

Table S5 Gene ontology (GO) enrichment analysis based on these target genes

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p. adjust	qvalue	geneID
BP	G0:0000082	G1/S transition of mitotic cell cycle	31/579	275/18862	4.57E-10	1.88E-06	1.47E-06	894/9134/5128/7029/8462/8452/123879/1871/1956
BP	G0:0044843	cell cycle G1/S phase transition	32/579	298/18862	8.21E-10	1.88E-06	1.47E-06	894/9134/5128/7029/8462/8452/123879/1871/1956
BP	G0:0048732	gland development	37/579	413/18862	6.16E-09	9.43E-06	7.37E-06	171023/7042/8452/1956/1969/6776/3082/10018/14853/5324
BP	G0:0016311	dephosphorylation	40/579	491/18862	2.17E-08	2.34E-05	1.83E-05	994/11261/7042/23239/23035/5494/84919/5789/108493/6992/5519/5537/55291
BP	G0:0006470	protein dephosphorylation	31/579	325/18862	2.55E-08	2.34E-05	1.83E-05	994/23239/23035/5494/84919/5789/10395/2280/17
BP	G0:0031647	regulation of protein stability	29/579	295/18862	3.73E-08	2.85E-05	2.23E-05	11261/3920/8452/2319/908/66036/80155/5621/572
BP	G0:0016570	histone modification	37/579	448/18862	5.23E-08	3.09E-05	2.42E-05	171023/8314/9575/79718/80312/200424/4297/8473/4602/26147/11108
BP	G0:0070646	protein modification by small protein removal	29/579	300/18862	5.39E-08	3.09E-05	2.42E-05	54532/171023/8314/8473/63967/54891/983/54726/
BP	G0:0016569	covalent chromatin modification	37/579	461/18862	1.08E-07	5.53E-05	4.33E-05	171023/8314/9575/79718/80312/200424/4297/8473/4602/26147/11108
BP	G0:0035303	regulation of dephosphorylation	23/579	210/18862	1.39E-07	6.39E-05	5.00E-05	11261/7042/84919/10395/2280/1760/8897/66036/2

BP	G0:00165 79	protein deubiquitination	27/579	283/188 62	2.03E- 07	8.46E- 05	6.62E-05	54532/171023/8314/8473/63967/54891/983/54726/
BP	G0:00181 05	peptidyl-serine phosphorylation	28/579	310/188 62	3.75E- 07	0.00013 39	0.0001047	5144/63967/1956/3082/253260/983/1147/1760/556
BP	G0:00030 07	heart morphogenesis	24/579	239/188 62	3.79E- 07	0.00013 39	0.0001047	10413/171023/7042/57534/8829/10395/2280/5915/
BP	G0:00508 21	protein stabilization	21/579	191/188 62	4.55E- 07	0.00014 93	0.0001167	11261/3920/2319/908/66036/80155/5728/57142/74
BP	G0:00182 09	peptidyl-serine modification	29/579	333/188 62	4.98E- 07	0.00015 23	0.0001191	5144/63967/1956/3082/253260/983/1147/1760/556
BP	G0:00457 87	positive regulation of cell cycle	32/579	395/188 62	6.47E- 07	0.00018 55	0.000145	894/9236/994/7029/7042/8452/1956/6421/10018/9
BP	G0:19019 90	regulation of mitotic cell cycle phase transition	34/579	439/188 62	8.14E- 07	0.00021 96	0.0001717	894/994/7532/7029/63967/8452/123879/1956/983/
BP	G0:00305 09	BMP signaling pathway	18/579	154/188 62	1.23E- 06	0.00031 4	0.0002456	7042/5494/90/4087/4090/7471/3516/6497/4088/40
BP	G0:00506 73	epithelial cell proliferation	33/579	428/188 62	1.30E- 06	0.00031 5	0.0002463	10413/7042/8829/5813/1956/1969/6776/3082/3146
BP	G0:00147 06	striated muscle tissue development	29/579	351/188 62	1.46E- 06	0.00032 26	0.0002523	10413/7042/56603/2280/150094/5915/90/1073/194
BP	G0:00719 00	regulation of protein serine/threonine kinase activity	36/579	492/188 62	1.48E- 06	0.00032 26	0.0002523	894/9134/7532/7074/1956/3082/3843/253260/983/

BP	G0:19019 87	regulation of cell cycle phase transition	35/579	478/188 62	2.04E- 06	0.00042 03	0.0003287	894/994/7532/7029/63967/8452/123879/1956/983/
BP	G0:00109 21	regulation of phosphatase activity	19/579	176/188 62	2.11E- 06	0.00042 03	0.0003287	11261/7042/84919/2280/1760/66036/22870/7184/3
BP	G0:20000 58	regulation of ubiquitin-dependent protein catabolic process	18/579	161/188 62	2.35E- 06	0.00045 02	0.0003521	9655/8473/5728/7471/7480/5887/255488/154214/4
BP	G0:00307 05	cytoskeleton- dependent intracellular transport	20/579	195/188 62	2.54E- 06	0.00046 69	0.0003651	3842/23299/5813/6421/55207/140735/23557/8976/
BP	G0:00431 61	proteasome-mediated ubiquitin-dependent protein catabolic process	32/579	425/188 62	3.12E- 06	0.00055 12	0.000431	23607/9354/9655/9575/79718/8473/8452/84961/98
BP	G0:00717 72	response to BMP	18/579	167/188 62	3.98E- 06	0.00065 24	0.0005101	7042/5494/90/4087/4090/7471/3516/6497/4088/40
BP	G0:00717 73	cellular response to BMP stimulus	18/579	167/188 62	3.98E- 06	0.00065 24	0.0005101	7042/5494/90/4087/4090/7471/3516/6497/4088/40
BP	G0:00605 37	muscle tissue development	29/579	371/188 62	4.39E- 06	0.00069 4	0.0005426	10413/7042/56603/2280/150094/5915/90/1073/194
BP	G0:19038 29	positive regulation of cellular protein localization	25/579	295/188 62	4.94E- 06	0.00075 58	0.000591	23607/11261/10413/7532/163/8314/7029/1956/196

BP	G0:00160 50	vesicle organization	27/579	339/188 62	6.63E- 06	0.00095 59	0.0007475	137492/9839/23607/11261/8675/10228/8452/10802
BP	G0:00487 38	cardiac muscle tissue development	20/579	208/188 62	6.82E- 06	0.00095 59	0.0007475	10413/7042/2280/150094/5915/90/1948/5728/1901
BP	G0:00016 55	urogenital system development	26/579	320/188 62	6.87E- 06	0.00095 59	0.0007475	10413/163/171023/7020/7042/56603/2045/5915/10
BP	G0:20000 45	regulation of G1/S transition of mitotic cell cycle	18/579	174/188 62	7.11E- 06	0.00095 95	0.0007503	894/7029/123879/1956/983/144455/5728/54617/99
BP	G0:00032 79	cardiac septum development	13/579	96/1886 2	7.35E- 06	0.00096 41	0.0007539	163/7042/8829/5915/90/23414/4194/3516/6299/40
BP	G0:00900 68	positive regulation of cell cycle process	25/579	303/188 62	7.89E- 06	0.00100 61	0.0007868	894/994/7029/8452/1956/6421/983/144455/7480/5
BP	G0:19028 06	regulation of cell cycle G1/S phase transition	19/579	195/188 62	9.53E- 06	0.00118 17	0.000924	894/7029/123879/1956/983/144455/5728/54617/99
BP	G0:00301 77	positive regulation of Wnt signaling pathway	18/579	179/188 62	1.05E- 05	0.00125 1	0.0009782	80351/10413/79718/5494/1956/139285/5715/7480/
BP	G0:19033 62	regulation of cellular protein catabolic process	22/579	251/188 62	1.07E- 05	0.00125 1	0.0009782	9655/8473/139285/5728/7471/7480/3949/10197/58
BP	G0:00165 71	histone methylation	15/579	130/188 62	1.10E- 05	0.00125 1	0.0009782	80312/200424/4297/8473/1786/3720/55870/10498/
BP	G0:19030 50	regulation of proteolysis involved	20/579	215/188 62	1.12E- 05	0.00125 1	0.0009782	9655/8473/5728/7471/7480/10197/5887/255488/15

		in cellular protein catabolic process						
BP	G0:0097191	extrinsic apoptotic signaling pathway	20/579	217/18862	1.28E-05	0.0013812	0.0010801	8795/10413/7042/3082/10018/90/2923/5728/55437
BP	G0:0048193	Golgi vesicle transport	28/579	372/18862	1.29E-05	0.0013812	0.0010801	23299/10228/64764/8452/10802/10890/51762/1407
BP	G0:0050678	regulation of epithelial cell proliferation	28/579	374/18862	1.43E-05	0.0014811	0.0011581	10413/7042/8829/1956/6776/3146/253260/54206/5
BP	G0:0035265	organ growth	17/579	166/18862	1.45E-05	0.0014811	0.0011581	10413/7042/5915/10018/5728/1901/4087/23414/37
BP	G0:0006605	protein targeting	31/579	441/18862	1.75E-05	0.0017446	0.0013642	137492/23471/11261/7532/8314/60559/3920/51762
BP	G0:0007265	Ras protein signal transduction	26/579	338/18862	1.80E-05	0.0017613	0.0013772	27/7042/7074/8829/8473/8452/10395/10672/57826
BP	G0:0001501	skeletal system development	33/579	486/18862	1.91E-05	0.0017872	0.0013975	171023/7020/7042/64764/56603/1969/3215/3696/5
BP	G0:0006479	protein methylation	17/579	170/18862	1.98E-05	0.0017872	0.0013975	80312/200424/4297/8473/1786/3720/55870/7832/1
BP	G0:0008213	protein alkylation	17/579	170/18862	1.98E-05	0.0017872	0.0013975	80312/200424/4297/8473/1786/3720/55870/7832/1
BP	G0:0001837	epithelial to mesenchymal transition	16/579	153/18862	1.99E-05	0.0017872	0.0013975	7042/7074/3082/90/5728/57142/4087/3516/4088/4
BP	G0:0051648	vesicle localization	20/579	224/18862	2.04E-05	0.0018007	0.0014081	11261/8452/10802/22870/5728/23557/8867/8976/1

