

Supplementary Table 2. Gene Ontology (GO) enrichment analysis based on 3 functional groups (biological processes (BP), cellular components (CC), and molecular functions (MF) in EVs isolated from RJ-treated ADSCs.

Biological processes (BP): Upregulated

Category	Term	Count	%	P-Value	FDR
GOTERM_BP_ALL	GO:0030198~extracellular matrix organization	51	7.112970711	3.27E-16	1.06E-12
GOTERM_BP_ALL	GO:0043062~extracellular structure organization	51	7.112970711	3.56E-16	1.06E-12
GOTERM_BP_ALL	GO:0030199~collagen fibril organization	14	1.952580195	2.15E-09	4.24E-06
GOTERM_BP_ALL	GO:0072359~circulatory system development	76	10.59972106	4.24E-09	5.03E-06
GOTERM_BP_ALL	GO:0072358~cardiovascular system development	76	10.59972106	4.24E-09	5.03E-06
GOTERM_BP_ALL	GO:0071840~cellular component organization or biogenesis	318	44.35146444	6.34E-09	6.26E-06
GOTERM_BP_ALL	GO:0001944~vasculature development	56	7.810320781	7.95E-09	6.73E-06
GOTERM_BP_ALL	GO:0001568~blood vessel development	53	7.391910739	2.00E-08	1.34E-05
GOTERM_BP_ALL	GO:0044259~multicellular organismal macromolecule metabolic process	21	2.928870293	2.04E-08	1.34E-05
GOTERM_BP_ALL	GO:0032963~collagen metabolic process	20	2.789400279	5.15E-08	2.59E-05
GOTERM_BP_ALL	GO:0016043~cellular component organization	307	42.81729428	5.16E-08	2.59E-05
GOTERM_BP_ALL	GO:0044236~multicellular organism metabolic process	22	3.068340307	5.23E-08	2.59E-05
GOTERM_BP_ALL	GO:0043170~macromolecule metabolic process	426	59.41422594	6.46E-08	2.94E-05
GOTERM_BP_ALL	GO:0022610~biological adhesion	111	15.48117155	9.72E-08	4.12E-05
GOTERM_BP_ALL	GO:0007155~cell adhesion	110	15.34170153	1.51E-07	5.98E-05
GOTERM_BP_ALL	GO:0030574~collagen catabolic process	14	1.952580195	1.18E-06	4.39E-04
GOTERM_BP_ALL	GO:0031589~cell-substrate adhesion	32	4.463040446	1.43E-06	4.99E-04
GOTERM_BP_ALL	GO:0030334~regulation of cell migration	54	7.531380753	2.00E-06	6.59E-04
GOTERM_BP_ALL	GO:0034976~response to endoplasmic reticulum stress	29	4.044630404	2.74E-06	8.56E-04
GOTERM_BP_ALL	GO:0009653~anatomical structure morphogenesis	148	20.64156206	3.36E-06	9.95E-04
GOTERM_BP_ALL	GO:0044243~multicellular organism catabolic process	14	1.952580195	3.97E-06	0.001120304
GOTERM_BP_ALL	GO:0007275~multicellular organism development	244	34.0306834	6.55E-06	0.001763704
GOTERM_BP_ALL	GO:0035987~endodermal cell differentiation	11	1.534170153	7.54E-06	0.001917167
GOTERM_BP_ALL	GO:0016477~cell migration	78	10.87866109	7.76E-06	0.001917167
GOTERM_BP_ALL	GO:0051674~localization of cell	85	11.85495119	8.90E-06	0.001997713
GOTERM_BP_ALL	GO:0048870~cell motility	85	11.85495119	8.90E-06	0.001997713
GOTERM_BP_ALL	GO:0044260~cellular macromolecule metabolic process	385	53.69595537	9.10E-06	0.001997713
GOTERM_BP_ALL	GO:0001501~skeletal system development	41	5.718270572	1.04E-05	0.002089266
GOTERM_BP_ALL	GO:0071704~organic substance metabolic process	473	65.9693166	1.04E-05	0.002089266
GOTERM_BP_ALL	GO:0010033~response to organic substance	154	21.47838215	1.07E-05	0.002089266
GOTERM_BP_ALL	GO:0048514~blood vessel morphogenesis	41	5.718270572	1.09E-05	0.002089266
GOTERM_BP_ALL	GO:0048731~system development	217	30.26499303	1.54E-05	0.002806703
GOTERM_BP_ALL	GO:2000145~regulation of cell motility	54	7.531380753	1.56E-05	0.002806703
GOTERM_BP_ALL	GO:0008152~metabolic process	485	67.64295676	1.95E-05	0.003390691
GOTERM_BP_ALL	GO:0016485~protein processing	25	3.486750349	2.05E-05	0.003469374
GOTERM_BP_ALL	GO:0050793~regulation of developmental process	121	16.87587169	2.30E-05	0.003785446
GOTERM_BP_ALL	GO:0010810~regulation of cell-substrate adhesion	21	2.928870293	2.59E-05	0.004147702
GOTERM_BP_ALL	GO:0048646~anatomical structure formation involved in morphogenesis	74	10.32078103	3.21E-05	0.004885607
GOTERM_BP_ALL	GO:0009888~tissue development	103	14.36541144	3.21E-05	0.004885607
GOTERM_BP_ALL	GO:0048856~anatomical structure development	264	36.82008368	3.75E-05	0.005563273
GOTERM_BP_ALL	GO:0001525~angiogenesis	35	4.881450488	4.08E-05	0.005800932
GOTERM_BP_ALL	GO:0001706~endoderm formation	11	1.534170153	4.11E-05	0.005800932
GOTERM_BP_ALL	GO:1904035~regulation of epithelial cell apoptotic process	12	1.673640167	4.77E-05	0.006529371
GOTERM_BP_ALL	GO:0040012~regulation of locomotion	54	7.531380753	4.85E-05	0.006529371
GOTERM_BP_ALL	GO:0006508~proteolysis	99	13.80753138	5.35E-05	0.007053073
GOTERM_BP_ALL	GO:0044767~single-organism developmental process	263	36.68061367	5.65E-05	0.007277681
GOTERM_BP_ALL	GO:2000026~regulation of multicellular organismal development	100	13.94700139	6.27E-05	0.007903283
GOTERM_BP_ALL	GO:0051604~protein maturation	26	3.626220363	7.05E-05	0.008708851
GOTERM_BP_ALL	GO:0048251~elastic fiber assembly	5	0.69735007	7.53E-05	0.009106442
GOTERM_BP_ALL	GO:0019538~protein metabolic process	261	36.40167364	8.36E-05	0.009904879
GOTERM_BP_ALL	GO:0030335~positive regulation of cell migration	33	4.60251046	9.30E-05	0.01081345
GOTERM_BP_ALL	GO:0040011~locomotion	90	12.55230126	1.03E-04	0.011713645
GOTERM_BP_ALL	GO:0044238~primary metabolic process	449	62.62203626	1.09E-04	0.012204685
GOTERM_BP_ALL	GO:0043412~macromolecule modification	202	28.17294282	1.14E-04	0.01250485
GOTERM_BP_ALL	GO:0032502~developmental process	267	37.23849372	1.23E-04	0.013276991

GOTERM_BP_ALL	GO:0051270~regulation of cellular component movement	54	7.531380753	1.52E-04	0.016070181
GOTERM_BP_ALL	GO:0044710~single-organism metabolic process	201	28.0334728	1.57E-04	0.016345285
GOTERM_BP_ALL	GO:0061448~connective tissue development	23	3.207810321	1.62E-04	0.016592633
GOTERM_BP_ALL	GO:2000147~positive regulation of cell motility	33	4.60251046	1.75E-04	0.017607844
GOTERM_BP_ALL	GO:1904019~epithelial cell apoptotic process	13	1.813110181	1.83E-04	0.018061456
GOTERM_BP_ALL	GO:0007160~cell-matrix adhesion	20	2.789400279	2.09E-04	0.020272211
GOTERM_BP_ALL	GO:0044267~cellular protein metabolic process	235	32.77545328	2.22E-04	0.02121456
GOTERM_BP_ALL	GO:0045595~regulation of cell differentiation	89	12.41283124	2.33E-04	0.02187489
GOTERM_BP_ALL	GO:0051272~positive regulation of cellular component movement	33	4.60251046	2.82E-04	0.026133907
GOTERM_BP_ALL	GO:0006928~movement of cell or subcellular component	100	13.94700139	2.98E-04	0.027088579
GOTERM_BP_ALL	GO:0006026~aminoglycan catabolic process	11	1.534170153	3.05E-04	0.027088579
GOTERM_BP_ALL	GO:0040017~positive regulation of locomotion	33	4.60251046	3.06E-04	0.027088579
GOTERM_BP_ALL	GO:0022603~regulation of anatomical structure morphogenesis	65	9.065550907	3.13E-04	0.027261612
GOTERM_BP_ALL	GO:0051216~cartilage development	19	2.649930265	3.27E-04	0.028088658
GOTERM_BP_ALL	GO:0085029~extracellular matrix assembly	7	0.976290098	3.36E-04	0.028484555
GOTERM_BP_ALL	GO:0060284~regulation of cell development	55	7.670850767	3.47E-04	0.028791894
GOTERM_BP_ALL	GO:0032879~regulation of localization	130	18.13110181	3.50E-04	0.028791894
GOTERM_BP_ALL	GO:0044707~single-multicellular organism process	276	38.49372385	3.84E-04	0.031210758
GOTERM_BP_ALL	GO:0006464~cellular protein modification process	187	26.08089261	5.04E-04	0.03979106
