO:0031327)	1374	526	354.64	+	1.48	7.68E-15
positive regulation of cell communication (GO:0010647)	1461	559	377.09	+	1.48	6.14E-16
positive regulation of RNA metabolic process (GO:0051254)	1383	529	356.96	+	1.48	7.07E-15
anatomical structure morphogenesis (GO:0009653)	2139	818	552.09	+	1.48	3.58E-25
ion transmembrane transport (GO:0034220)	709	271	183.00	+	1.48	3.13E-06
mRNA metabolic process (GO:0016071)	398	152	102.73	+	1.48	2.19E-02
positive regulation of MAPK cascade (GO:0043410)	474	181	122.34	+	1.48	2.63E-03
inorganic ion homeostasis (GO:0098771)	571	218	147.38	+	1.48	1.75E-04
negative regulation of nucleic acid-templated transcription (GO:1903507)	1095	418	282.63	+	1.48	5.54E-11
cell proliferation (GO:0008283)	566	216	146.09	+	1.48	2.09E-04
ion homeostasis (GO:0050801)	577	220	148.93	+	1.48	1.67E-04
eye development (GO:0001654)	383	146	98.85	+	1.48	3.74E-02
positive regulation of macromolecule biosynthetic process (GO:0010557)	1564	596	403.68	+	1.48	7.30E-17
regulation of system process (GO:0044057)	496	189	128.02	+	1.48	1.67E-03
nucleobase-containing compound biosynthetic process (GO:0034654)	1475	562	380.71	+	1.48	1.10E-15
positive regulation of nitrogen compound metabolic process (GO:0051173)	1727	658	445.75	+	1.48	5.39E-19
negative regulation of cellular metabolic process (GO:0031324)	2237	852	577.38	+	1.48	6.75E-26
negative regulation of macromolecule metabolic process (GO:0010605)	2186	832	564.22	+	1.47	4.48E-25
negative regulation of gene expression (GO:0010629)	1390	529	358.77	+	1.47	1.79E-14
anatomical structure development (GO:0048856)	4940	1880	1275.04	+	1.47	9.54E-70

single-organism developmental process (GO:0044767)	5217	1985	1346.53	+	1.47	5.06E-75
positive regulation of metabolic process (GO:0009893)	2913	1108	751.86	+	1.47	2.08E-35
aromatic compound biosynthetic process (GO:0019438)	1546	588	399.03	+	1.47	2.04E-16
negative regulation of transcription, DNA-templated (GO:0045892)	1076	409	277.72	+	1.47	2.00E-10
positive regulation of cellular biosynthetic process (GO:0031328)	1689	642	435.94	+	1.47	3.31E-18
developmental process (GO:0032502)	5248	1994	1354.54	+	1.47	5.47E-75
heterocycle biosynthetic process (GO:0018130)	1532	582	395.42	+	1.47	4.13E-16
positive regulation of signal transduction (GO:0009967)	1306	496	337.09	+	1.47	3.24E-13
negative regulation of metabolic process (GO:0009892)	2389	907	616.61	+	1.47	1.76E-27
lipid metabolic process (GO:0006629)	959	364	247.52	+	1.47	6.81E-09
positive regulation of biosynthetic process (GO:0009891)	1726	655	445.49	+	1.47	1.71E-18
cellular component organization (GO:0016043)	4702	1784	1213.61	+	1.47	4.49E-64
positive regulation of cell migration (GO:0030335)	427	162	110.21	+	1.47	1.51E-02
skeletal system development (GO:0001501)	456	173	117.70	+	1.47	6.92E-03
negative regulation of RNA biosynthetic process (GO:1902679)	1110	421	286.50	+	1.47	1.12E-10
chordate embryonic development (GO:0043009)	699	265	180.42	+	1.47	1.02E-05
metal ion homeostasis (GO:0055065)	488	185	125.96	+	1.47	3.09E-03
organic cyclic compound biosynthetic process (GO:1901362)	1636	620	422.26	+	1.47	3.57E-17
embryo development ending in birth or egg hatching (GO:0009792)	708	268	182.74	+	1.47	9.47E-06
positive regulation of nucleobase-containing compound metabolic process (GO:0045935)	1617	611	417.36	+	1.46	1.33E-16
circulatory system development (GO:0072359)	854	322	220.42	+	1.46	3.02E-07
cardiovascular system development (GO:0072358)	854	322	220.42	+	1.46	3.02E-07
negative regulation of RNA metabolic process (GO:0051253)	1157	436	298.63	+	1.46	9.48E-11