BP	G0:2001236	regulation of extrinsic apoptotic signaling pathway	16/579	154/18862	2.15E-05	0.0018374	0.0014368	8795/10413/3082/90/2923/5728/55437/10197/6198
BP	G0:1901992	positive regulation of mitotic cell cycle phase transition	12/579	91/18862	2.16E-05	0.0018374	0.0014368	894/994/8452/1956/983/7480/595/993/996/1654/1
BP	G0:0042176	regulation of protein catabolic process	28/579	383/18862	2.20E-05	0.0018374	0.0014368	9655/8473/1956/139285/5728/7471/7480/3949/419
BP	G0:0001889	liver development	15/579	138/18862	2.27E-05	0.0018594	0.001454	8452/1956/3082/144455/7471/3720/5774/4088/704
BP	G0:0003281	ventricular septum development	10/579	64/18862	2.34E-05	0.0018849	0.0014739	163/7042/90/23414/4194/3516/6299/4092/7049/77
BP	G0:0061008	hepaticobiliary system development	15/579	140/18862	2.69E-05	0.0021307	0.0016661	8452/1956/3082/144455/7471/3720/5774/4088/704
BP	G0:0019058	viral life cycle	26/579	348/18862	2.98E-05	0.0022463	0.0017565	137492/104/3839/8829/1956/1969/983/128866/165
BP	G0:0045599	negative regulation of fat cell differentiation	9/579	53/18862	3.02E-05	0.0022463	0.0017565	10413/171023/7471/7480/23414/862/4088/89780/2
BP	G0:0072001	renal system development	23/579	288/18862	3.03E-05	0.0022463	0.0017565	10413/163/171023/7020/7042/56603/2045/5915/10
BP	G0:0032147	activation of protein kinase activity	25/579	328/18862	3.03E-05	0.0022463	0.0017565	8795/7042/57498/8649/63967/1956/3082/3146/253
BP	G0:0033135	regulation of peptidyl-serine phosphorylation	15/579	143/18862	3.46E-05	0.0025201	0.0019706	5144/1956/3082/253260/5562/5728/4092/7422/897

BP	G0:00600 70	canonical Wnt signaling pathway	25/579	333/188 62	3.90E- 05	0.00279 36	0.0021845	80351/10413/79718/5494/8452/1956/139285/5715/
BP	G0:00070 50	cell cycle arrest	20/579	235/188 62	4.06E- 05	0.00285 52	0.0022326	7029/7042/8649/5494/983/144455/5562/5621/5543
BP	G0:00104 98	proteasomal protein catabolic process	32/579	483/188 62	4.11E- 05	0.00285 52	0.0022326	23607/9354/9655/9575/79718/8473/8452/84961/98
BP	G0:00216 75	nerve development	10/579	69/1886 2	4.58E- 05	0.00313 76	0.0024535	104/7020/8829/23405/4884/9935/6299/627/3200/9
BP	G0:00715 59	response to transforming growth factor beta	21/579	257/188 62	4.78E- 05	0.00314 81	0.0024617	7042/5494/3696/90/4087/4090/7471/6497/4088/40
BP	G0:00902 63	positive regulation of canonical Wnt signaling pathway	15/579	147/188 62	4.78E- 05	0.00314 81	0.0024617	80351/10413/79718/5494/1956/139285/5715/7480/
BP	G0:00071 78	transmembrane receptor protein serine/threonine kinase signaling pathway	26/579	358/188 62	4.80E- 05	0.00314 81	0.0024617	7042/5494/2280/3696/651/90/4087/4090/60436/74
BP	G0:00510 56	regulation of small GTPase mediated signal transduction	24/579	319/188 62	5.35E- 05	0.00342 37	0.0026772	23607/27/7042/7074/8829/8473/8452/10395/10672
BP	G0:00071 79	transforming growth factor beta receptor signaling pathway	18/579	202/188 62	5.37E- 05	0.00342 37	0.0026772	7042/5494/3696/90/4087/4090/7471/6497/4088/40

BP	G0:0050679	positive regulation of epithelial cell proliferation	18/579	203/18862	5.73E-05	0.0035356	0.0027647	10413/8829/1956/6776/3146/253260/57142/7422/8
BP	G0:0001822	kidney development	22/579	280/18862	5.73E-05	0.0035356	0.0027647	10413/163/171023/7020/7042/56603/2045/5915/10
BP	G0:0001933	negative regulation of protein phosphorylation	26/579	362/18862	5.78E-05	0.0035356	0.0027647	11261/7532/104/9655/5144/84919/3082/3843/2286
BP	G0:0032924	activin receptor signaling pathway	8/579	45/18862	5.94E-05	0.0035407	0.0027687	2280/90/4087/60436/6497/4088/4092/92
BP	G0:0048538	thymus development	8/579	45/18862	5.94E-05	0.0035407	0.0027687	171023/10018/3720/9935/5894/64919/1399/3200
BP	G0:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	12/579	101/18862	6.19E-05	0.0036405	0.0028467	894/9134/1956/3843/5728/2965/595/898/905/993/
BP	G0:0060038	cardiac muscle cell proliferation	9/579	58/18862	6.33E-05	0.0036768	0.0028751	10413/7042/5728/23414/3720/3516/7049/2247/529
BP	G0:0031396	regulation of protein ubiquitination	18/579	205/18862	6.51E-05	0.0036783	0.0028763	11261/8473/8452/123879/2280/57561/139285/5728
BP	G0:0030111	regulation of Wnt signaling pathway	26/579	365/18862	6.62E-05	0.0036783	0.0028763	80351/10413/79718/7074/5494/8452/1956/139285/
BP	G0:0014855	striated muscle cell proliferation	10/579	72/18862	6.65E-05	0.0036783	0.0028763	10413/7042/5728/23414/3720/3516/7049/2247/383
BP	G0:0099518	vesicle cytoskeletal trafficking	10/579	72/18862	6.65E-05	0.0036783	0.0028763	23557/8976/22906/3064/23095/9371/3798/4644/46

BP	G0:00329 25	regulation of activin receptor signaling pathway	6/579	24/1886 2	6.84E- 05	0.00369 99	0.0028932	2280/90/4087/6497/4092/92
BP	G0:00459 31	positive regulation of mitotic cell cycle	13/579	118/188 62	6.85E- 05	0.00369 99	0.0028932	894/994/8452/1956/983/7480/6198/595/993/996/1
BP	G0:00328 69	cellular response to insulin stimulus	19/579	226/188 62	7.41E- 05	0.00391 57	0.0030619	7532/526/8473/2885/10890/51762/54206/64710/55
BP	G0:00454 46	endothelial cell differentiation	13/579	119/188 62	7.48E- 05	0.00391 57	0.0030619	6935/8829/5144/3215/57826/90/1901/3551/3516/5
BP	G0:20012 37	negative regulation of extrinsic apoptotic signaling pathway	12/579	103/188 62	7.51E- 05	0.00391 57	0.0030619	8795/10413/3082/90/55437/10197/6198/5894/1654
BP	G0:00009 10	cytokinesis	16/579	171/188 62	7.74E- 05	0.00399 19	0.0031215	994/8452/55165/128866/144455/23503/9928/6651/
BP	G0:00465 78	regulation of Ras protein signal transduction	17/579	190/188 62	8.17E- 05	0.00404 82	0.0031655	27/7042/8829/8473/8452/10395/2885/90627/9928/
BP	G0:00604 85	mesenchyme development	22/579	287/188 62	8.26E- 05	0.00404 82	0.0031655	10413/7042/7074/8829/3082/90/139285/5728/5714
BP	G0:00608 28	regulation of canonical Wnt signaling pathway	22/579	287/188 62	8.26E- 05	0.00404 82	0.0031655	80351/10413/79718/5494/8452/1956/139285/5715/
BP	G0:00031 58	endothelium development	14/579	137/188 62	8.34E- 05	0.00404 82	0.0031655	6935/8829/5144/3215/57826/90/1901/90627/3551/

BP	G0:00516 50	establishment of vesicle localization	18/579	209/188 62	8.36E- 05	0.00404 82	0.0031655	11261/8452/10802/22870/23557/8867/8976/128637
BP	G0:00434 34	response to peptide hormone	29/579	435/188 62	8.38E- 05	0.00404 82	0.0031655	7532/526/8473/6775/6776/2885/10890/51762/1147
BP	G0:19040 29	regulation of cyclin-dependent protein kinase activity	12/579	105/188 62	9.07E- 05	0.00433 37	0.0033888	894/9134/1956/3843/5728/2965/595/898/905/993/
BP	G0:00109 70	transport along microtubule	15/579	156/188 62	9.46E- 05	0.00441 64	0.0034535	3842/23299/5813/6421/55207/140735/23557/22906
BP	G0:00310 60	regulation of histone methylation	9/579	61/1886 2	9.50E- 05	0.00441 64	0.0034535	80312/4297/8473/1786/3720/4302/4524/4602/2614
BP	G0:00310 62	positive regulation of histone methylation	7/579	36/1886 2	9.53E- 05	0.00441 64	0.0034535	80312/4297/8473/1786/3720/4602/26147
BP	G0:00162 36	macroautophagy	23/579	311/188 62	9.87E- 05	0.00451 79	0.0035328	137492/526/3920/8649/22863/128866/140735/8897
BP	G0:01501 15	cell-substrate junction organization	12/579	106/188 62	9.94E- 05	0.00451 79	0.0035328	8829/10395/51762/5728/3678/5795/4088/7414/742
BP	G0:00715 60	cellular response to transforming growth factor beta stimulus	20/579	251/188 62	0.00010 16	0.00452 86	0.0035412	7042/5494/3696/90/4087/4090/7471/6497/4088/40
BP	G0:00900 92	regulation of transmembrane receptor protein serine/threonine	20/579	251/188 62	0.00010 16	0.00452 86	0.0035412	7042/5494/2280/651/90/4087/7471/3516/6497/408