GOTERM_BP_ALL	GO:0036211~protein modification process	187	26.08089261	5.04E-04	0.03979106
GOTERM_BP_ALL	GO:0051239~regulation of multicellular organismal process	137	19.10739191	5.41E-04	0.042160913
GOTERM_BP_ALL	GO:0006027~glycosaminoglycan catabolic process	10	1.394700139	5.90E-04	0.044894173
GOTERM_BP_ALL	GO:0044237~cellular metabolic process	442	61.64574616	5.91E-04	0.044894173
GOTERM_BP_ALL	GO:0007167~enzyme linked receptor protein signaling pathway	59	8.228730823	6.11E-04	0.045845639
GOTERM_BP_ALL	GO:0008285~negative regulation of cell proliferation	44	6.136680614	6.36E-04	0.047102748
GOTERM_BP_ALL	GO:0006865~amino acid transport	12	1.673640167	6.50E-04	0.047594835
GOTERM_BP_ALL	GO:0003206~cardiac chamber morphogenesis	14	1.952580195	7.46E-04	0.053918134
GOTERM_BP_ALL	GO:0044085~cellular component biogenesis	147	20.50209205	7.80E-04	0.055726024
GOTERM_BP_ALL	GO:0007492~endoderm development	11	1.534170153	8.38E-04	0.058827911
GOTERM_BP_ALL	GO:0071310~cellular response to organic substance	115	16.0390516	8.44E-04	0.058827911
GOTERM_BP_ALL	GO:0097435~fibril organization	6	0.836820084	8.76E-04	0.060360353
GOTERM_BP_ALL	GO:0030155~regulation of cell adhesion	43	5.9972106	9.00E-04	0.061248525
GOTERM_BP_ALL	GO:0043206~extracellular fibril organization	5	0.69735007	9.09E-04	0.061248525
GOTERM_BP_ALL	GO:0010811~positive regulation of cell-substrate adhesion	13	1.813110181	9.25E-04	0.061618307
GOTERM_BP_ALL	GO:0008625~extrinsic apoptotic signaling pathway via death domain receptors	11	1.534170153	0.001025661	0.067545473
GOTERM_BP_ALL	GO:2000351~regulation of endothelial cell apoptotic process	8	1.115760112	0.001141105	0.074322329
GOTERM_BP_ALL	GO:0051179~localization	269	37.51743375	0.001229288	0.079195516
GOTERM_BP_ALL	GO:0040013~negative regulation of locomotion	22	3.068340307	0.001339938	0.085395833
GOTERM_BP_ALL	GO:0051271~negative regulation of cellular component movement	22	3.068340307	0.001414143	0.089166211
GOTERM_BP_ALL	GO:0007417~central nervous system development	55	7.670850767	0.001442755	0.090012711
GOTERM_BP_ALL	GO:0018193~peptidyl-amino acid modification	68	9.483960948	0.001596324	0.098556378
GOTERM_BP_ALL	GO:0022607~cellular component assembly	132	18.41004184	0.001671799	0.101919907
GOTERM_BP_ALL	GO:0040007~growth	56	7.810320781	0.001685195	0.101919907
GOTERM_BP_ALL	GO:0043933~macromolecular complex subunit organization	125	17.43375174	0.001723803	0.103201843
GOTERM_BP_ALL	GO:0051128~regulation of cellular component organization	119	16.59693166	0.001747886	0.103597224
GOTERM_BP_ALL	GO:0003007~heart morphogenesis	20	2.789400279	0.001883626	0.110216193
GOTERM_BP_ALL	GO:0060348~bone development	17	2.370990237	0.001896752	0.110216193
GOTERM_BP_ALL	GO:0050900~leukocyte migration	28	3.905160391	0.001948917	0.112147869
GOTERM_BP_ALL	GO:0032330~regulation of chondrocyte differentiation	8	1.115760112	0.001976888	0.112183349
GOTERM_BP_ALL	GO:0007507~heart development	35	4.881450488	0.001987388	0.112183349
GOTERM_BP_ALL	GO:0000904~cell morphogenesis involved in differentiation	47	6.555090656	0.002018249	0.112850603
GOTERM_BP_ALL	GO:0051094~positive regulation of developmental process	63	8.786610879	0.002058927	0.114049183
GOTERM_BP_ALL	GO:0010467~gene expression	244	34.0306834	0.002096366	0.115047812
GOTERM_BP_ALL	GO:0009719~response to endogenous stimulus	84	11.71548117	0.002139058	0.116313717
GOTERM_BP_ALL	GO:0072577~endothelial cell apoptotic process	8	1.115760112	0.002245557	0.120223782
GOTERM_BP_ALL	GO:0048513~animal organ development	153	21.33891213	0.002251534	0.120223782
GOTERM_BP_ALL	GO:0022617~extracellular matrix disassembly	11	1.534170153	0.002345111	0.124102414
GOTERM_BP_ALL	GO:0016458~gene silencing	21	2.928870293	0.002429601	0.127014417
GOTERM_BP_ALL	GO:0007166~cell surface receptor signaling pathway	133	18.54951185	0.002442997	0.127014417
GOTERM_BP_ALL	GO:0051093~negative regulation of developmental process	46	6.415620642	0.002471529	0.127380455
GOTERM_BP_ALL	GO:0009887~organ morphogenesis	58	8.089260809	0.002537421	0.129649087

GOTERM_BP_ALL	GO:0048519~negative regulation of biological process	215	29.986053	0.002697721	0.136661456
GOTERM_BP_ALL	GO:0051240~positive regulation of multicellular organismal process	78	10.87866109	0.002895695	0.145447338
GOTERM_BP_ALL	GO:0071711~basement membrane organization	5	0.69735007	0.002949508	0.146905309
GOTERM_BP_ALL	GO:0008283~cell proliferation	97	13.52859135	0.00309086	0.152446074
GOTERM_BP_ALL	GO:0035966~response to topologically incorrect protein	17	2.370990237	0.003112194	0.152446074
GOTERM_BP_ALL	GO:0030433~ER-associated ubiquitin-dependent protein catabolic process	10	1.394700139	0.003150281	0.153046834
GOTERM_BP_ALL	GO:0048523~negative regulation of cellular process	201	28.0334728	0.003201904	0.154290118
GOTERM_BP_ALL	GO:0036503~ERAD pathway	11	1.534170153	0.003258175	0.155621386
GOTERM_BP_ALL	GO:0006986~response to unfolded protein	16	2.231520223	0.003282044	0.155621386
GOTERM_BP_ALL	GO:1904036~negative regulation of epithelial cell apoptotic process	7	0.976290098	0.003399875	0.159929018
GOTERM_BP_ALL	GO:0019511~peptidyl-proline hydroxylation	5	0.69735007	0.003738426	0.174469713
GOTERM_BP_ALL	GO:2000146~negative regulation of cell motility	19	2.649930265	0.003782714	0.174778224
GOTERM_BP_ALL	GO:0071495~cellular response to endogenous stimulus	66	9.205020921	0.003804014	0.174778224
GOTERM_BP_ALL	GO:0045597~positive regulation of cell differentiation	50	6.973500697	0.003880717	0.176930849
GOTERM_BP_ALL	GO:0010812~negative regulation of cell-substrate adhesion	8	1.115760112	0.004034712	0.181315574
GOTERM_BP_ALL	GO:0010769~regulation of cell morphogenesis involved in differentiation	25	3.486750349	0.004038073	0.181315574
GOTERM_BP_ALL	GO:0043589~skin morphogenesis	4	0.557880056	0.004250826	0.189415613
GOTERM_BP_ALL	GO:2000352~negative regulation of endothelial cell apoptotic process	6	0.836820084	0.004282384	0.189415613
GOTERM_BP_ALL	GO:0051241~negative regulation of multicellular organismal process	58	8.089260809	0.004393609	0.191626835
GOTERM_BP_ALL	GO:0009100~glycoprotein metabolic process	28	3.905160391	0.004415682	0.191626835
GOTERM_BP_ALL	GO:0034446~substrate adhesion-dependent cell spreading	10	1.394700139	0.004437044	0.191626835
GOTERM_BP_ALL	GO:0007040~lysosome organization	8	1.115760112	0.004494657	0.191626835
GOTERM_BP_ALL	GO:0080171~lytic vacuole organization	8	1.115760112	0.004494657	0.191626835
GOTERM_BP_ALL	GO:0048762~mesenchymal cell differentiation	16	2.231520223	0.004526364	0.191626835
GOTERM_BP_ALL	GO:0048518~positive regulation of biological process	240	33.47280335	0.004612221	0.193101536
GOTERM_BP_ALL	GO:0015813~L-glutamate transport	5	0.69735007	0.004658937	0.193101536
GOTERM_BP_ALL	GO:0018126~protein hydroxylation	5	0.69735007	0.004658937	0.193101536
GOTERM_BP_ALL	GO:0030336~negative regulation of cell migration	18	2.510460251	0.004756809	0.195788922
GOTERM_BP_ALL	GO:0042127~regulation of cell proliferation	82	11.43654114	0.004897115	0.200173795
GOTERM_BP_ALL	GO:0010720~positive regulation of cell development	32	4.463040446	0.005154093	0.209235015
GOTERM_BP_ALL	GO:0030162~regulation of proteolysis	43	5.9972106	0.005218743	0.210418279