cellular protein metabolic process (GO:0044267)	3251	1225	839.10	+	1.46	3.14E-38
anatomical structure formation involved in morphogenesis (GO:0048646)	990	373	255.52	+	1.46	8.88E-09
protein complex assembly (GO:0006461)	921	347	237.71	+	1.46	5.62E-08
protein complex biogenesis (GO:0070271)	921	347	237.71	+	1.46	5.62E-08
cellular response to oxygen-containing compound (GO:1901701)	937	353	241.84	+	1.46	3.71E-08
cellular homeostasis (GO:0019725)	733	276	189.19	+	1.46	8.71E-06
regulation of proteolysis (GO:0030162)	656	247	169.32	+	1.46	6.53E-05
gland development (GO:0048732)	537	202	138.60	+	1.46	1.56E-03
heart development (GO:0007507)	553	208	142.73	+	1.46	1.04E-03
positive regulation of locomotion (GO:0040017)	455	171	117.44	+	1.46	1.37E-02
positive regulation of gene expression (GO:0010628)	1650	620	425.87	+	1.46	2.19E-16
cellular cation homeostasis (GO:0030003)	482	181	124.41	+	1.45	7.27E-03
positive regulation of phosphorylation (GO:0042327)	919	345	237.20	+	1.45	9.79E-08
response to inorganic substance (GO:0010035)	629	236	162.35	+	1.45	1.84E-04
response to oxygen-containing compound (GO:1901700)	1710	641	441.36	+	1.45	7.69E-17

cellular component organization or biogenesis (GO:0071840)	4917	1843	1269.10	+	1.45	4.81E-63
reproductive structure development (GO:0048608)	502	188	129.57	+	1.45	5.34E-03
negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	1299	486	335.28	+	1.45	8.10E-12
single-organism metabolic process (GO:0044710)	2872	1074	741.28	+	1.45	3.18E-31
response to nutrient levels (GO:0031667)	567	212	146.35	+	1.45	1.20E-03
positive regulation of phosphorus metabolic process (GO:0010562)	1037	387	267.66	+	1.45	1.11E-08
positive regulation of phosphate metabolic process (GO:0045937)	1037	387	267.66	+	1.45	1.11E-08
microtubule-based process (GO:0007017)	528	197	136.28	+	1.45	3.72E-03
regulation of response to stimulus (GO:0048583)	3270	1220	844.00	+	1.45	3.95E-36
reproductive system development (GO:0061458)	507	189	130.86	+	1.44	6.64E-03
response to extracellular stimulus (GO:0009991)	593	221	153.06	+	1.44	8.29E-04
animal organ development (GO:0048513)	3159	1177	815.35	+	1.44	2.65E-34
cellular response to chemical stimulus (GO:0070887)	2174	810	561.12	+	1.44	1.15E-21
cell cycle (GO:0007049)	760	283	196.16	+	1.44	1.50E-05
positive regulation of establishment of protein localization (GO:1904951)	521	194	134.47	+	1.44	5.14E-03
cation transport (GO:0006812)	720	268	185.84	+	1.44	4.18E-05
inorganic ion transmembrane transport (GO:0098660)	551	205	142.22	+	1.44	2.65E-03
localization of cell (GO:0051674)	793	295	204.68	+	1.44	7.47E-06
cell motility (GO:0048870)	793	295	204.68	+	1.44	7.47E-06
response to organic substance (GO:0010033)	2713	1009	700.24	+	1.44	4.46E-28
positive regulation of protein phosphorylation (GO:0001934)	877	326	226.36	+	1.44	1.05E-06
positive regulation of multicellular organismal process (GO:0051240)	1543	573	398.26	+	1.44	6.78E-14
response to lipid (GO:0033993)	1099	408	283.66	+	1.44	5.32E-09
cellular ion homeostasis (GO:0006873)	496	184	128.02	+	1.44	1.23E-02
small molecule metabolic process (GO:0044281)	1428	529	368.57	+	1.44	2.16E-12
positive regulation of cellular component movement (GO:0051272)	452	167	116.66	+	1.43	4.54E-02
response to wounding (GO:0009611)	455	168	117.44	+	1.43	4.41E-02
cellular component assembly (GO:0022607)	1865	688	481.37	+	1.43	9.25E-17
embryo development (GO:0009790)	1049	386	270.75	+	1.43	6.90E-08
cellular response to DNA damage stimulus (GO:0006974)	582	214	150.22	+	1.42	3.30E-03