		kinase signaling pathway						
BP	G0:0060284	regulation of cell development	31/579	485/18862	0.0001044	0.0046068	0.0036023	10413/9575/7074/8829/5789/2045/23405/5728/571
BP	G0:1901989	positive regulation of cell cycle phase transition	12/579	107/18862	0.0001089	0.0047608	0.0037228	894/994/8452/1956/983/7480/595/993/996/1654/1
BP	G0:0060043	regulation of cardiac muscle cell proliferation	8/579	49/18862	0.0001116	0.0047864	0.0037428	10413/5728/23414/3720/3516/7049/2247/5292
BP	G0:0072132	mesenchyme morphogenesis	8/579	49/18862	0.0001116	0.0047864	0.0037428	7042/90/4087/4194/3516/4088/55273/89780
BP	G0:0031056	regulation of histone modification	14/579	141/18862	0.0001139	0.0048379	0.0037831	80312/4297/8473/1786/9252/3720/6497/7422/1111
BP	G0:0055017	cardiac muscle tissue growth	11/579	92/18862	0.0001174	0.0049437	0.0038658	10413/7042/5728/1901/23414/3720/3516/7049/224
BP	G0:0035304	regulation of protein dephosphorylation	14/579	142/18862	0.0001228	0.0051241	0.0040069	84919/10395/2280/1760/22870/7529/7184/3551/80
BP	G0:0034504	protein localization to nucleus	21/579	275/18862	0.0001255	0.0051899	0.0040583	3842/10628/23607/11261/10413/3839/1871/3843/9
BP	G0:0007517	muscle organ development	23/579	317/18862	0.0001312	0.0052848	0.0041325	104/7042/56603/2280/8087/1073/5562/1901/7480/
BP	G0:0031098	stress-activated protein kinase signaling cascade	21/579	276/18862	0.0001321	0.0052848	0.0041325	7042/23008/23239/1956/3082/3146/1147/55437/35

BP	G0:00448 39	cell cycle G2/M phase transition	21/579	276/188 62	0.00013 21	0.00528 48	0.0041325	994/7532/63967/983/5715/7480/9928/10197/57551
BP	G0:00015 70	vasculogenesis	10/579	78/1886 2	0.00013 24	0.00528 48	0.0041325	10413/1969/3696/23414/161742/7049/55273/7422/
BP	G0:00160 49	cell growth	30/579	470/188 62	0.00013 77	0.00540 76	0.0042286	8314/7042/7074/8829/123879/1956/2045/214/5714
BP	G0:19033 20	regulation of protein modification by small protein conjugation or removal	19/579	237/188 62	0.00013 89	0.00540 76	0.0042286	11261/8473/8452/123879/2280/57561/139285/5472
BP	G0:00604 11	cardiac septum morphogenesis	9/579	64/1886 2	0.00013 91	0.00540 76	0.0042286	7042/8829/5915/90/23414/3516/4092/7049/4853
BP	G0:00486 38	regulation of developmental growth	23/579	319/188 62	0.00014 4	0.00555 33	0.0043425	80351/10413/8829/2045/57678/6776/10018/5728/5
BP	G0:19054 77	positive regulation of protein localization to membrane	13/579	127/188 62	0.00014 58	0.00557 6	0.0043602	11261/7532/163/7029/1956/1969/22841/5621/7529
BP	G0:00000 86	G2/M transition of mitotic cell cycle	20/579	258/188 62	0.00014 76	0.00559 87	0.004378	994/7532/63967/983/5715/7480/9928/10197/57551
BP	G0:00482 78	vesicle docking	9/579	65/1886 2	0.00015 71	0.00585 55	0.0045788	8675/10228/10890/51762/201475/55014/6814/2627
BP	G0:00459 30	negative regulation of mitotic cell cycle	23/579	321/188 62	0.00015 79	0.00585 55	0.0045788	7029/63967/123879/1956/983/144455/5715/5728/4
BP	G0:00423 26	negative regulation of phosphorylation	27/579	407/188 62	0.00015 82	0.00585 55	0.0045788	11261/7532/104/9655/5144/84919/3082/3843/2286

BP	G0:00611 36	regulation of proteasomal protein catabolic process	16/579	182/188 62	0.00016 11	0.00591 55	0.0046257	9655/8473/7480/10197/5887/255488/154214/4092/
BP	G0:00514 03	stress-activated MAPK cascade	20/579	261/188 62	0.00017 24	0.00623 43	0.004875	7042/23008/23239/1956/3082/3146/1147/55437/35
BP	G0:00000 45	autophagosome assembly	11/579	96/1886 2	0.00017 25	0.00623 43	0.004875	22863/128866/8897/81671/51715/57154/55014/261
BP	G0:00330 02	muscle cell proliferation	18/579	222/188 62	0.00017 94	0.00643 28	0.0050302	10413/7042/1956/1786/5728/1901/23414/3720/351
BP	G0:00000 77	DNA damage checkpoint	14/579	148/188 62	0.00019 06	0.00672 12	0.0052557	9575/7029/63967/983/144455/4194/65975/57551/7
BP	G0:00066 23	protein targeting to vacuole	7/579	40/1886 2	0.00019 13	0.00672 12	0.0052557	137492/3920/57154/64089/27183/10490/23163
BP	G0:00069 86	response to unfolded protein	16/579	185/188 62	0.00019 46	0.00672 12	0.0052557	821/84919/64764/153222/10018/7184/58477/51768
BP	G0:19022 75	regulation of chromatin organization	16/579	185/188 62	0.00019 46	0.00672 12	0.0052557	80312/4297/8473/1786/9252/3720/6497/6749/9874
BP	G0:00509 18	positive chemotaxis	9/579	67/1886 2	0.00019 9	0.00672 12	0.0052557	8829/3082/3146/1901/5795/4088/7422/2247/3673
BP	G0:00427 70	signal transduction in response to DNA damage	13/579	131/188 62	0.00019 92	0.00672 12	0.0052557	7029/2885/983/144455/7471/4194/161742/65975/7
BP	G0:00720 73	kidney epithelium development	13/579	131/188 62	0.00019 92	0.00672 12	0.0052557	10413/171023/2045/5915/4087/4090/7471/6299/40

BP	G0:00182 05	peptidyl-lysine modification	26/579	391/188 62	0.00020 07	0.00672 12	0.0052557	9575/200424/4297/8473/55683/1786/5562/9252/37
BP	G0:19016 53	cellular response to peptide	26/579	391/188 62	0.00020 07	0.00672 12	0.0052557	7532/526/8462/8473/6776/2885/10890/51762/1001
BP	G0:20012 33	regulation of apoptotic signaling pathway	24/579	348/188 62	0.00020 38	0.00677 85	0.0053005	8795/10413/3082/6421/10018/90/2923/5728/55437
BP	G0:00324 34	regulation of proteasomal ubiquitin-dependent protein catabolic process	13/579	132/188 62	0.00021 49	0.00705 88	0.0055197	9655/8473/7480/5887/255488/154214/4092/25820/
BP	G0:19049 51	positive regulation of establishment of protein localization	23/579	328/188 62	0.00021 62	0.00705 88	0.0055197	23607/11261/7532/8314/7029/7042/5494/1956/384
BP	G0:00359 66	response to topologically incorrect protein	17/579	206/188 62	0.00021 82	0.00705 88	0.0055197	821/84919/64764/153222/8452/10018/7184/58477/
BP	G0:00074 09	axonogenesis	29/579	460/188 62	0.00021 84	0.00705 88	0.0055197	104/10678/7074/8829/9378/1969/2045/2885/10890
BP	G0:00435 25	positive regulation of neuron apoptotic process	8/579	54/1886 2	0.00022 51	0.00722 32	0.0056483	7020/7042/2045/10018/5621/23621/55294/4602
BP	G0:19050 37	autophagosome organization	11/579	99/1886 2	0.00022 7	0.00723 55	0.0056579	22863/128866/8897/81671/51715/57154/55014/261

BP	G0:00020 64	epithelial cell development	17/579	207/188 62	0.00023 12	0.00731 59	0.0057208	10413/171023/9575/5144/1969/57826/5915/3551/7
BP	G0:00032 05	cardiac chamber development	14/579	151/188 62	0.00023 52	0.00739 19	0.0057802	163/7042/8829/2280/5915/90/23414/4194/3516/62
BP	G0:00605 62	epithelial tube morphogenesis	22/579	309/188 62	0.00023 82	0.00743 55	0.0058142	10413/7042/57534/8829/10395/1969/2045/90/1282
BP	G0:00344 97	protein localization to phagophore assembly site	4/579	11/1886 2	0.00024 42	0.00757 04	0.0059197	55014/26100/79065/9927
BP	G0:00604 19	heart growth	11/579	100/188 62	0.00024 82	0.00764 24	0.0059761	10413/7042/5728/1901/23414/3720/3516/7049/224
BP	G0:00080 88	axo-dendritic transport	9/579	69/1886 2	0.00024 98	0.00764 24	0.0059761	5813/6421/55207/23557/22906/23095/9371/3798/5
BP	G0:00018 44	protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	6/579	30/1886 2	0.00025 81	0.00774 23	0.0060542	7532/7029/10018/7529/7533/10971
BP	G0:00331 37	negative regulation of peptidyl-serine phosphorylation	6/579	30/1886 2	0.00025 81	0.00774 23	0.0060542	5144/3082/5728/4092/9770/152559
BP	G0:00600 45	positive regulation of cardiac muscle cell proliferation	6/579	30/1886 2	0.00025 81	0.00774 23	0.0060542	10413/23414/3516/7049/2247/5292
BP	G0:00513 02	regulation of cell division	15/579	171/188 62	0.00026 2	0.00780 78	0.0061054	10628/994/7042/346389/8452/144455/23503/9928/