GOTERM_BP_ALL	GO:0050769~positive regulation of neurogenesis	27	3.765690377	0.005594996	0.224064485
GOTERM_BP_ALL	GO:0048869~cellular developmental process	186	25.94142259	0.005695163	0.226545185
GOTERM_BP_ALL	GO:0030968~endoplasmic reticulum unfolded protein response	13	1.813110181	0.005848469	0.231092487
GOTERM_BP_ALL	GO:1904380~endoplasmic reticulum mannose trimming	4	0.557880056	0.005896522	0.231448239
GOTERM_BP_ALL	GO:0035967~cellular response to topologically incorrect protein	14	1.952580195	0.005951399	0.232065401
GOTERM_BP_ALL	GO:0051962~positive regulation of nervous system development	30	4.184100418	0.006154455	0.238414735
GOTERM_BP_ALL	GO:0014031~mesenchymal cell development	15	2.092050209	0.006253623	0.240683268
GOTERM_BP_ALL	GO:0015807~L-amino acid transport	7	0.976290098	0.006363359	0.243326656
GOTERM_BP_ALL	GO:0045765~regulation of angiogenesis	18	2.510460251	0.006688308	0.253553008
GOTERM_BP_ALL	GO:0001704~formation of primary germ layer	12	1.673640167	0.006769037	0.253553008
GOTERM_BP_ALL	GO:0031399~regulation of protein modification process	86	11.9944212	0.006800546	0.253553008
GOTERM_BP_ALL	GO:0051259~protein oligomerization	31	4.323570432	0.006808029	0.253553008
GOTERM_BP_ALL	GO:0010975~regulation of neuron projection development	28	3.905160391	0.006911824	0.253553008
GOTERM_BP_ALL	GO:0015800~acidic amino acid transport	5	0.69735007	0.006931483	0.253553008
GOTERM_BP_ALL	GO:0007035~vacuolar acidification	5	0.69735007	0.006931483	0.253553008
GOTERM_BP_ALL	GO:0034620~cellular response to unfolded protein	13	1.813110181	0.006973029	0.253553008
GOTERM_BP_ALL	GO:0060322~head development	43	5.9972106	0.007098345	0.254981505
GOTERM_BP_ALL	GO:0033627~cell adhesion mediated by integrin	7	0.976290098	0.007128962	0.254981505
GOTERM_BP_ALL	GO:0006342~chromatin silencing	12	1.673640167	0.007202206	0.254981505
GOTERM_BP_ALL	GO:0010771~negative regulation of cell morphogenesis involved in differentiation	12	1.673640167	0.007202206	0.254981505
GOTERM_BP_ALL	GO:0000902~cell morphogenesis	67	9.344490934	0.007240229	0.254981505
GOTERM_BP_ALL	GO:0046165~alcohol biosynthetic process	11	1.534170153	0.007270436	0.254981505
GOTERM_BP_ALL	GO:0009056~catabolic process	101	14.08647141	0.007612639	0.265412428
GOTERM_BP_ALL	GO:0009057~macromolecule catabolic process	65	9.065550907	0.007947655	0.274069306
GOTERM_BP_ALL	GO:0007420~brain development	41	5.718270572	0.00795342	0.274069306
GOTERM_BP_ALL	GO:0071822~protein complex subunit organization	86	11.9944212	0.008017576	0.274683079
GOTERM_BP_ALL	GO:1901342~regulation of vasculature development	19	2.649930265	0.008202596	0.278272288
GOTERM_BP_ALL	GO:0003205~cardiac chamber development	14	1.952580195	0.008216239	0.278272288
GOTERM_BP_ALL	GO:1903792~negative regulation of anion transport	5	0.69735007	0.008300614	0.279532607

GOTERM_BP_ALL	GO:0042060~wound healing	34	4.741980474	0.008652954	0.289751741
GOTERM_BP_ALL	GO:0090101~negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	11	1.534170153	0.008846845	0.294580059
GOTERM_BP_ALL	GO:0032989~cellular component morphogenesis	70	9.762900976	0.008975995	0.29721073
GOTERM_BP_ALL	GO:0030154~cell differentiation	170	23.70990237	0.009049432	0.297977692
GOTERM_BP_ALL	GO:0010976~positive regulation of neuron projection development	18	2.510460251	0.009103571	0.298104235
GOTERM_BP_ALL	GO:0015849~organic acid transport	12	1.673640167	0.009155079	0.298143715
GOTERM_BP_ALL	GO:0001932~regulation of protein phosphorylation	69	9.623430962	0.009257772	0.299840509
GOTERM_BP_ALL	GO:0009611~response to wounding	39	5.439330544	0.009336061	0.300732781
GOTERM_BP_ALL	GO:0018208~peptidyl-proline modification	8	1.115760112	0.009723921	0.30811722
GOTERM_BP_ALL	GO:1905039~carboxylic acid transmembrane transport	8	1.115760112	0.009723921	0.30811722
GOTERM_BP_ALL	GO:0042325~regulation of phosphorylation	73	10.18131102	0.009835079	0.30811722
GOTERM_BP_ALL	GO:0090181~regulation of cholesterol metabolic process	5	0.69735007	0.009835454	0.30811722
GOTERM_BP_ALL	GO:0045785~positive regulation of cell adhesion	26	3.626220363	0.00985507	0.30811722
GOTERM_BP_ALL	GO:0050808~synapse organization	18	2.510460251	0.009877218	0.30811722
GOTERM_BP_ALL	GO:0002062~chondrocyte differentiation	10	1.394700139	0.010119229	0.312837686
GOTERM_BP_ALL	GO:0071560~cellular response to transforming growth factor beta stimulus	17	2.370990237	0.010137553	0.312837686
GOTERM_BP_ALL	GO:0036066~protein O-linked fucosylation	4	0.557880056	0.010194351	0.312837686
GOTERM_BP_ALL	GO:0009790~embryo development	53	7.391910739	0.010239668	0.312837686
GOTERM_BP_ALL	GO:0065008~regulation of biological quality	165	23.0125523	0.010343961	0.313240052
GOTERM_BP_ALL	GO:0006396~RNA processing	51	7.112970711	0.010406258	0.313240052
GOTERM_BP_ALL	GO:0070085~glycosylation	21	2.928870293	0.010411387	0.313240052
GOTERM_BP_ALL	GO:0006695~cholesterol biosynthetic process	7	0.976290098	0.010864046	0.325208074
GOTERM_BP_ALL	GO:0071559~response to transforming growth factor beta	17	2.370990237	0.011021796	0.327001104
GOTERM_BP_ALL	GO:0045666~positive regulation of neuron differentiation	22	3.068340307	0.011034287	0.327001104
GOTERM_BP_ALL	GO:0010955~negative regulation of protein processing	6	0.836820084	0.011291923	0.33132291
GOTERM_BP_ALL	GO:1903318~negative regulation of protein maturation	6	0.836820084	0.011291923	0.33132291
GOTERM_BP_ALL	GO:0048522~positive regulation of cellular process	214	29.84658298	0.011420249	0.333437512
GOTERM_BP_ALL	GO:0032835~glomerulus development	8	1.115760112	0.011533489	0.333736911
GOTERM_BP_ALL	GO:0006517~protein deglycosylation	5	0.69735007	0.011543119	0.333736911
GOTERM_BP_ALL	GO:0016070~RNA metabolic process	210	29.28870293	0.011631561	0.334661461
GOTERM_BP_ALL	GO:0023056~positive regulation of signaling	80	11.15760112	0.011786733	0.335033281
GOTERM_BP_ALL	GO:1902653~secondary alcohol biosynthetic process	7	0.976290098	0.011979968	0.335033281
GOTERM_BP_ALL	GO:0046718~viral entry into host cell	11	1.534170153	0.01204017	0.335033281
GOTERM_BP_ALL	GO:0051828~entry into other organism involved in symbiotic interaction	11	1.534170153	0.01204017	0.335033281
GOTERM_BP_ALL	GO:0030260~entry into host cell	11	1.534170153	0.01204017	0.335033281
GOTERM_BP_ALL	GO:0044409~entry into host	11	1.534170153	0.01204017	0.335033281
GOTERM_BP_ALL	GO:0051806~entry into cell of other organism involved in symbiotic interaction	11	1.534170153	0.01204017	0.335033281
GOTERM_BP_ALL	GO:0050767~regulation of neurogenesis	40	5.578800558	0.012420563	0.341047851
GOTERM_BP_ALL	GO:0051960~regulation of nervous system development	44	6.136680614	0.01251096	0.341047851
GOTERM_BP_ALL	GO:1903825~organic acid transmembrane transport	8	1.115760112	0.012524245	0.341047851
GOTERM_BP_ALL	GO:0061035~regulation of cartilage development	8	1.115760112	0.012524245	0.341047851
GOTERM_BP_ALL	GO:0009101~glycoprotein biosynthetic process	24	3.347280335	0.012870718	0.341047851
GOTERM_BP_ALL	GO:0036507~protein demannosylation	4	0.557880056	0.012870781	0.341047851
GOTERM_BP_ALL	GO:0071028~nuclear mRNA surveillance	4	0.557880056	0.012870781	0.341047851