cellular response to organic substance (GO:0071310)	1771	650	457.10	+	1.42	3.73E-15
positive regulation of protein transport (GO:0051222)	485	178	125.18	+	1.42	3.32E-02
tissue development (GO:0009888)	1608	590	415.03	+	1.42	2.10E-13
epithelium development (GO:0060429)	1009	370	260.43	+	1.42	2.85E-07
cell cycle process (GO:0022402)	723	265	186.61	+	1.42	1.87E-04
macromolecular complex subunit organization (GO:0043933)	1743	638	449.88	+	1.42	1.45E-14
chromatin organization (GO:0006325)	564	206	145.57	+	1.42	8.30E-03
cellular macromolecule metabolic process (GO:0044260)	5345	1950	1379.57	+	1.41	3.64E-59

cellular metabolic process (GO:0044237)	7028	2558	1813.96	+	1.41	1.14E-86
RNA metabolic process (GO:0016070)	2014	733	519.82	+	1.41	1.01E-16
sensory organ development (GO:0007423)	589	214	152.02	+	1.41	7.33E-03
transmembrane transport (GO:0055085)	1042	378	268.95	+	1.41	6.17E-07
regulation of macromolecule metabolic process (GO:0060255)	5150	1863	1329.24	+	1.40	5.00E-53
regulation of primary metabolic process (GO:0080090)	5149	1862	1328.98	+	1.40	6.92E-53
regulation of cellular metabolic process (GO:0031323)	5218	1883	1346.79	+	1.40	4.45E-53
regulation of metabolic process (GO:0019222)	5499	1982	1419.32	+	1.40	1.34E-56
homeostatic process (GO:0042592)	1407	507	363.15	+	1.40	8.09E-10
nucleobase-containing compound metabolic process (GO:0006139)	2943	1059	759.60	+	1.39	1.11E-24
cellular aromatic compound metabolic process (GO:0006725)	3120	1121	805.29	+	1.39	2.84E-26
cellular component biogenesis (GO:0044085)	2108	756	544.09	+	1.39	7.59E-16
heterocycle metabolic process (GO:0046483)	3061	1097	790.06	+	1.39	3.59E-25
regulation of response to stress (GO:0080134)	1142	409	294.76	+	1.39	4.89E-07
organic cyclic compound metabolic process (GO:1901360)	3285	1173	847.88	+	1.38	8.53E-27
regulation of nitrogen compound metabolic process (GO:0051171)	3740	1332	965.31	+	1.38	4.94E-31
macromolecular complex assembly (GO:0065003)	1206	429	311.27	+	1.38	3.85E-07
regulation of gene expression (GO:0010468)	3647	1295	941.31	+	1.38	2.23E-29
nucleic acid metabolic process (GO:0090304)	2470	877	637.52	+	1.38	6.69E-18
regulation of macromolecule biosynthetic process (GO:0010556)	3463	1229	893.82	+	1.37	2.24E-27
organ morphogenesis (GO:0009887)	933	331	240.81	+	1.37	8.73E-05
regulation of cell proliferation (GO:0042127)	1562	554	403.16	+	1.37	7.26E-10
regulation of cellular macromolecule biosynthetic process (GO:2000112)	3355	1189	865.94	+	1.37	5.20E-26
organic substance biosynthetic process (GO:1901576)	3177	1125	820.00	+	1.37	4.11E-24
positive regulation of response to stimulus (GO:0048584)	1778	629	458.91	+	1.37	1.97E-11
biosynthetic process (GO:0009058)	3255	1151	840.13	+	1.37	1.33E-24
primary metabolic process (GO:0044238)	7212	2547	1861.45	+	1.37	9.43E-73
regulation of biosynthetic process (GO:0009889)	3696	1303	953.96	+	1.37	2.65E-28
regulation of nucleic acid-templated transcription (GO:1903506)	3003	1058	775.09	+	1.37	1.41E-21
regulation of nucleobase-containing compound metabolic process (GO:0019219)	3481	1226	898.46	+	1.36	5.34E-26
regulation of cell adhesion (GO:0030155)	619	218	159.77	+	1.36	4.36E-02
organic substance metabolic process (GO:0071704)	7647	2693	1973.73	+	1.36	4.04E-78
regulation of RNA biosynthetic process (GO:2001141)	3010	1060	776.90	+	1.36	1.44E-21
regulation of cellular biosynthetic process (GO:0031326)	3632	1279	937.44	+	1.36	1.97E-27
regulation of transcription, DNA-templated (GO:0006355)	2977	1048	768.38	+	1.36	3.32E-21
regulation of RNA metabolic process (GO:0051252)	3133	1102	808.64	+	1.36	1.74E-22