BP	G0:00456 64	regulation of neuron differentiation	16/579	190/188 62	0.00026 38	0.00780 9	0.0061063	6935/7532/7074/57534/5915/1656/5728/60436/653
BP	G0:00512 22	positive regulation of protein transport	22/579	312/188 62	0.00027 26	0.00801 79	0.0062697	23607/11261/7532/8314/7029/7042/5494/1956/384
BP	G0:00313 98	positive regulation of protein ubiquitination	12/579	118/188 62	0.00027 64	0.00807 98	0.0063181	8452/123879/2280/57561/139285/5728/4092/8945/
BP	G0:00510 58	negative regulation of small GTPase mediated signal transduction	8/579	56/1886 2	0.00029 12	0.00832 69	0.0065113	23607/27/7042/8452/10395/94134/201163/9927
BP	G0:00487 62	mesenchymal cell differentiation	18/579	231/188 62	0.00029 27	0.00832 69	0.0065113	7042/7074/8829/3082/90/139285/5728/57142/4087
BP	G0:00017 01	in utero embryonic development	23/579	335/188 62	0.00029 29	0.00832 69	0.0065113	10413/80312/57498/57534/8452/2885/10018/90/14
BP	G0:00447 73	mitotic DNA damage checkpoint	11/579	102/188 62	0.00029 55	0.00832 69	0.0065113	7029/63967/983/144455/4194/65975/57551/7832/1
BP	G0:00466 20	regulation of organ growth	11/579	102/188 62	0.00029 55	0.00832 69	0.0065113	10413/10018/5728/23414/3720/3516/6532/7049/22
BP	G0:00436 66	regulation of phosphoprotein phosphatase activity	12/579	119/188 62	0.00029 9	0.00832 69	0.0065113	84919/2280/1760/22870/7184/3551/8036/57181/30
BP	G0:00305 12	negative regulation of transforming growth factor beta	10/579	86/1886 2	0.00029 94	0.00832 69	0.0065113	5494/4087/7471/6497/4088/4092/57154/161742/70

		receptor signaling pathway						
BP	G0:0051781	positive regulation of cell division	10/579	86/18862	0.0002994	0.0083269	0.0065113	994/7042/346389/8452/9928/7422/8555/2247/9493
BP	G0:0007623	circadian rhythm	17/579	212/18862	0.0003063	0.0084662	0.0066202	9575/4297/10135/8473/23239/1956/6421/150094/9
BP	G0:0046856	phosphatidylinositol dephosphorylation	6/579	31/18862	0.0003119	0.0085185	0.0066612	22908/8897/66036/5728/8867/9110
BP	G0:0060317	cardiac epithelial to mesenchymal transition	6/579	31/18862	0.0003119	0.0085185	0.0066612	7042/90/57142/3516/7049/55273
BP	G0:0034329	cell junction assembly	27/579	425/18862	0.0003162	0.0085859	0.0067138	8829/9378/5789/10395/1969/2045/1948/5728/8167
BP	G0:0045927	positive regulation of growth	19/579	253/18862	0.0003207	0.0086565	0.006769	10413/7042/8829/1956/57678/23414/54617/3516/6
BP	G0:0006457	protein folding	18/579	233/18862	0.0003251	0.0087234	0.0068214	821/55466/2280/908/10681/2923/7184/9761/5887/
BP	G0:0031570	DNA integrity checkpoint	14/579	156/18862	0.0003294	0.0087892	0.0068728	9575/7029/63967/983/144455/4194/65975/57551/7
BP	G0:0017038	protein import	16/579	194/18862	0.0003336	0.008797	0.0068789	3842/10628/11261/3839/3920/1871/3843/51762/51
BP	G0:1905475	regulation of protein localization to membrane	16/579	194/18862	0.0003336	0.008797	0.0068789	11261/7532/163/7029/1956/1969/22841/5621/7529
BP	G0:0090287	regulation of cellular response to	21/579	296/18862	0.0003433	0.0090029	0.0070399	5494/25778/4087/7471/3678/3516/6497/4088/4092

		growth factor stimulus						
BP	G0:19037 47	regulation of establishment of protein localization to mitochondrion	9/579	72/1886 2	0.00034 59	0.00901 79	0.0070517	7532/8314/7029/5562/7529/7533/10971/9530/5529
BP	G0:20000 60	positive regulation of ubiquitin-dependent protein catabolic process	11/579	104/188 62	0.00035 01	0.00907 69	0.0070978	9655/5728/255488/154214/4092/57154/25820/863/
BP	G0:00609 76	coronary vasculature development	7/579	44/1886 2	0.00035 37	0.00911 96	0.0071312	163/8829/161742/7049/7422/8862/187
BP	G0:00070 33	vacuole organization	15/579	176/188 62	0.00035 75	0.00916 56	0.0071672	22863/128866/8897/51552/83871/23557/81671/517
BP	G0:00313 31	positive regulation of cellular catabolic process	25/579	384/188 62	0.00036 32	0.00925 94	0.0072405	23112/9655/22849/3146/10018/139285/5049/5562/
BP	G0:19037 49	positive regulation of establishment of protein localization to mitochondrion	8/579	58/1886 2	0.00037 24	0.00944 29	0.007384	7532/8314/7029/5562/7529/7533/10971/55294
BP	G0:00328 68	response to insulin	20/579	278/188 62	0.00039 42	0.00993 91	0.007772	7532/526/8473/2885/10890/51762/54206/64710/55
BP	G0:00070 93	mitotic cell cycle checkpoint	14/579	159/188 62	0.00040 02	0.01003 62	0.0078479	7029/63967/983/144455/4194/65975/57551/27183/

BP	G0:19037 93	positive regulation of anion transport	29/579	478/188 62	0.00041 13	0.01024 47	0.008011	23607/11261/7532/8314/7029/7042/5494/1956/384
BP	G0:00447 74	mitotic DNA integrity checkpoint	11/579	106/188 62	0.00041 3	0.01024 47	0.008011	7029/63967/983/144455/4194/65975/57551/7832/1
BP	G0:00903 16	positive regulation of intracellular protein transport	15/579	179/188 62	0.00042 81	0.01056 19	0.008259	11261/7532/8314/7029/5494/3843/5562/5621/6432
BP	G0:00324 65	regulation of cytokinesis	10/579	90/1886 2	0.00043 36	0.01064 12	0.008321	994/8452/144455/23503/9928/27183/8555/201163/
BP	G0:00726 55	establishment of protein localization to mitochondrion	13/579	142/188 62	0.00043 95	0.01072 86	0.0083894	7532/8314/7029/10018/5562/7529/23409/7533/109
BP	G0:00093 06	protein secretion	24/579	367/188 62	0.00044 36	0.01076	0.0084139	23607/821/9575/7042/7074/1956/10890/22841/517
BP	G0:19027 49	regulation of cell cycle G2/M phase transition	17/579	219/188 62	0.00044 64	0.01076	0.0084139	994/7532/63967/983/5715/7480/9928/10197/57551
BP	G0:00349 68	histone lysine methylation	11/579	107/188 62	0.00044 78	0.01076	0.0084139	200424/4297/8473/1786/3720/55870/2145/8085/43
BP	G0:00313 45	negative regulation of cell projection organization	15/579	180/188 62	0.00045 41	0.01085 4	0.0084874	10413/8829/2045/1948/5621/5728/57142/23557/89
BP	G0:00355 92	establishment of protein localization to extracellular region	24/579	368/188 62	0.00046 13	0.01096 75	0.0085761	23607/821/9575/7042/7074/1956/10890/22841/517

BP	G0:00316 48	protein destabilization	7/579	46/1886 2	0.00046 86	0.01101 9	0.0086164	8452/5621/8945/440193/55294/23163/3064
BP	G0:00474 96	vesicle transport along microtubule	7/579	46/1886 2	0.00046 86	0.01101 9	0.0086164	23557/22906/3064/23095/9371/3798/5048
BP	G0:00102 56	endomembrane system organization	29/579	482/188 62	0.00047 06	0.01101 9	0.0086164	137492/23471/8675/10228/7042/10890/23204/983/
BP	G0:00713 75	cellular response to peptide hormone stimulus	22/579	325/188 62	0.00047 71	0.01111 37	0.0086905	7532/526/8473/6776/2885/10890/51762/54206/647
BP	G0:00224 06	membrane docking	15/579	181/188 62	0.00048 15	0.01115 96	0.0087264	11261/7532/8675/10228/10890/51762/22863/983/2
BP	G0:00071 83	SMAD protein complex assembly	4/579	13/1886 2	0.00050 37	0.01155 73	0.0090374	5494/2280/4087/4088
BP	G0:00602 13	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	4/579	13/1886 2	0.00050 37	0.01155 73	0.0090374	23112/22849/27327/7832
BP	G0:00514 43	positive regulation of ubiquitin-protein transferase activity	6/579	34/1886 2	0.00052 69	0.01202 92	0.0094064	123879/57561/5728/8945/8555/55294
BP	G0:00319 52	regulation of protein autophosphorylation	7/579	47/1886 2	0.00053 62	0.01208 99	0.0094539	11261/2045/57826/54206/7422/9770/1654
BP	G0:00381 27	ERBB signaling pathway	13/579	145/188 62	0.00053 71	0.01208 99	0.0094539	9655/1956/2885/54206/9052/9252/57142/5795/577