GOTERM_BP_ALL	GO:0071027~nuclear RNA surveillance	4	0.557880056	0.012870781	0.341047851
GOTERM_BP_ALL	GO:0045540~regulation of cholesterol biosynthetic process	4	0.557880056	0.012870781	0.341047851
GOTERM_BP_ALL	GO:0036508~protein alpha-1,2-demannosylation	4	0.557880056	0.012870781	0.341047851
GOTERM_BP_ALL	GO:0007162~negative regulation of cell adhesion	17	2.370990237	0.012889273	0.341047851
GOTERM_BP_ALL	GO:0031401~positive regulation of protein modification process	61	8.507670851	0.013187029	0.347048668
GOTERM_BP_ALL	GO:0010256~endomembrane system organization	34	4.741980474	0.01323317	0.347048668
GOTERM_BP_ALL	GO:0035295~tube development	35	4.881450488	0.013374116	0.349199934
GOTERM_BP_ALL	GO:0031175~neuron projection development	46	6.415620642	0.014032473	0.362572205
GOTERM_BP_ALL	GO:0070887~cellular response to chemical stimulus	126	17.57322176	0.014130935	0.362572205
GOTERM_BP_ALL	GO:0048536~spleen development	6	0.836820084	0.014221651	0.362572205
GOTERM_BP_ALL	GO:0045542~positive regulation of cholesterol biosynthetic process	3	0.418410042	0.01425193	0.362572205
GOTERM_BP_ALL	GO:0010757~negative regulation of plasminogen activation	3	0.418410042	0.01425193	0.362572205
GOTERM_BP_ALL	GO:0001935~endothelial cell proliferation	11	1.534170153	0.014333813	0.362572205
GOTERM_BP_ALL	GO:0006486~protein glycosylation	20	2.789400279	0.014375648	0.362572205
GOTERM_BP_ALL	GO:0043413~macromolecule glycosylation	20	2.789400279	0.014375648	0.362572205

GOTERM_BP_ALL	GO:0010647~positive regulation of cell communication	79	11.0181311	0.0145189	0.364551627
GOTERM_BP_ALL	GO:0006629~lipid metabolic process	69	9.623430962	0.014577145	0.364551627
GOTERM_BP_ALL	GO:0006399~tRNA metabolic process	15	2.092050209	0.014643488	0.364672066
GOTERM_BP_ALL	GO:0001667~ameboidal-type cell migration	22	3.068340307	0.015311559	0.379713854
GOTERM_BP_ALL	GO:1904037~positive regulation of epithelial cell apoptotic process	5	0.69735007	0.015502301	0.381253676
GOTERM_BP_ALL	GO:0006465~signal peptide processing	5	0.69735007	0.015502301	0.381253676
GOTERM_BP_ALL	GO:0051966~regulation of synaptic transmission, glutamatergic	7	0.976290098	0.015807614	0.387155908
GOTERM_BP_ALL	GO:0044255~cellular lipid metabolic process	56	7.810320781	0.015900667	0.387832314
GOTERM_BP_ALL	GO:0097191~extrinsic apoptotic signaling pathway	17	2.370990237	0.016264022	0.395069087
GOTERM_BP_ALL	GO:0001558~regulation of cell growth	26	3.626220363	0.016724019	0.40458474
GOTERM_BP_ALL	GO:0001936~regulation of endothelial cell proliferation	10	1.394700139	0.016849438	0.405961858
GOTERM_BP_ALL	GO:0033554~cellular response to stress	88	12.27336123	0.017102495	0.410390643
GOTERM_BP_ALL	GO:0070848~response to growth factor	37	5.160390516	0.017241661	0.410648782
GOTERM_BP_ALL	GO:0003333~amino acid transmembrane transport	7	0.976290098	0.017251822	0.410648782
GOTERM_BP_ALL	GO:0044723~single-organism carbohydrate metabolic process	38	5.29986053	0.017744597	0.419493095
GOTERM_BP_ALL	GO:0050820~positive regulation of coagulation	5	0.69735007	0.017764935	0.419493095
GOTERM_BP_ALL	GO:0003231~cardiac ventricle development	11	1.534170153	0.017880818	0.420554002
GOTERM_BP_ALL	GO:0010721~negative regulation of cell development	21	2.928870293	0.018335175	0.427796166
GOTERM_BP_ALL	GO:0045814~negative regulation of gene expression, epigenetic	12	1.673640167	0.018399352	0.427796166
GOTERM_BP_ALL	GO:0007369~gastrulation	14	1.952580195	0.018405268	0.427796166
GOTERM_BP_ALL	GO:0060548~negative regulation of cell death	49	6.834030683	0.018646453	0.431709087
GOTERM_BP_ALL	GO:0016126~sterol biosynthetic process	7	0.976290098	0.018784164	0.433205207
GOTERM_BP_ALL	GO:0071025~RNA surveillance	4	0.557880056	0.019316871	0.443763943
GOTERM_BP_ALL	GO:0006665~sphingolipid metabolic process	13	1.813110181	0.019406415	0.444099706
GOTERM_BP_ALL	GO:0006468~protein phosphorylation	91	12.69177127	0.019697994	0.447646026
GOTERM_BP_ALL	GO:0036498~IRE1-mediated unfolded protein response	8	1.115760112	0.019787963	0.447646026
GOTERM_BP_ALL	GO:0010717~regulation of epithelial to mesenchymal transition	8	1.115760112	0.019787963	0.447646026
GOTERM_BP_ALL	GO:0010941~regulation of cell death	76	10.59972106	0.019914171	0.448788183
GOTERM_BP_ALL	GO:0051246~regulation of protein metabolic process	119	16.59693166	0.020051393	0.450168961
GOTERM_BP_ALL	GO:0044712~single-organism catabolic process	46	6.415620642	0.020394049	0.456134068
GOTERM_BP_ALL	GO:0090205~positive regulation of cholesterol metabolic process	3	0.418410042	0.020824937	0.460557462
GOTERM_BP_ALL	GO:0032914~positive regulation of transforming growth factor beta1 production	3	0.418410042	0.020824937	0.460557462
GOTERM_BP_ALL	GO:1903224~regulation of endodermal cell differentiation	3	0.418410042	0.020824937	0.460557462
GOTERM_BP_ALL	GO:0098657~import into cell	8	1.115760112	0.021234695	0.466140881
GOTERM_BP_ALL	GO:0071260~cellular response to mechanical stimulus	8	1.115760112	0.021234695	0.466140881
GOTERM_BP_ALL	GO:0030324~lung development	14	1.952580195	0.021801354	0.476814125
GOTERM_BP_ALL	GO:1903036~positive regulation of response to wounding	7	0.976290098	0.022122129	0.48031386
GOTERM_BP_ALL	GO:0007033~vacuole organization	16	2.231520223	0.022123449	0.48031386
GOTERM_BP_ALL	GO:0003208~cardiac ventricle morphogenesis	8	1.115760112	0.022753257	0.49218451
GOTERM_BP_ALL	GO:0098739~import across plasma membrane	5	0.69735007	0.022879323	0.49311181
GOTERM_BP_ALL	GO:0060841~venous blood vessel development	4	0.557880056	0.023093955	0.495934326
GOTERM_BP_ALL	GO:0060255~regulation of macromolecule metabolic process	254	35.42538354	0.02341861	0.499300424
GOTERM_BP_ALL	GO:0005975~carbohydrate metabolic process	43	5.9972106	0.023419186	0.499300424
GOTERM_BP_ALL	GO:0006509~membrane protein ectodomain proteolysis	6	0.836820084	0.023664159	0.50106934
GOTERM_BP_ALL	GO:0007229~integrin-mediated signaling pathway	10	1.394700139	0.023707024	0.50106934
GOTERM_BP_ALL	GO:0007169~transmembrane receptor protein tyrosine kinase signaling pathway	37	5.160390516	0.023755776	0.50106934
GOTERM_BP_ALL	GO:0052547~regulation of peptidase activity	25	3.486750349	0.023907969	0.502491259
GOTERM_BP_ALL	GO:0006914~autophagy	26	3.626220363	0.024187936	0.506579149
GOTERM_BP_ALL	GO:0001934~positive regulation of protein phosphorylation	48	6.694560669	0.024467219	0.510623965
GOTERM_BP_ALL	GO:0080090~regulation of primary metabolic process	253	35.28591353	0.024897377	0.515866115
GOTERM_BP_ALL	GO:0002576~platelet degranulation	10	1.394700139	0.025018491	0.515866115
GOTERM_BP_ALL	GO:0030168~platelet activation	13	1.813110181	0.02525132	0.515866115
GOTERM_BP_ALL	GO:0071363~cellular response to growth factor stimulus	35	4.881450488	0.025283049	0.515866115
GOTERM_BP_ALL	GO:1902533~positive regulation of intracellular signal transduction	49	6.834030683	0.025351318	0.515866115
GOTERM_BP_ALL	GO:0071496~cellular response to external stimulus	18	2.510460251	0.02536884	0.515866115
GOTERM_BP_ALL	GO:0050878~regulation of body fluid levels	30	4.184100418	0.025492521	0.515866115
GOTERM_BP_ALL	GO:0048468~cell development	95	13.24965132	0.025503327	0.515866115