biological adhesion (GO:0022610)	882	310	227.65	+	1.36	5.89E-04
cellular biosynthetic process (GO:0044249)	3109	1092	802.45	+	1.36	5.12E-22

protein metabolic process (GO:0019538)	3867	1355	998.09	+	1.36	1.24E-28
cell adhesion (GO:0007155)	871	305	224.81	+	1.36	1.03E-03
macromolecule metabolic process (GO:0043170)	6052	2112	1562.05	+	1.35	4.03E-51
metabolic process (GO:0008152)	8072	2810	2083.43	+	1.35	4.42E-78
organic acid metabolic process (GO:0006082)	771	267	199.00	+	1.34	1.42E-02
positive regulation of cell proliferation (GO:0008284)	887	307	228.94	+	1.34	2.54E-03
nitrogen compound metabolic process (GO:0006807)	4129	1425	1065.72	+	1.34	1.21E-27
chromosome organization (GO:0051276)	841	290	217.07	+	1.34	7.19E-03
response to external stimulus (GO:0009605)	1979	679	510.79	+	1.33	4.92E-10
cell surface receptor signaling pathway (GO:0007166)	1656	568	427.42	+	1.33	7.52E-08
macromolecule biosynthetic process (GO:0009059)	2384	815	615.32	+	1.32	2.02E-12
cellular macromolecule biosynthetic process (GO:0034645)	2357	805	608.35	+	1.32	3.96E-12
response to stress (GO:0006950)	2989	1016	771.48	+	1.32	7.23E-16
cellular nitrogen compound metabolic process (GO:0034641)	3794	1283	979.25	+	1.31	9.41E-21
reproductive process (GO:0022414)	1402	472	361.86	+	1.30	4.94E-05
reproduction (GO:0000003)	1405	473	362.64	+	1.30	4.77E-05
gene expression (GO:0010467)	2601	869	671.33	+	1.29	3.46E-11
cellular nitrogen compound biosynthetic process (GO:0044271)	2277	759	587.71	+	1.29	4.16E-09
proteolysis (GO:0006508)	1066	353	275.14	+	1.28	1.82E-02
single organism reproductive process (GO:0044702)	1261	417	325.47	+	1.28	2.49E-03
organonitrogen compound metabolic process (GO:1901564)	1778	573	458.91	+	1.25	4.03E-04
cellular process (GO:0009987)	14095	4461	3637.99	+	1.23	1.02E-102
biological regulation (GO:0065007)	11690	3691	3017.25	+	1.22	5.68E-63
single-organism cellular process (GO:0044763)	10837	3415	2797.09	+	1.22	1.67E-52
single-organism process (GO:0044699)	12411	3897	3203.34	+	1.22	1.21E-67
regulation of biological process (GO:0050789)	11093	3468	2863.16	+	1.21	3.37E-50
regulation of cellular process (GO:0050794)	10637	3322	2745.47	+	1.21	1.61E-45
multi-organism process (GO:0051704)	1944	602	501.76	+	1.20	2.49E-02
biological_process (GO:0008150)	17404	5331	4492.06	+	1.19	4.92E-145
multicellular organismal process (GO:0032501)	7149	2160	1845.19	+	1.17	2.66E-14
response to stimulus (GO:0050896)	8233	2402	2124.98	+	1.13	8.03E-10
cellular response to stimulus (GO:0051716)	6618	1879	1708.14	+	1.10	6.26E-03
system process (GO:0003008)	2700	486	696.88	-	.70	2.51E-15
neurological system process (GO:0050877)	2229	326	575.32	-	.57	2.29E-28
Unclassified (UNCLASSIFIED)	6377	807	1645.94	-	.49	0.00E00
G-protein coupled receptor signaling pathway (GO:0007186)	2278	234	587.96	-	.40	4.43E-63
sensory perception (GO:0007600)	1865	150	481.37	-	.31	3.12E-70
detection of stimulus (GO:0051606)	1605	75	414.26	-	< 0.2	5.06E-94

detection of stimulus involved in sensory perception (GO:0050906)	1509	50	389.48	-	< 0.2	3.91E-105
sensory perception of chemical stimulus (GO:0007606)	1510	44	389.74	-	< 0.2	6.97E-111
detection of chemical stimulus (GO:0009593)	1477	39	381.22	-	< 0.2	2.63E-112
sensory perception of smell (GO:0007608)	1427	36	368.32	-	< 0.2	5.41E-110
detection of chemical stimulus involved in sensory perception (GO:0050907)	1445	27	372.96	-	< 0.2	8.84E-122
detection of chemical stimulus involved in sensory perception of smell (GO:0050911)	1389	25	358.51	-	< 0.2	6.55E-118