BP	G0:00064 69	negative regulation of protein kinase activity	18/579	243/188 62	0.00053 74	0.01208 99	0.0094539	11261/7532/104/9655/3843/54206/9052/5728/7529
BP	G0:00170 15	regulation of transforming growth factor beta receptor signaling pathway	12/579	127/188 62	0.00054 32	0.01215 93	0.0095081	5494/4087/7471/6497/4088/4092/57154/161742/70
BP	G0:20012 52	positive regulation of chromosome organization	14/579	164/188 62	0.00054 71	0.01218 72	0.0095299	80351/80312/4297/8473/6421/908/1786/9252/3720
BP	G0:00103 89	regulation of G2/M transition of mitotic cell cycle	16/579	203/188 62	0.00055 1	0.01221 54	0.009552	994/7532/63967/983/5715/7480/9928/10197/57551
BP	G0:00165 78	histone deubiquitination	5/579	23/1886 2	0.00056 95	0.01241 43	0.0097075	171023/8314/9958/9960/56970
BP	G0:00340 63	stress granule assembly	5/579	23/1886 2	0.00056 95	0.01241 43	0.0097075	1656/5562/7812/1654/23215
BP	G0:00020 40	sprouting angiogenesis	15/579	184/188 62	0.00057 23	0.01241 43	0.0097075	8829/1969/3146/144455/1948/90627/3678/8434/16
BP	G0:00512 05	protein insertion into membrane	9/579	77/1886 2	0.00057 25	0.01241 43	0.0097075	23471/7532/7029/1956/10018/7529/7533/10971/55
BP	G0:00705 85	protein localization to mitochondrion	13/579	146/188 62	0.00057 35	0.01241 43	0.0097075	7532/8314/7029/10018/5562/7529/23409/7533/109
BP	G0:00300 99	myeloid cell differentiation	26/579	419/188 62	0.00057 77	0.01244 52	0.0097317	23112/4297/3930/1969/3146/3696/192670/4090/27

BP	G0:00716 92	protein localization to extracellular region	24/579	375/188 62	0.00060 28	0.01292 69	0.0101084	23607/821/9575/7042/7074/1956/10890/22841/517
BP	G0:00420 59	negative regulation of epidermal growth factor receptor signaling pathway	7/579	48/1886 2	0.00061 14	0.01298 99	0.0101576	9655/1956/2885/54206/9052/5795/5774
BP	G0:00512 04	protein insertion into mitochondrial membrane	7/579	48/1886 2	0.00061 14	0.01298 99	0.0101576	7532/7029/10018/7529/7533/10971/55750
BP	G0:00018 25	blastocyst formation	6/579	35/1886 2	0.00061 96	0.01310 27	0.0102458	10413/80312/8452/57142/2551/9113
BP	G0:00519 60	regulation of nervous system development	26/579	422/188 62	0.00064 21	0.01351 57	0.0105688	10413/7074/8829/9378/5789/2045/3082/5915/2340
BP	G0:00352 64	multicellular organism growth	12/579	130/188 62	0.00067 02	0.01391 59	0.0108817	80351/104/57678/6776/5915/6712/6895/23038/593
BP	G0:19001 80	regulation of protein localization to nucleus	12/579	130/188 62	0.00067 02	0.01391 59	0.0108817	23607/11261/10413/3843/908/983/51715/4088/297
BP	G0:19038 44	regulation of cellular response to transforming growth factor beta stimulus	12/579	130/188 62	0.00067 02	0.01391 59	0.0108817	5494/4087/7471/6497/4088/4092/57154/161742/70
BP	G0:00027 90	peptide secretion	25/579	401/188 62	0.00068 41	0.01414 21	0.0110586	23607/821/9575/7042/7074/1956/10890/22841/517

BP	G0:00346 20	cellular response to unfolded protein	13/579	149/188 62	0.00069 53	0.01424 68	0.0111405	821/84919/64764/153222/10018/7184/58477/51768
BP	G0:00359 67	cellular response to topologically incorrect protein	14/579	168/188 62	0.00069 54	0.01424 68	0.0111405	821/84919/64764/153222/8452/10018/7184/58477/
BP	G0:19055 64	positive regulation of vascular endothelial cell proliferation	5/579	24/1886 2	0.00070 14	0.01430 57	0.0111865	3146/10000/8862/2247/2260
BP	G0:00991 11	microtubule-based transport	15/579	188/188 62	0.00071 57	0.01453 16	0.0113631	3842/23299/5813/6421/55207/140735/23557/22906
BP	G0:00315 72	G2 DNA damage checkpoint	6/579	36/1886 2	0.00072 44	0.01461 07	0.011425	63967/983/57551/8555/1111/8091
BP	G0:19011 84	regulation of ERBB signaling pathway	10/579	96/1886 2	0.00072 59	0.01461 07	0.011425	9655/1956/2885/54206/9052/57142/5795/5774/351
BP	G0:00720 89	stem cell proliferation	8/579	64/1886 2	0.00073 23	0.01467 53	0.0114755	10413/7471/7480/84133/898/2247/8091/5292
BP	G0:19033 64	positive regulation of cellular protein catabolic process	13/579	150/188 62	0.00074 05	0.01477 42	0.0115529	9655/139285/5728/3949/255488/154214/4092/5715
BP	G0:00000 75	cell cycle checkpoint	16/579	209/188 62	0.00075 56	0.01501 01	0.0117373	9575/7029/63967/983/144455/4194/65975/57551/2
BP	G0:00032 31	cardiac ventricle development	11/579	114/188 62	0.00076 74	0.01511 08	0.0118161	163/7042/2280/90/23414/4194/3516/6299/4092/70
BP	G0:00308 79	mammary gland development	12/579	132/188 62	0.00076 79	0.01511 08	0.0118161	1969/6776/10018/57142/7422/89780/8862/8945/59

BP	G0:0000209	protein polyubiquitination	22/579	337/18862	0.0007738	0.0151108	0.0118161	80351/9354/8452/84961/165918/5715/84937/10197
BP	G0:0007059	chromosome segregation	22/579	337/18862	0.0007738	0.0151108	0.0118161	9134/8452/6421/8780/192670/55207/128866/54617
BP	G0:0048639	positive regulation of developmental growth	14/579	170/18862	0.0007815	0.0151968	0.0118833	10413/8829/57678/23414/3516/6198/4092/57154/7
BP	G0:0060412	ventricular septum morphogenesis	6/579	37/18862	0.0008425	0.0163135	0.0127566	7042/90/23414/3516/4092/7049
BP	G0:0062009	secondary palate development	5/579	25/18862	0.0008548	0.0164826	0.0128888	7042/3696/4087/7049/89780
BP	G0:0061458	reproductive system development	25/579	408/18862	0.0008756	0.0167064	0.0130638	7042/3696/2885/152006/10018/192670/144455/572
BP	G0:0140056	organelle localization by membrane tethering	14/579	172/18862	0.0008765	0.0167064	0.0130638	7532/8675/10228/10890/51762/22863/983/201475/
BP	G0:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	12/579	134/18862	0.0008774	0.0167064	0.0130638	5494/90/4087/7471/6497/4088/4092/57154/161742
BP	G0:0000186	activation of MAPKK activity	7/579	51/18862	0.0008882	0.0168269	0.013158	57498/8649/1956/4216/4293/5894/1399
BP	G0:0007034	vacuolar transport	13/579	153/18862	0.000891	0.0168269	0.013158	137492/3920/22863/128866/201475/23557/57154/6

BP	G0:00602 11	regulation of nuclear-transcribed mRNA poly(A) tail shortening	4/579	15/1886 2	0.00091 57	0.01722 2	0.0134669	23112/22849/27327/7832
BP	G0:00198 82	antigen processing and presentation	17/579	234/188 62	0.00094 18	0.01763 98	0.0137937	163/821/10802/10890/51762/1147/140735/2923/57
BP	G0:00604 15	muscle tissue morphogenesis	8/579	67/1886 2	0.00099 6	0.01842 27	0.0144058	104/7042/2280/1901/23414/3516/4092/7049
BP	G0:00070 44	cell-substrate junction assembly	10/579	100/188 62	0.00099 9	0.01842 27	0.0144058	8829/10395/5728/3678/5795/4088/7414/7422/3673
BP	G0:00455 98	regulation of fat cell differentiation	12/579	136/188 62	0.00099 95	0.01842 27	0.0144058	168455/10413/171023/7471/7480/23414/862/4088/
BP	G0:00726 66	establishment of protein localization to vacuole	7/579	52/1886 2	0.00099 96	0.01842 27	0.0144058	137492/3920/57154/64089/27183/10490/23163
BP	G0:00427 52	regulation of circadian rhythm	11/579	118/188 62	0.00102 26	0.01872 04	0.0146386	9575/23239/6421/150094/983/5562/8239/463/8945
BP	G0:19007 39	regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway	5/579	26/1886 2	0.00103 19	0.01872 04	0.0146386	7532/7029/7529/7533/10971
BP	G0:19007 40	positive regulation of protein insertion into mitochondrial	5/579	26/1886 2	0.00103 19	0.01872 04	0.0146386	7532/7029/7529/7533/10971

		membrane involved in apoptotic signaling pathway						
BP	G0:00435 34	blood vessel endothelial cell migration	14/579	175/188 62	0.00103 7	0.01872 04	0.0146386	8829/1969/6776/3146/1948/90627/161742/7422/10
BP	G0:00521 26	movement in host environment	14/579	175/188 62	0.00103 7	0.01872 04	0.0146386	3839/8829/1956/1969/2885/983/128866/1948/3678
BP	G0:19018 88	regulation of cell junction assembly	15/579	195/188 62	0.00104 02	0.01872 04	0.0146386	8829/9378/5789/10395/1969/2045/5728/3551/5795
BP	G0:19033 22	positive regulation of protein modification by small protein conjugation or removal	12/579	137/188 62	0.00106 57	0.01910 28	0.0149376	8452/123879/2280/57561/139285/5728/4092/8945/
BP	G0:00350 23	regulation of Rho protein signal transduction	9/579	84/1886 2	0.00108 13	0.01930 79	0.015098	27/8829/8452/10395/90627/5894/396/56990/20116
BP	G0:00988 40	protein transport along microtubule	8/579	68/1886 2	0.00109 9	0.01947 21	0.0152264	3842/5813/6421/140735/403/80173/9371/3798
BP	G0:00991 18	microtubule-based protein transport	8/579	68/1886 2	0.00109 9	0.01947 21	0.0152264	3842/5813/6421/140735/403/80173/9371/3798
BP	G0:00181 08	peptidyl-tyrosine phosphorylation	23/579	369/188 62	0.00110 72	0.01949 91	0.0152476	27/9655/8829/25778/1956/1969/2045/3082/57826/