GOTERM_BP_ALL	GO:1904018~positive regulation of vasculature development	12	1.673640167	0.025604742	0.515866115
GOTERM_BP_ALL	GO:0030323~respiratory tube development	14	1.952580195	0.025644099	0.515866115
GOTERM_BP_ALL	GO:0032268~regulation of cellular protein metabolic process	111	15.48117155	0.025675806	0.515866115

GOTERM_BP_ALL	GO:0061061~muscle structure development	34	4.741980474	0.025780448	0.516218634
GOTERM_BP_ALL	GO:0022604~regulation of cell morphogenesis	33	4.60251046	0.026174614	0.522346596
GOTERM_BP_ALL	GO:0007219~Notch signaling pathway	13	1.813110181	0.026338507	0.523853467
GOTERM_BP_ALL	GO:0006925~inflammatory cell apoptotic process	4	0.557880056	0.027241569	0.540002603
GOTERM_BP_ALL	GO:0051641~cellular localization	119	16.59693166	0.027363314	0.540607874
GOTERM_BP_ALL	GO:0009612~response to mechanical stimulus	15	2.092050209	0.027724058	0.54291416
GOTERM_BP_ALL	GO:1901136~carbohydrate derivative catabolic process	14	1.952580195	0.027742529	0.54291416
GOTERM_BP_ALL	GO:0016525~negative regulation of angiogenesis	8	1.115760112	0.027754849	0.54291416
GOTERM_BP_ALL	GO:0048598~embryonic morphogenesis	33	4.60251046	0.027928371	0.544511356
GOTERM_BP_ALL	GO:0032270~positive regulation of cellular protein metabolic process	71	9.90237099	0.028151031	0.544811303
GOTERM_BP_ALL	GO:0045766~positive regulation of angiogenesis	11	1.534170153	0.028163239	0.544811303
GOTERM_BP_ALL	GO:0044273~sulfur compound catabolic process	6	0.836820084	0.028352326	0.544811303
GOTERM_BP_ALL	GO:2000542~negative regulation of gastrulation	3	0.418410042	0.028403356	0.544811303
GOTERM_BP_ALL	GO:0048050~post-embryonic eye morphogenesis	3	0.418410042	0.028403356	0.544811303
GOTERM_BP_ALL	GO:0042981~regulation of apoptotic process	70	9.762900976	0.029265802	0.559454315
GOTERM_BP_ALL	GO:0006915~apoptotic process	85	11.85495119	0.029355541	0.559454315
GOTERM_BP_ALL	GO:0006835~dicarboxylic acid transport	8	1.115760112	0.029575354	0.561836938
GOTERM_BP_ALL	GO:0007399~nervous system development	103	14.36541144	0.029723809	0.562031757
GOTERM_BP_ALL	GO:0001952~regulation of cell-matrix adhesion	9	1.255230126	0.029850607	0.562031757
GOTERM_BP_ALL	GO:0019222~regulation of metabolic process	267	37.23849372	0.029870087	0.562031757
GOTERM_BP_ALL	GO:0045596~negative regulation of cell differentiation	36	5.020920502	0.030623755	0.574389219
GOTERM_BP_ALL	GO:0040029~regulation of gene expression, epigenetic	18	2.510460251	0.030810267	0.576064519
GOTERM_BP_ALL	GO:0006643~membrane lipid metabolic process	15	2.092050209	0.030916008	0.576223834
GOTERM_BP_ALL	GO:2000181~negative regulation of blood vessel morphogenesis	8	1.115760112	0.03147469	0.584797769
GOTERM_BP_ALL	GO:0016075~rRNA catabolic process	4	0.557880056	0.031758095	0.586675429
GOTERM_BP_ALL	GO:0009967~positive regulation of signal transduction	71	9.90237099	0.031773716	0.586675429
GOTERM_BP_ALL	GO:0007517~muscle organ development	23	3.207810321	0.031879044	0.586792211
GOTERM_BP_ALL	GO:0003209~cardiac atrium morphogenesis	5	0.69735007	0.032073958	0.588552165
GOTERM_BP_ALL	GO:0014070~response to organic cyclic compound	48	6.694560669	0.032218612	0.589381834
GOTERM_BP_ALL	GO:0042327~positive regulation of phosphorylation	49	6.834030683	0.033357386	0.60451898
GOTERM_BP_ALL	GO:0043067~regulation of programmed cell death	70	9.762900976	0.033410341	0.60451898
GOTERM_BP_ALL	GO:0050673~epithelial cell proliferation	22	3.068340307	0.033446637	0.60451898
GOTERM_BP_ALL	GO:0007041~lysosomal transport	8	1.115760112	0.033454062	0.60451898
GOTERM_BP_ALL	GO:0010632~regulation of epithelial cell migration	13	1.813110181	0.034922805	0.629141238
GOTERM_BP_ALL	GO:0031647~regulation of protein stability	16	2.231520223	0.035540152	0.636643935
GOTERM_BP_ALL	GO:0001937~negative regulation of endothelial cell proliferation	5	0.69735007	0.035554099	0.636643935
GOTERM_BP_ALL	GO:0097190~apoptotic signaling pathway	33	4.60251046	0.035904023	0.640973329
GOTERM_BP_ALL	GO:0060411~cardiac septum morphogenesis	7	0.976290098	0.036876538	0.654778132
GOTERM_BP_ALL	GO:0072102~glomerulus morphogenesis	3	0.418410042	0.036898245	0.654778132
GOTERM_BP_ALL	GO:0010594~regulation of endothelial cell migration	10	1.394700139	0.037406589	0.660819461
GOTERM_BP_ALL	GO:0090304~nucleic acid metabolic process	225	31.38075314	0.037461674	0.660819461
GOTERM_BP_ALL	GO:0007584~response to nutrient	13	1.813110181	0.037703492	0.662138891
GOTERM_BP_ALL	GO:0031325~positive regulation of cellular metabolic process	130	18.13110181	0.037759903	0.662138891
GOTERM_BP_ALL	GO:0016049~cell growth	26	3.626220363	0.037987713	0.664168661
GOTERM_BP_ALL	GO:0040008~regulation of growth	36	5.020920502	0.038439333	0.669061238
GOTERM_BP_ALL	GO:0033157~regulation of intracellular protein transport	23	3.207810321	0.038493316	0.669061238
GOTERM_BP_ALL	GO:0033036~macromolecule localization	129	17.9916318	0.039541276	0.685266505
GOTERM_BP_ALL	GO:0022411~cellular component disassembly	29	4.044630404	0.039874184	0.689021257
GOTERM_BP_ALL	GO:0009725~response to hormone	45	6.276150628	0.040273296	0.693894833
GOTERM_BP_ALL	GO:0001654~eye development	21	2.928870293	0.04074237	0.698046246
GOTERM_BP_ALL	GO:0043542~endothelial cell migration	12	1.673640167	0.040749789	0.698046246
GOTERM_BP_ALL	GO:0032331~negative regulation of chondrocyte differentiation	4	0.557880056	0.041882882	0.711288949
GOTERM_BP_ALL	GO:0060445~branching involved in salivary gland morphogenesis	4	0.557880056	0.041882882	0.711288949
GOTERM_BP_ALL	GO:1902932~positive regulation of alcohol biosynthetic process	4	0.557880056	0.041882882	0.711288949
GOTERM_BP_ALL	GO:0010952~positive regulation of peptidase activity	12	1.673640167	0.042380186	0.717678177
GOTERM_BP_ALL	GO:0099587~inorganic ion import into cell	5	0.69735007	0.043143905	0.720476202
GOTERM_BP_ALL	GO:1902930~regulation of alcohol biosynthetic process	5	0.69735007	0.043143905	0.720476202
GOTERM_BP_ALL	GO:0098659~inorganic cation import into cell	5	0.69735007	0.043143905	0.720476202
GOTERM_BP_ALL	GO:0017015~regulation of transforming growth factor beta receptor signaling pathway	9	1.255230126	0.043153206	0.720476202
GOTERM_BP_ALL	GO:1903844~regulation of cellular response to transforming growth factor beta stimulus	9	1.255230126	0.043153206	0.720476202

GOTERM_BP_ALL	GO:0060485~mesenchyme development	16	2.231520223	0.043430224	0.723064424
GOTERM_BP_ALL	GO:0045862~positive regulation of proteolysis	22	3.068340307	0.04370739	0.723074563
GOTERM_BP_ALL	GO:0050817~coagulation	22	3.068340307	0.04370739	0.723074563
GOTERM_BP_ALL	GO:0042221~response to chemical	182	25.38354254	0.043833831	0.723074563
GOTERM_BP_ALL	GO:0046942~carboxylic acid transport	18	2.510460251	0.043918819	0.723074563
GOTERM_BP_ALL	GO:0031344~regulation of cell projection organization	32	4.463040446	0.044228449	0.726155174
GOTERM_BP_ALL	GO:1901343~negative regulation of vasculature development	8	1.115760112	0.044588638	0.728035413
GOTERM_BP_ALL	GO:0070613~regulation of protein processing	8	1.115760112	0.044588638	0.728035413
GOTERM_BP_ALL	GO:0034332~adherens junction organization	10	1.394700139	0.044946383	0.731860476
GOTERM_BP_ALL	GO:0051234~establishment of localization	209	29.14923291	0.045261017	0.734964508
GOTERM_BP_ALL	GO:0090303~positive regulation of wound healing	6	0.836820084	0.045764692	0.740491806
GOTERM_BP_ALL	GO:0032905~transforming growth factor beta1 production	3	0.418410042	0.046226079	0.740491806
GOTERM_BP_ALL	GO:0032908~regulation of transforming growth factor beta1 production	3	0.418410042	0.046226079	0.740491806
GOTERM_BP_ALL	GO:1901409~positive regulation of phosphorylation of RNA polymerase II C-terminal domain	3	0.418410042	0.046226079	0.740491806
GOTERM_BP_ALL	GO:0048563~post-embryonic organ morphogenesis	3	0.418410042	0.046226079	0.740491806
GOTERM_BP_ALL	GO:0043066~negative regulation of apoptotic process	43	5.9972106	0.046852704	0.74487632
GOTERM_BP_ALL	GO:1903317~regulation of protein maturation	8	1.115760112	0.047069488	0.74487632
GOTERM_BP_ALL	GO:0051897~positive regulation of protein kinase B signaling	8	1.115760112	0.047069488	0.74487632
GOTERM_BP_ALL	GO:0043277~apoptotic cell clearance	5	0.69735007	0.047253838	0.74487632
GOTERM_BP_ALL	GO:2000736~regulation of stem cell differentiation	5	0.69735007	0.047253838	0.74487632
GOTERM_BP_ALL	GO:0003230~cardiac atrium development	5	0.69735007	0.047253838	0.74487632
GOTERM_BP_ALL	GO:0051701~interaction with host	12	1.673640167	0.047539872	0.747397407
GOTERM_BP_ALL	GO:0031667~response to nutrient levels	24	3.347280335	0.048306218	0.753773583
GOTERM_BP_ALL	GO:0000377~RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	19	2.649930265	0.048326972	0.753773583
GOTERM_BP_ALL	GO:0000398~mRNA splicing, via spliceosome	19	2.649930265	0.048326972	0.753773583
GOTERM_BP_ALL	GO:0051291~protein heterooligomerization	10	1.394700139	0.049071504	0.759744372
GOTERM_BP_ALL	GO:0048729~tissue morphogenesis	34	4.741980474	0.049166645	0.759744372
GOTERM_BP_ALL	GO:0007156~homophilic cell adhesion via plasma membrane adhesion molecules	12	1.673640167	0.049350697	0.759744372
GOTERM_BP_ALL	GO:0031047~gene silencing by RNA	12	1.673640167	0.049350697	0.759744372
GOTERM_BP_ALL	GO:0007179~transforming growth factor beta receptor signaling pathway	12	1.673640167	0.049350697	0.759744372
GOTERM_BP_ALL	GO:0007596~blood coagulation	21	2.928870293	0.0498629	0.765640948
GOTERM_BP_ALL	GO:0031323~regulation of cellular metabolic process	251	35.0069735	0.049994894	0.765684067
GOTERM_BP_ALL	GO:0006807~nitrogen compound metabolic process	295	41.14365411	0.050223001	0.767195174
GOTERM_BP_ALL	GO:0010595~positive regulation of endothelial cell migration	7	0.976290098	0.050547884	0.770173034
GOTERM_BP_ALL	GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	20	2.789400279	0.051246771	0.778819511
GOTERM_BP_ALL	GO:1990138~neuron projection extension	11	1.534170153	0.051558704	0.781393216
GOTERM_BP_ALL	GO:0042063~gliogenesis	16	2.231520223	0.051789127	0.781393216
GOTERM_BP_ALL	GO:0022008~neurogenesis	70	9.762900976	0.051811631	0.781393216
GOTERM_BP_ALL	GO:0009966~regulation of signal transduction	124	17.29428173	0.052015972	0.782434681
GOTERM_BP_ALL	GO:0006493~protein O-linked glycosylation	9	1.255230126	0.052276722	0.782434681
GOTERM_BP_ALL	GO:0001837~epithelial to mesenchymal transition	9	1.255230126	0.052276722	0.782434681
GOTERM_BP_ALL	GO:0016310~phosphorylation	103	14.36541144	0.052567183	0.783769331
GOTERM_BP_ALL	GO:0051049~regulation of transport	85	11.85495119	0.052760206	0.783769331
GOTERM_BP_ALL	GO:0045664~regulation of neuron differentiation	31	4.323570432	0.052902136	0.783769331
GOTERM_BP_ALL	GO:0046903~secretion	55	7.670850767	0.052984528	0.783769331
GOTERM_BP_ALL	GO:2001236~regulation of extrinsic apoptotic signaling pathway	12	1.673640167	0.053111121	0.783769331
GOTERM_BP_ALL	GO:0000375~RNA splicing, via transesterification reactions	19	2.649930265	0.053229224	0.783769331
GOTERM_BP_ALL	GO:0098743~cell aggregation	4	0.557880056	0.053423791	0.783769331
GOTERM_BP_ALL	GO:0001502~cartilage condensation	4	0.557880056	0.053423791	0.783769331
GOTERM_BP_ALL	GO:0010001~glial cell differentiation	13	1.813110181	0.053962216	0.785536237
GOTERM_BP_ALL	GO:0006996~organelle organization	166	23.15202232	0.054032165	0.785536237
GOTERM_BP_ALL	GO:0030258~lipid modification	17	2.370990237	0.054253449	0.785536237
GOTERM_BP_ALL	GO:0006810~transport	203	28.31241283	0.054327307	0.785536237
GOTERM_BP_ALL	GO:0070727~cellular macromolecule localization	77	10.73919107	0.054575042	0.785536237
GOTERM_BP_ALL	GO:0010604~positive regulation of macromolecule metabolic process	129	17.9916318	0.054638884	0.785536237
GOTERM_BP_ALL	GO:1903827~regulation of cellular protein localization	31	4.323570432	0.054656563	0.785536237
GOTERM_BP_ALL	GO:0008104~protein localization	112	15.62064156	0.054727071	0.785536237

GOTERM_BP_ALL	GO:2001237~negative regulation of extrinsic apoptotic signaling pathway	9	1.255230126	0.054737045	0.785536237
GOTERM_BP_ALL	GO:0048666~neuron development	49	6.834030683	0.055285384	0.788126772
GOTERM_BP_ALL	GO:0071526~semaphorin-plexin signaling pathway	5	0.69735007	0.056100546	0.788126772
GOTERM_BP_ALL	GO:0032964~collagen biosynthetic process	5	0.69735007	0.056100546	0.788126772
GOTERM_BP_ALL	GO:0016032~viral process	49	6.834030683	0.056252151	0.788126772
GOTERM_BP_ALL	GO:0032940~secretion by cell	49	6.834030683	0.056252151	0.788126772
GOTERM_BP_ALL	GO:1901407~regulation of phosphorylation of RNA polymerase II C-terminal domain	3	0.418410042	0.056308468	0.788126772
GOTERM_BP_ALL	GO:0071404~cellular response to low-density lipoprotein particle stimulus	3	0.418410042	0.056308468	0.788126772
GOTERM_BP_ALL	GO:0010755~regulation of plasminogen activation	3	0.418410042	0.056308468	0.788126772
GOTERM_BP_ALL	GO:0048845~venous blood vessel morphogenesis	3	0.418410042	0.056308468	0.788126772
GOTERM_BP_ALL	GO:0042493~response to drug	24	3.347280335	0.05656903	0.788126772
GOTERM_BP_ALL	GO:0009893~positive regulation of metabolic process	137	19.10739191	0.056575059	0.788126772
GOTERM_BP_ALL	GO:0043069~negative regulation of programmed cell death	43	5.9972106	0.056655435	0.788126772
GOTERM_BP_ALL	GO:0002040~sprouting angiogenesis	7	0.976290098	0.056779168	0.788126772
GOTERM_BP_ALL	GO:0008593~regulation of Notch signaling pathway	7	0.976290098	0.056779168	0.788126772
GOTERM_BP_ALL	GO:0046834~lipid phosphorylation	9	1.255230126	0.057270108	0.791235267
GOTERM_BP_ALL	GO:0048675~axon extension	9	1.255230126	0.057270108	0.791235267
GOTERM_BP_ALL	GO:0060541~respiratory system development	14	1.952580195	0.057832122	0.795712488
GOTERM_BP_ALL	GO:0051453~regulation of intracellular pH	8	1.115760112	0.057862676	0.795712488
GOTERM_BP_ALL	GO:0002009~morphogenesis of an epithelium	29	4.044630404	0.05802515	0.796099683
GOTERM_BP_ALL	GO:2000116~regulation of cysteine-type endopeptidase activity	15	2.092050209	0.058713744	0.803686739
GOTERM_BP_ALL	GO:1901617~organic hydroxy compound biosynthetic process	12	1.673640167	0.059103971	0.805308595
GOTERM_BP_ALL	GO:0010770~positive regulation of cell morphogenesis involved in differentiation	12	1.673640167	0.059103971	0.805308595
GOTERM_BP_ALL	GO:0009991~response to extracellular stimulus	25	3.486750349	0.059771917	0.812541638