BP	G0:00514 38	regulation of ubiquitin-protein transferase activity	7/579	53/1886 2	0.00112 18	0.01949 91	0.0152476	123879/57561/5728/4092/8945/8555/55294
BP	G0:00515 68	histone H3-K4 methylation	7/579	53/1886 2	0.00112 18	0.01949 91	0.0152476	200424/4297/8473/1786/55870/8085/4602
BP	G0:00901 51	establishment of protein localization to mitochondrial membrane	7/579	53/1886 2	0.00112 18	0.01949 91	0.0152476	7532/7029/10018/7529/7533/10971/55750
BP	G0:19011 85	negative regulation of ERBB signaling pathway	7/579	53/1886 2	0.00112 18	0.01949 91	0.0152476	9655/1956/2885/54206/9052/5795/5774
BP	G0:00451 37	development of primary sexual characteristics	16/579	217/188 62	0.00112 63	0.01950 45	0.0152517	7042/152006/10018/192670/23414/6299/7422/92/8
BP	G0:00024 78	antigen processing and presentation of exogenous peptide antigen	14/579	177/188 62	0.00115 72	0.01996 46	0.0156115	163/821/10802/1147/140735/2923/5715/3551/1019
BP	G0:00016 66	response to hypoxia	22/579	348/188 62	0.00117 47	0.02018 92	0.0157872	7042/5562/5715/5728/7184/4194/10197/3516/2340
BP	G0:00031 98	epithelial to mesenchymal transition involved in endocardial cushion formation	4/579	16/1886 2	0.00119 15	0.02032 63	0.0158944	7042/90/3516/55273

BP	G0:00609 77	coronary vasculature morphogenesis	4/579	16/1886 2	0.00119 15	0.02032 63	0.0158944	8829/161742/7049/7422
BP	G0:00488 13	dendrite morphogenesis	12/579	139/188 62	0.00120 89	0.02049 57	0.0160269	7074/57498/8829/5789/22903/5728/8976/4891/753
BP	G0:01501 16	regulation of cell- substrate junction organization	8/579	69/1886 2	0.00121 04	0.02049 57	0.0160269	8829/10395/5728/5795/4088/7414/7422/5295
BP	G0:00182 12	peptidyl-tyrosine modification	23/579	372/188 62	0.00123 21	0.02069 16	0.01618	27/9655/8829/25778/1956/1969/2045/3082/57826/
BP	G0:00109 71	positive regulation of G2/M transition of mitotic cell cycle	5/579	27/1886 2	0.00123 48	0.02069 16	0.01618	994/983/7480/595/993
BP	G0:00323 88	positive regulation of intracellular transport	16/579	219/188 62	0.00124	0.02069 16	0.01618	11261/7532/8314/7029/5494/3843/5562/5621/6432
BP	G0:00517 01	biological process involved in interaction with host	16/579	219/188 62	0.00124	0.02069 16	0.01618	3839/8829/1956/1969/2885/10018/983/128866/194
BP	G0:00434 14	macromolecule methylation	20/579	305/188 62	0.00124 95	0.02077 51	0.0162454	80312/200424/4297/8473/8731/1786/3720/55870/7
BP	G0:00016 57	ureteric bud development	9/579	86/1886 2	0.00127 98	0.02094 35	0.016377	5915/4087/4090/7471/6299/4088/4092/7422/2247
BP	G0:00310 58	positive regulation of histone modification	9/579	86/1886 2	0.00127 98	0.02094 35	0.016377	80312/4297/8473/1786/9252/3720/7422/4602/2614

BP	G0:00190 68	virion assembly	6/579	40/1886 2	0.00128 7	0.02094 35	0.016377	137492/128866/1656/128637/27183/10015
BP	G0:00324 67	positive regulation of cytokinesis	6/579	40/1886 2	0.00128 7	0.02094 35	0.016377	994/8452/9928/8555/9493/9371
BP	G0:00550 23	positive regulation of cardiac muscle tissue growth	6/579	40/1886 2	0.00128 7	0.02094 35	0.016377	10413/23414/3516/7049/2247/5292
BP	G0:00716 34	regulation of transforming growth factor beta production	6/579	40/1886 2	0.00128 7	0.02094 35	0.016377	23607/7042/2280/3696/4088/4602
BP	G0:00002 81	mitotic cytokinesis	8/579	70/1886 2	0.00133 05	0.02149 94	0.0168117	55165/128866/23503/6651/27183/403/9493/10015
BP	G0:00550 21	regulation of cardiac muscle tissue growth	8/579	70/1886 2	0.00133 05	0.02149 94	0.0168117	10413/5728/23414/3720/3516/7049/2247/5292
BP	G0:00353 35	peptidyl-tyrosine dephosphorylation	10/579	104/188 62	0.00135 1	0.02175 31	0.0170101	994/5789/8897/5728/5795/5774/5775/8555/993/91
BP	G0:00454 44	fat cell differentiation	16/579	221/188 62	0.00136 31	0.02187 22	0.0171033	168455/10413/171023/6041/7471/7480/23414/9935
BP	G0:00721 63	mesonephric epithelium development	9/579	87/1886 2	0.00138 94	0.02213 93	0.0173121	5915/4087/4090/7471/6299/4088/4092/7422/2247
BP	G0:00721 64	mesonephric tubule development	9/579	87/1886 2	0.00138 94	0.02213 93	0.0173121	5915/4087/4090/7471/6299/4088/4092/7422/2247
BP	G0:00485 88	developmental cell growth	16/579	222/188 62	0.00142 85	0.02257 07	0.0176494	7074/8829/2045/214/57142/10479/4092/57154/823

BP	G0:0007173	epidermal growth factor receptor signaling pathway	11/579	123/18862	0.0014362	0.0225707	0.0176494	9655/1956/2885/54206/9052/9252/5795/5774/9770
BP	G0:0007498	mesoderm development	11/579	123/18862	0.0014362	0.0225707	0.0176494	10413/1969/90/4087/23414/4088/7422/89780/92/8
BP	G0:0018022	peptidyl-lysine methylation	11/579	123/18862	0.0014362	0.0225707	0.0176494	200424/4297/8473/1786/3720/55870/2145/8085/43
BP	G0:0072665	protein localization to vacuole	8/579	71/18862	0.00146	0.0228668	0.017881	137492/3920/57142/57154/64089/27183/10490/231
BP	G0:0045017	glycerolipid biosynthetic process	18/579	266/18862	0.0015168	0.0234946	0.0183719	55500/57678/150094/22908/8897/66036/5728/5155
BP	G0:0048339	paraxial mesoderm development	4/579	17/18862	0.0015206	0.0234946	0.0183719	10413/4087/4088/89780
BP	G0:0061952	midbody abscission	4/579	17/18862	0.0015206	0.0234946	0.0183719	55165/128866/27183/10015
BP	G0:0080182	histone H3-K4 trimethylation	4/579	17/18862	0.0015206	0.0234946	0.0183719	200424/4297/8473/8085
BP	G0:0006606	protein import into nucleus	12/579	143/18862	0.0015436	0.0237065	0.0185375	3842/10628/11261/3839/1871/3843/51715/4088/10
BP	G0:0045785	positive regulation of cell adhesion	25/579	425/18862	0.0015446	0.0237065	0.0185375	151887/29126/9655/7042/8829/57678/3146/2885/2
BP	G0:2001234	negative regulation of apoptotic signaling pathway	16/579	224/18862	0.0015672	0.0239723	0.0187454	8795/10413/3082/90/55437/10197/6198/7178/5894
BP	G0:0071902	positive regulation of protein	20/579	311/18862	0.001577	0.0240293	0.01879	894/7074/1956/3082/253260/983/5562/4216/4293/

		serine/threonine kinase activity						
BP	G0:0033673	negative regulation of kinase activity	18/579	267/18862	0.0015814	0.0240293	0.01879	11261/7532/104/9655/3843/54206/9052/5728/7529
BP	G0:0033627	cell adhesion mediated by integrin	8/579	72/18862	0.0015993	0.0242214	0.0189402	7042/1969/3696/3678/1399/80173/3673/5140
BP	G0:0009896	positive regulation of catabolic process	26/579	450/18862	0.0016155	0.0243865	0.0190693	23112/9655/22849/3146/10018/139285/5049/5562/
BP	G0:0051098	regulation of binding	22/579	357/18862	0.0016246	0.024443	0.0191134	9236/7074/8829/2280/3146/9044/64710/57326/408
BP	G0:0035051	cardiocyte differentiation	12/579	144/18862	0.0016382	0.0245238	0.0191767	7042/1956/150094/5915/90/1948/3516/55553/7049
BP	G0:0060560	developmental growth involved in morphogenesis	16/579	225/18862	0.0016406	0.0245238	0.0191767	10413/7074/8829/2045/214/57142/1901/6299/1047
BP	G0:1901988	negative regulation of cell cycle phase transition	18/579	268/18862	0.0016482	0.0245577	0.0192032	7029/63967/123879/983/144455/5715/5728/4194/1
BP	G0:0031641	regulation of myelination	6/579	42/18862	0.0016702	0.0246448	0.0192713	3082/5915/23405/5728/9928/8604
BP	G0:0062208	positive regulation of pattern recognition receptor signaling pathway	6/579	42/18862	0.0016702	0.0246448	0.0192713	85364/3146/57142/9958/1654/3304