GOTERM_BP_ALL	GO:0048592~eye morphogenesis	11	1.534170153	0.060089757	0.814993105
GOTERM_BP_ALL	GO:0051896~regulation of protein kinase B signaling	10	1.394700139	0.060453192	0.816701966
GOTERM_BP_ALL	GO:0044764~multi-organism cellular process	49	6.834030683	0.060518212	0.816701966
GOTERM_BP_ALL	GO:0052548~regulation of endopeptidase activity	22	3.068340307	0.060629132	0.816701966
GOTERM_BP_ALL	GO:0050818~regulation of coagulation	8	1.115760112	0.060780824	0.816888765
GOTERM_BP_ALL	GO:0051649~establishment of localization in cell	93	12.9707113	0.061310075	0.821976287
GOTERM_BP_ALL	GO:0044419~interspecies interaction between organisms	50	6.973500697	0.061575413	0.821976287
GOTERM_BP_ALL	GO:0044403~symbiosis, encompassing mutualism through parasitism	50	6.973500697	0.061575413	0.821976287
GOTERM_BP_ALL	GO:0051276~chromosome organization	58	8.089260809	0.062014019	0.825970985
GOTERM_BP_ALL	GO:0051260~protein homooligomerization	17	2.370990237	0.062440002	0.829780029
GOTERM_BP_ALL	GO:0051247~positive regulation of protein metabolic process	72	10.041841	0.06279156	0.829802035
GOTERM_BP_ALL	GO:0051017~actin filament bundle assembly	10	1.394700139	0.062915985	0.829802035
GOTERM_BP_ALL	GO:0090288~negative regulation of cellular response to growth factor stimulus	10	1.394700139	0.062915985	0.829802035
GOTERM_BP_ALL	GO:0023051~regulation of signaling	137	19.10739191	0.063001673	0.829802035
GOTERM_BP_ALL	GO:0030641~regulation of cellular pH	8	1.115760112	0.063787591	0.834926686
GOTERM_BP_ALL	GO:0007034~vacuolar transport	18	2.510460251	0.063968813	0.834926686
GOTERM_BP_ALL	GO:0034660~ncRNA metabolic process	31	4.323570432	0.064082039	0.834926686
GOTERM_BP_ALL	GO:0033993~response to lipid	44	6.136680614	0.06413791	0.834926686
GOTERM_BP_ALL	GO:0010646~regulation of cell communication	135	18.82845188	0.064226474	0.834926686
GOTERM_BP_ALL	GO:1902041~regulation of extrinsic apoptotic signaling pathway via death domain receptors	6	0.836820084	0.064235966	0.834926686
GOTERM_BP_ALL	GO:1903034~regulation of response to wounding	11	1.534170153	0.064679968	0.838858137
GOTERM_BP_ALL	GO:0010631~epithelial cell migration	15	2.092050209	0.065619446	0.846263507
GOTERM_BP_ALL	GO:0035850~epithelial cell differentiation involved in kidney development	5	0.69735007	0.065773127	0.846263507
GOTERM_BP_ALL	GO:0030030~cell projection organization	63	8.786610879	0.065799507	0.846263507
GOTERM_BP_ALL	GO:0035411~catenin import into nucleus	4	0.557880056	0.066316718	0.846263507
GOTERM_BP_ALL	GO:0007064~mitotic sister chromatid cohesion	4	0.557880056	0.066316718	0.846263507
GOTERM_BP_ALL	GO:0036065~fucosylation	4	0.557880056	0.066316718	0.846263507
GOTERM_BP_ALL	GO:0016601~Rac protein signal transduction	4	0.557880056	0.066316718	0.846263507
GOTERM_BP_ALL	GO:0032436~positive regulation of proteasomal ubiquitin-dependent protein catabolic process	7	0.976290098	0.066953817	0.846263507
GOTERM_BP_ALL	GO:0060415~muscle tissue morphogenesis	7	0.976290098	0.066953817	0.846263507
GOTERM_BP_ALL	GO:0019220~regulation of phosphate metabolic process	76	10.59972106	0.067065523	0.846263507
GOTERM_BP_ALL	GO:0070102~interleukin-6-mediated signaling pathway	3	0.418410042	0.067071881	0.846263507

GOTERM_BP_ALL	GO:0051248~negative regulation of protein metabolic process	52	7.252440725	0.067372631	0.846263507
GOTERM_BP_ALL	GO:0010562~positive regulation of phosphorus metabolic process	52	7.252440725	0.067372631	0.846263507
GOTERM_BP_ALL	GO:0045937~positive regulation of phosphate metabolic process	52	7.252440725	0.067372631	0.846263507
GOTERM_BP_ALL	GO:0010605~negative regulation of macromolecule metabolic process	106	14.78382148	0.067392673	0.846263507
GOTERM_BP_ALL	GO:0033619~membrane protein proteolysis	6	0.836820084	0.068364773	0.856655414
GOTERM_BP_ALL	GO:0051174~regulation of phosphorus metabolic process	76	10.59972106	0.068799924	0.860289339
GOTERM_BP_ALL	GO:0065003~macromolecular complex assembly	80	11.15760112	0.069934916	0.872640526
GOTERM_BP_ALL	GO:0070482~response to oxygen levels	19	2.649930265	0.07034635	0.875930288
GOTERM_BP_ALL	GO:0010977~negative regulation of neuron projection development	10	1.394700139	0.070682637	0.87827252
GOTERM_BP_ALL	GO:0048699~generation of neurons	65	9.065550907	0.07106539	0.88078828
GOTERM_BP_ALL	GO:0007599~hemostasis	21	2.928870293	0.071435925	0.88078828
GOTERM_BP_ALL	GO:1901137~carbohydrate derivative biosynthetic process	39	5.439330544	0.071481075	0.88078828
GOTERM_BP_ALL	GO:0009059~macromolecule biosynthetic process	222	30.9623431	0.071644892	0.88078828
GOTERM_BP_ALL	GO:0044283~small molecule biosynthetic process	27	3.765690377	0.071770689	0.88078828
GOTERM_BP_ALL	GO:0090132~epithelium migration	15	2.092050209	0.07177674	0.88078828
GOTERM_BP_ALL	GO:0032880~regulation of protein localization	48	6.694560669	0.072275206	0.885072619
GOTERM_BP_ALL	GO:0035195~gene silencing by miRNA	6	0.836820084	0.072637161	0.885977112
GOTERM_BP_ALL	GO:1900048~positive regulation of hemostasis	4	0.557880056	0.073245957	0.885977112
GOTERM_BP_ALL	GO:0071354~cellular response to interleukin-6	4	0.557880056	0.073245957	0.885977112
GOTERM_BP_ALL	GO:0034661~ncRNA catabolic process	4	0.557880056	0.073245957	0.885977112
GOTERM_BP_ALL	GO:0032365~intracellular lipid transport	4	0.557880056	0.073245957	0.885977112
GOTERM_BP_ALL	GO:0030194~positive regulation of blood coagulation	4	0.557880056	0.073245957	0.885977112
GOTERM_BP_ALL	GO:0061572~actin filament bundle organization	10	1.394700139	0.073398282	0.886011441
GOTERM_BP_ALL	GO:0048705~skeletal system morphogenesis	14	1.952580195	0.073579887	0.886148272
GOTERM_BP_ALL	GO:0001503~ossification	21	2.928870293	0.073708638	0.886148272
GOTERM_BP_ALL	GO:0032434~regulation of proteasomal ubiquitin-dependent protein catabolic process	9	1.255230126	0.074013955	0.888017637
GOTERM_BP_ALL	GO:0042592~homeostatic process	77	10.73919107	0.074908566	0.896935495
GOTERM_BP_ALL	GO:0045861~negative regulation of proteolysis	19	2.649930265	0.075416029	0.900930559
GOTERM_BP_ALL	GO:0090092~regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	14	1.952580195	0.075726048	0.900930559
GOTERM_BP_ALL	GO:1902531~regulation of intracellular signal transduction	80	11.15760112	0.075843231	0.900930559
GOTERM_BP_ALL	GO:0032527~protein exit from endoplasmic reticulum	5	0.69735007	0.076253516	0.900930559
GOTERM_BP_ALL	GO:0009791~post-embryonic development	8	1.115760112	0.07670358	0.900930559
GOTERM_BP_ALL	GO:0045807~positive regulation of endocytosis	9	1.255230126	0.077064014	0.900930559
GOTERM_BP_ALL	GO:1904235~regulation of substrate-dependent cell migration, cell attachment to substrate	2	0.278940028	0.077066272	0.900930559
GOTERM_BP_ALL	GO:0055095~lipoprotein particle mediated signaling	2	0.278940028	0.077066272	0.900930559
GOTERM_BP_ALL	GO:1904237~positive regulation of substrate-dependent cell migration, cell attachment to substrate	2	0.278940028	0.077066272	0.900930559
GOTERM_BP_ALL	GO:0001300~chronological cell aging	2	0.278940028	0.077066272	0.900930559
GOTERM_BP_ALL	GO:0055096~low-density lipoprotein particle mediated signaling	2	0.278940028	0.077066272	0.900930559