BP	G0:0071604	transforming growth factor beta production	6/579	42/18862	0.0016702	0.0246448	0.0192713	23607/7042/2280/3696/4088/4602
BP	G0:0010975	regulation of neuron projection development	25/579	428/18862	0.0016998	0.0250008	0.0195497	27/7074/57498/8829/5789/64764/2045/3082/1948/
BP	G0:0048608	reproductive structure development	24/579	405/18862	0.0017249	0.0250797	0.0196114	7042/3696/2885/152006/10018/192670/144455/572
BP	G0:0001773	myeloid dendritic cell activation	5/579	29/18862	0.001727	0.0250797	0.0196114	3146/3696/3516/3662/4853
BP	G0:0048008	platelet-derived growth factor receptor signaling pathway	7/579	57/18862	0.0017317	0.0250797	0.0196114	10628/8829/5728/5795/7422/9860/59338
BP	G0:0055008	cardiac muscle tissue morphogenesis	7/579	57/18862	0.0017317	0.0250797	0.0196114	7042/2280/1901/23414/3516/4092/7049
BP	G0:0003151	outflow tract morphogenesis	8/579	73/18862	0.0017489	0.0250797	0.0196114	7042/8829/5915/23414/3516/7049/7422/1399
BP	G0:0048644	muscle organ morphogenesis	8/579	73/18862	0.0017489	0.0250797	0.0196114	104/7042/2280/1901/23414/3516/4092/7049
BP	G0:0072401	signal transduction involved in DNA integrity checkpoint	8/579	73/18862	0.0017489	0.0250797	0.0196114	7029/983/144455/4194/7832/10498/8555/1111
BP	G0:0072422	signal transduction involved in DNA damage checkpoint	8/579	73/18862	0.0017489	0.0250797	0.0196114	7029/983/144455/4194/7832/10498/8555/1111

BP	G0:00198 84	antigen processing and presentation of exogenous antigen	14/579	185/188 62	0.00176 14	0.02518 09	0.0196905	163/821/10802/1147/140735/2923/5715/3551/1019
BP	G0:00331 57	regulation of intracellular protein transport	17/579	248/188 62	0.00176 74	0.02518 78	0.0196959	11261/7532/8314/7029/5494/3843/5562/5621/6432
BP	G0:00019 38	positive regulation of endothelial cell proliferation	10/579	108/188 62	0.00179 78	0.02554 27	0.0199734	8829/6776/3146/253260/7422/10000/8862/187/224
BP	G0:00362 93	response to decreased oxygen levels	22/579	360/188 62	0.00180 4	0.02555 16	0.0199804	7042/5562/5715/5728/7184/4194/10197/3516/2340
BP	G0:00017 63	morphogenesis of a branching structure	14/579	186/188 62	0.00185 26	0.02607 5	0.0203897	10413/8829/1969/2045/3082/2885/90/1282/57142/
BP	G0:00309 68	endoplasmic reticulum unfolded protein response	11/579	127/188 62	0.00185 8	0.02607 5	0.0203897	821/84919/64764/153222/10018/7184/58477/51283
BP	G0:19030 52	positive regulation of proteolysis involved in cellular protein catabolic process	11/579	127/188 62	0.00185 8	0.02607 5	0.0203897	9655/5728/255488/154214/4092/57154/25820/863/
BP	G0:00516 56	establishment of organelle localization	25/579	431/188 62	0.00186 81	0.02613 66	0.0204378	11261/23299/8452/10802/128866/22870/23557/886
BP	G0:00613 83	trabecula morphogenesis	6/579	43/1886 2	0.00189 15	0.02638 34	0.0206308	7042/2280/1901/7480/3516/7049

BP	G0:00018 23	mesonephros development	9/579	91/1886 2	0.00190 62	0.02642 8	0.0206657	5915/4087/4090/7471/6299/4088/4092/7422/2247
BP	G0:00305 10	regulation of BMP signaling pathway	9/579	91/1886 2	0.00190 62	0.02642 8	0.0206657	5494/4087/7471/3516/6497/4092/57154/51232/485
BP	G0:19019 91	negative regulation of mitotic cell cycle phase transition	17/579	250/188 62	0.00192 44	0.02659 9	0.0207994	7029/63967/123879/983/144455/5715/5728/4194/1
BP	G0:00485 11	rhythmic process	19/579	294/188 62	0.00193 15	0.02661 78	0.0208141	9575/7042/4297/10135/8473/23239/1956/6421/150
BP	G0:00063 67	transcription initiation from RNA polymerase II promoter	14/579	187/188 62	0.00194 78	0.02676 12	0.0209262	10413/7182/1871/3146/5915/983/5728/6908/7480/
BP	G0:00022 21	pattern recognition receptor signaling pathway	15/579	208/188 62	0.00197 49	0.02701 38	0.0211237	85364/3146/8780/22841/1147/54726/57142/7184/3
BP	G0:00456 67	regulation of osteoblast differentiation	11/579	128/188 62	0.00197 79	0.02701 38	0.0211237	10413/3082/90/4090/7480/6497/4088/9770/92/831
BP	G0:00069 13	nucleocytoplasmic transport	21/579	340/188 62	0.00199 67	0.02718 98	0.0212614	3842/10628/11261/3839/5494/1871/3843/84271/55
BP	G0:00434 91	protein kinase B signaling	18/579	273/188 62	0.00201 96	0.02719 39	0.0212645	23239/23035/1956/1969/3082/253260/2885/5728/5
BP	G0:00613 84	heart trabecula morphogenesis	5/579	30/1886 2	0.00202 07	0.02719 39	0.0212645	7042/2280/1901/3516/7049

BP	G0:01501 17	positive regulation of cell-substrate junction organization	5/579	30/1886 2	0.00202 07	0.02719 39	0.0212645	8829/5795/4088/7422/5295
BP	G0:19027 51	positive regulation of cell cycle G2/M phase transition	5/579	30/1886 2	0.00202 07	0.02719 39	0.0212645	994/983/7480/595/993
BP	G0:19012 16	positive regulation of neuron death	9/579	92/1886 2	0.00205 68	0.02759 85	0.021581	7020/7042/2045/10018/1948/5621/23621/55294/46
BP	G0:00513 48	negative regulation of transferase activity	19/579	296/188 62	0.00208 53	0.02789 98	0.0218165	11261/7532/104/9655/3843/54206/9052/5728/7529
BP	G0:00305 22	intracellular receptor signaling pathway	18/579	274/188 62	0.00210 18	0.02803 79	0.0219245	85364/10413/171023/9575/7182/56603/57678/5915
BP	G0:00989 30	axonal transport	7/579	59/1886 2	0.00212	0.02812 08	0.0219894	55207/23557/22906/23095/9371/3798/5048
BP	G0:00069 04	vesicle docking involved in exocytosis	6/579	44/1886 2	0.00213 43	0.02812 08	0.0219894	10890/51762/201475/6814/26276/10490
BP	G0:00550 10	ventricular cardiac muscle tissue morphogenesis	6/579	44/1886 2	0.00213 43	0.02812 08	0.0219894	7042/2280/23414/3516/4092/7049
BP	G0:00604 21	positive regulation of heart growth	6/579	44/1886 2	0.00213 43	0.02812 08	0.0219894	10413/23414/3516/7049/2247/5292
BP	G0:00709 97	neuron death	21/579	342/188 62	0.00214 24	0.02812 08	0.0219894	54532/11261/104/163/7020/7042/10314/2045/1001

BP	G0:00215 37	telencephalon development	16/579	231/188 62	0.00214 48	0.02812 08	0.0219894	5915/22903/5728/57142/9928/6299/6497/89780/64
BP	G0:00485 68	embryonic organ development	24/579	412/188 62	0.00215 94	0.02823 25	0.0220768	10413/7020/7042/4297/57534/1969/3215/5915/288
BP	G0:00726 59	protein localization to plasma membrane	18/579	275/188 62	0.00218 67	0.02850 8	0.0222922	1956/1969/10890/22841/51762/2319/201475/83871
BP	G0:00020 42	cell migration involved in sprouting angiogenesis	9/579	93/1886 2	0.00221 67	0.02876 02	0.0224894	8829/1948/90627/161742/7422/10000/29775/55294
BP	G0:00511 69	nuclear transport	21/579	343/188 62	0.00221 86	0.02876 02	0.0224894	3842/10628/11261/3839/5494/1871/3843/84271/55
BP	G0:00097 91	post-embryonic development	8/579	76/1886 2	0.00226 48	0.02919 4	0.0228286	10018/4087/7422/55870/64919/3482/3708/59338
BP	G0:00723 95	signal transduction involved in cell cycle checkpoint	8/579	76/1886 2	0.00226 48	0.02919 4	0.0228286	7029/983/144455/4194/7832/10498/8555/1111
BP	G0:00458 62	positive regulation of proteolysis	22/579	367/188 62	0.00228 96	0.02943 11	0.023014	8795/444/9655/8473/10395/3146/10018/5728/1019
BP	G0:00435 35	regulation of blood vessel endothelial cell migration	12/579	150/188 62	0.00231 14	0.02962 87	0.0231685	1969/6776/3146/90627/161742/7422/10000/29775/
BP	G0:00303 26	embryonic limb morphogenesis	10/579	112/188 62	0.00235 73	0.02998 32	0.0234457	7020/7042/56603/5915/10018/8434/6299/6497/320
BP	G0:00351 13	embryonic appendage morphogenesis	10/579	112/188 62	0.00235 73	0.02998 32	0.0234457	7020/7042/56603/5915/10018/8434/6299/6497/320

BP	G0:00312 90	retinal ganglion cell axon guidance	4/579	19/1886 2	0.00235 87	0.02998 32	0.0234457	8829/2045/214/7422
BP	G0:00084 06	gonad development	15/579	212/188 62	0.00237 47	0.03010 34	0.0235397	7042/152006/10018/192670/23414/6299/7422/92/5
BP	G0:00468 39	phospholipid dephosphorylation	6/579	45/1886 2	0.00239 99	0.03017 31	0.0235942	22908/8897/66036/5728/8867/9110
BP	G0:00616 47	histone H3-K9 modification	6/579	45/1886 2	0.00239 99	0.03017 31	0.0235942	4297/1786/3720/55870/1111/4602
BP	G0:19000 87	positive regulation of G1/S transition of mitotic cell cycle	6/579	45/1886 2	0.00239 99	0.03017 31	0.0235942	894/1956/595/1654/134353/5356
BP	G0:00604 20	regulation of heart growth	8/579	77/1886 2	0.00246 1	0.03085 64	0.0241285	10413/5728/23414/3720/3516/7049/2247/5292
BP	G0:00085 43	fibroblast growth factor receptor signaling pathway	10/579	113/188 62	0.00251 69	0.03144 87	0.0245917	25778/3185/2885/51552/8036/161742/8862/1399/2
BP	G0:00109 77	negative regulation of neuron projection development	11/579	132/188 62	0.00252 19	0.03144 87	0.0245917	8829/2045/1948/5728/57142/23557/89780/396/104
BP	G0:00076 11	learning or memory	16/579	235/188 62	0.00254 8	0.03168 74	0.0247783	9378/22849/1956/5621/5728/8867/3678/3949/6198
BP	G0:19012 14	regulation of neuron death	19/579	302/188 62	0.00261 01	0.03237 28	0.0253143	11261/163/7020/7042/10314/2045/10018/128866/1
BP	G0:00507 67	regulation of neurogenesis	21/579	348/188 62	0.00263 47	0.03258 93	0.0254835	10413/7074/8829/5789/2045/23405/5728/57142/39