GOTERM_BP_ALL	GO:0097359~UDP-glucosylation	2	0.278940028	0.077066272	0.900930559
GOTERM_BP_ALL	GO:0019218~regulation of steroid metabolic process	7	0.976290098	0.078121682	0.904586897
GOTERM_BP_ALL	GO:0034613~cellular protein localization	75	10.46025105	0.078262683	0.904586897
GOTERM_BP_ALL	GO:0071402~cellular response to lipoprotein particle stimulus	3	0.418410042	0.078447387	0.904586897
GOTERM_BP_ALL	GO:0035413~positive regulation of catenin import into nucleus	3	0.418410042	0.078447387	0.904586897
GOTERM_BP_ALL	GO:0042340~keratan sulfate catabolic process	3	0.418410042	0.078447387	0.904586897
GOTERM_BP_ALL	GO:0071712~ER-associated misfolded protein catabolic process	3	0.418410042	0.078447387	0.904586897
GOTERM_BP_ALL	GO:0060394~negative regulation of pathway-restricted SMAD protein phosphorylation	3	0.418410042	0.078447387	0.904586897
GOTERM_BP_ALL	GO:0032269~negative regulation of cellular protein metabolic process	49	6.834030683	0.079078756	0.909326189
GOTERM_BP_ALL	GO:0006351~transcription, DNA-templated	158	22.0362622	0.079165229	0.909326189
GOTERM_BP_ALL	GO:0008219~cell death	90	12.55230126	0.0793949	0.910200339
GOTERM_BP_ALL	GO:0030182~neuron differentiation	59	8.228730823	0.079654891	0.911418029
GOTERM_BP_ALL	GO:0016071~mRNA metabolic process	35	4.881450488	0.079912893	0.912084971
GOTERM_BP_ALL	GO:0048589~developmental growth	31	4.323570432	0.080142562	0.912084971
GOTERM_BP_ALL	GO:0014044~Schwann cell development	4	0.557880056	0.080482612	0.912084971
GOTERM_BP_ALL	GO:0061037~negative regulation of cartilage development	4	0.557880056	0.080482612	0.912084971
GOTERM_BP_ALL	GO:0071604~transforming growth factor beta production	4	0.557880056	0.080482612	0.912084971
GOTERM_BP_ALL	GO:0044093~positive regulation of molecular function	85	11.85495119	0.080676953	0.912542556
GOTERM_BP_ALL	GO:0030163~protein catabolic process	41	5.718270572	0.081074996	0.915298102

GOTERM_BP_ALL	GO:0048645~organ formation	6	0.836820084	0.081608572	0.919570352
GOTERM_BP_ALL	GO:0010883~regulation of lipid storage	5	0.69735007	0.081789238	0.919857329
GOTERM_BP_ALL	GO:0008203~cholesterol metabolic process	9	1.255230126	0.083387027	0.934251
GOTERM_BP_ALL	GO:0050807~regulation of synapse organization	9	1.255230126	0.083387027	0.934251
GOTERM_BP_ALL	GO:0003279~cardiac septum development	8	1.115760112	0.083694582	0.934251
GOTERM_BP_ALL	GO:0001649~osteoblast differentiation	13	1.813110181	0.083798484	0.934251
GOTERM_BP_ALL	GO:0048812~neuron projection morphogenesis	29	4.044630404	0.083857184	0.934251
GOTERM_BP_ALL	GO:0050803~regulation of synapse structure or activity	15	2.092050209	0.084335371	0.936059449
GOTERM_BP_ALL	GO:0090130~tissue migration	15	2.092050209	0.084335371	0.936059449
GOTERM_BP_ALL	GO:0050730~regulation of peptidyl-tyrosine phosphorylation	14	1.952580195	0.084701959	0.93806623
GOTERM_BP_ALL	GO:1901700~response to oxygen-containing compound	69	9.623430962	0.084832715	0.93806623
GOTERM_BP_ALL	GO:0070271~protein complex biogenesis	68	9.483960948	0.085938544	0.948524671
GOTERM_BP_ALL	GO:0014033~neural crest cell differentiation	7	0.976290098	0.086114483	0.948699893
GOTERM_BP_ALL	GO:0048585~negative regulation of response to stimulus	65	9.065550907	0.086376592	0.949175082
GOTERM_BP_ALL	GO:0043408~regulation of MAPK cascade	35	4.881450488	0.086477905	0.949175082
GOTERM_BP_ALL	GO:0006461~protein complex assembly	68	9.483960948	0.086921745	0.950210497
GOTERM_BP_ALL	GO:0006885~regulation of pH	8	1.115760112	0.087322691	0.950210497
GOTERM_BP_ALL	GO:1901215~negative regulation of neuron death	12	1.673640167	0.087433156	0.950210497
GOTERM_BP_ALL	GO:0050821~protein stabilization	10	1.394700139	0.087931811	0.950210497
GOTERM_BP_ALL	GO:0051603~proteolysis involved in cellular protein catabolic process	34	4.741980474	0.087977365	0.950210497
GOTERM_BP_ALL	GO:0035412~regulation of catenin import into nucleus	4	0.557880056	0.088015111	0.950210497
GOTERM_BP_ALL	GO:0030970~retrograde protein transport, ER to cytosol	4	0.557880056	0.088015111	0.950210497
GOTERM_BP_ALL	GO:1903513~endoplasmic reticulum to cytosol transport	4	0.557880056	0.088015111	0.950210497
GOTERM_BP_ALL	GO:0033028~myeloid cell apoptotic process	4	0.557880056	0.088015111	0.950210497
GOTERM_BP_ALL	GO:0032990~cell part morphogenesis	41	5.718270572	0.088998893	0.958184973
GOTERM_BP_ALL	GO:0061024~membrane organization	50	6.973500697	0.089786516	0.958184973
GOTERM_BP_ALL	GO:0048878~chemical homeostasis	51	7.112970711	0.08998893	0.958184973
GOTERM_BP_ALL	GO:0044802~single-organism membrane organization	43	5.9972106	0.090260564	0.958184973
GOTERM_BP_ALL	GO:0002821~positive regulation of adaptive immune response	7	0.976290098	0.090273377	0.958184973
GOTERM_BP_ALL	GO:0033197~response to vitamin E	3	0.418410042	0.090370407	0.958184973
GOTERM_BP_ALL	GO:0055098~response to low-density lipoprotein particle	3	0.418410042	0.090370407	0.958184973
GOTERM_BP_ALL	GO:0072015~glomerular visceral epithelial cell development	3	0.418410042	0.090370407	0.958184973
GOTERM_BP_ALL	GO:0006878~cellular copper ion homeostasis	3	0.418410042	0.090370407	0.958184973
GOTERM_BP_ALL	GO:1900025~negative regulation of substrate adhesion-dependent cell spreading	3	0.418410042	0.090370407	0.958184973
GOTERM_BP_ALL	GO:0031346~positive regulation of cell projection organization	18	2.510460251	0.091116499	0.959478976
GOTERM_BP_ALL	GO:0060968~regulation of gene silencing	6	0.836820084	0.09113998	0.959478976
GOTERM_BP_ALL	GO:0016441~posttranscriptional gene silencing	6	0.836820084	0.09113998	0.959478976
GOTERM_BP_ALL	GO:0035194~posttranscriptional gene silencing by RNA	6	0.836820084	0.09113998	0.959478976
GOTERM_BP_ALL	GO:0012501~programmed cell death	85	11.85495119	0.091672297	0.963371814
GOTERM_BP_ALL	GO:0072001~renal system development	17	2.370990237	0.09201812	0.96529451
GOTERM_BP_ALL	GO:0046907~intracellular transport	74	10.32078103	0.092702512	0.97052929
GOTERM_BP_ALL	GO:0043393~regulation of protein binding	12	1.673640167	0.092844628	0.97052929
GOTERM_BP_ALL	GO:0008333~endosome to lysosome transport	5	0.69735007	0.093433803	0.974968577
GOTERM_BP_ALL	GO:0072006~nephron development	10	1.394700139	0.094190908	0.981141498
GOTERM_BP_ALL	GO:0032092~positive regulation of protein binding	7	0.976290098	0.094539539	0.981323728
GOTERM_BP_ALL	GO:0048644~muscle organ morphogenesis	7	0.976290098	0.094539539	0.981323728
GOTERM_BP_ALL	GO:0033674~positive regulation of kinase activity	27	3.765690377	0.095067444	0.98373444
GOTERM_BP_ALL	GO:0034612~response to tumor necrosis factor	16	2.231520223	0.095241471	0.98373444
GOTERM_BP_ALL	GO:0048708~astrocyte differentiation	6	0.836820084	0.096111653	0.98373444
GOTERM_BP_ALL	GO:0043281~regulation of cysteine-type endopeptidase activity involved in apoptotic process	13	1.813110181	0.096547728	0.98373444
GOTERM_BP_ALL	GO:0031669~cellular response to nutrient levels	11	1.534170153	0.096868844	0.98373444
GOTERM_BP_ALL	GO:1901576~organic substance biosynthetic process	262	36.54114365	0.098011329	0.98373444
GOTERM_BP_ALL	GO:0010629~negative regulation of gene expression	69	9.623430962	0.098717642	0.98373444