BP	G0:01400 29	exocytic process	8/579	78/1886 2	0.00267 02	0.03294 02	0.025758	10890/51762/201475/23557/8867/6814/26276/1049
BP	G0:00357 67	endothelial cell chemotaxis	5/579	32/1886 2	0.00271 52	0.03333 76	0.0260687	8829/3146/7422/2247/2260
BP	G0:00355 67	non-canonical Wnt signaling pathway	12/579	153/188 62	0.00272 43	0.03333 76	0.0260687	23112/163/7074/192670/166336/5715/27327/7471/
BP	G0:00466 61	male sex differentiation	12/579	153/188 62	0.00272 43	0.03333 76	0.0260687	7042/152006/10018/192670/4090/23414/92/595/13
BP	G0:00480 02	antigen processing and presentation of peptide antigen	14/579	194/188 62	0.00273 33	0.03335 97	0.026086	163/821/10802/1147/140735/2923/5715/3551/1019
BP	G0:00315 71	mitotic G1 DNA damage checkpoint	7/579	62/1886 2	0.00282 46	0.03424 93	0.0267816	7029/983/144455/4194/7832/10498/595
BP	G0:00518 98	negative regulation of protein kinase B signaling	7/579	62/1886 2	0.00282 46	0.03424 93	0.0267816	23239/23035/1969/5728/5795/201163/59338
BP	G0:00072 66	Rho protein signal transduction	11/579	134/188 62	0.00283 61	0.03424 93	0.0267816	27/8829/8452/10395/10672/1147/90627/5894/396/
BP	G0:00085 84	male gonad development	11/579	134/188 62	0.00283 61	0.03424 93	0.0267816	7042/152006/10018/192670/23414/92/595/1399/78
BP	G0:00032 06	cardiac chamber morphogenesis	10/579	115/188 62	0.00286 23	0.03447 49	0.026958	7042/8829/2280/5915/90/23414/3516/4092/7049/4
BP	G0:00430 11	myeloid dendritic cell differentiation	4/579	20/1886 2	0.00287 75	0.03456 81	0.0270309	3696/3516/3662/4853

BP	G0:00342 48	regulation of cellular amide metabolic process	27/579	494/188 62	0.00289 72	0.03471 33	0.0271445	23112/84919/5813/22849/9728/192670/8087/1656/
BP	G0:00483 40	paraxial mesoderm morphogenesis	3/579	10/1886 2	0.00293 87	0.03511 85	0.0274613	4087/4088/89780
BP	G0:00465 46	development of primary male sexual characteristics	11/579	135/188 62	0.00300 46	0.03572 2	0.0279333	7042/152006/10018/192670/23414/92/595/1399/78
BP	G0:00080 89	anterograde axonal transport	6/579	47/1886 2	0.00300 47	0.03572 2	0.0279333	55207/23557/22906/23095/9371/3798
BP	G0:19907 78	protein localization to cell periphery	20/579	329/188 62	0.00302 89	0.03591 68	0.0280855	1956/1969/10890/22841/51762/2319/201475/83871
BP	G0:00066 61	phosphatidylinositol biosynthetic process	10/579	116/188 62	0.00304 86	0.03605 64	0.0281947	22908/8897/66036/5728/51552/8867/2247/9110/52
BP	G0:00447 83	G1 DNA damage checkpoint	7/579	63/1886 2	0.00309 54	0.03638 99	0.0284555	7029/983/144455/4194/7832/10498/595
BP	G0:00448 19	mitotic G1/S transition checkpoint	7/579	63/1886 2	0.00309 54	0.03638 99	0.0284555	7029/983/144455/4194/7832/10498/595
BP	G0:00032 03	endocardial cushion morphogenesis	5/579	33/1886 2	0.00312 05	0.03638 99	0.0284555	7042/90/4194/3516/55273
BP	G0:00109 22	positive regulation of phosphatase activity	5/579	33/1886 2	0.00312 05	0.03638 99	0.0284555	84919/66036/57181/4088/3673
BP	G0:00070 32	endosome organization	8/579	80/1886 2	0.00313 03	0.03638 99	0.0284555	137492/10228/128866/8867/23023/26276/27183/10

BP	G0:00075 48	sex differentiation	17/579	262/188 62	0.00313 23	0.03638 99	0.0284555	7042/152006/10018/192670/4090/23414/6299/7422
BP	G0:00507 30	regulation of peptidyl-tyrosine phosphorylation	17/579	262/188 62	0.00313 23	0.03638 99	0.0284555	9655/8829/1956/2045/3082/57826/253260/90/5420
BP	G0:00616 40	cytoskeleton- dependent cytokinesis	9/579	98/1886 2	0.00317 07	0.03674 35	0.028732	55165/128866/23503/6651/27183/10097/403/9493/
BP	G0:00182 15	protein phosphopantetheinylat ion	20/579	331/188 62	0.00324 38	0.03749 54	0.02932	54532/444/8314/8473/285203/54726/2923/57478/7
BP	G0:00457 78	positive regulation of ossification	6/579	48/1886 2	0.00334 66	0.03830 94	0.0299565	7020/7042/90/7480/4088/92
BP	G0:00610 28	establishment of endothelial barrier	6/579	48/1886 2	0.00334 66	0.03830 94	0.0299565	5144/57826/3551/7414/7422/2194
BP	G0:00300 10	establishment of cell polarity	11/579	137/188 62	0.00336 57	0.03830 94	0.0299565	56603/253260/10890/22841/2319/7465/154810/139
BP	G0:00092 67	cellular response to starvation	12/579	157/188 62	0.00336 59	0.03830 94	0.0299565	3920/150094/22863/8897/5562/27327/81929/26100
BP	G0:00723 84	organelle transport along microtubule	8/579	81/1886 2	0.00338 23	0.03830 94	0.0299565	23299/23557/22906/3064/23095/9371/3798/5048
BP	G0:00518 93	regulation of focal adhesion assembly	7/579	64/1886 2	0.00338 57	0.03830 94	0.0299565	8829/10395/5728/5795/4088/7414/7422
BP	G0:00713 00	cellular response to retinoic acid	7/579	64/1886 2	0.00338 57	0.03830 94	0.0299565	10413/27/56603/7480/6532/89780/4602

BP	G0:0090109	regulation of cell-substrate junction assembly	7/579	64/18862	0.0033857	0.0383094	0.0299565	8829/10395/5728/5795/4088/7414/7422
BP	G0:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	9/579	99/18862	0.0033954	0.0383094	0.0299565	163/821/10802/140735/6712/830/9493/9371/3798
BP	G0:0031667	response to nutrient levels	25/579	451/18862	0.0033977	0.0383094	0.0299565	65084/3920/8473/56603/1956/150094/22863/8897/
BP	G0:0008090	retrograde axonal transport	4/579	21/18862	0.0034693	0.0386428	0.0302171	23557/23095/3798/5048
BP	G0:0034629	cellular protein-containing complex localization	4/579	21/18862	0.0034693	0.0386428	0.0302171	23557/8976/81929/4092
BP	G0:0035024	negative regulation of Rho protein signal transduction	4/579	21/18862	0.0034693	0.0386428	0.0302171	27/8452/10395/201163
BP	G0:0039702	viral budding via host ESCRT complex	4/579	21/18862	0.0034693	0.0386428	0.0302171	137492/128866/27183/10015
BP	G0:0043984	histone H4-K16 acetylation	4/579	21/18862	0.0034693	0.0386428	0.0302171	4297/8473/55683/284058
BP	G0:0006473	protein acetylation	14/579	200/18862	0.0035987	0.0399861	0.0312676	9575/4297/8473/55683/80155/5562/9252/284058/5
BP	G0:0007369	gastrulation	13/579	179/18862	0.0036129	0.0400475	0.0313156	8452/1969/90/4087/60436/3678/4088/89780/92/88

BP	G0:00107 17	regulation of epithelial to mesenchymal transition	9/579	100/188 62	0.00363 24	0.04007	0.0313332	7042/7074/90/5728/4087/4088/4092/161742/8313
BP	G0:19052 69	positive regulation of chromatin organization	9/579	100/188 62	0.00363 24	0.04007	0.0313332	80312/4297/8473/1786/9252/3720/7422/4602/2614
BP	G0:00073 68	determination of left/right symmetry	10/579	119/188 62	0.00366 61	0.04024 81	0.0314725	57534/90/4087/5681/4088/89780/92/80173/9371/4
BP	G0:20001 34	negative regulation of G1/S transition of mitotic cell cycle	10/579	119/188 62	0.00366 61	0.04024 81	0.0314725	7029/123879/983/144455/5728/4194/7465/7832/10
BP	G0:00603 89	pathway-restricted SMAD protein phosphorylation	7/579	65/1886 2	0.00369 61	0.04038 48	0.0315793	7042/651/90/4092/7049/9958/92
BP	G0:19048 88	cranial skeletal system development	7/579	65/1886 2	0.00369 61	0.04038 48	0.0315793	7020/7042/55165/4087/51715/4088/1399
BP	G0:00465 80	negative regulation of Ras protein signal transduction	6/579	49/1886 2	0.00371 67	0.04051 25	0.0316792	27/7042/8452/10395/201163/9927
BP	G0:00322 59	methylation	21/579	359/188 62	0.00378 56	0.04116 58	0.0321901	80312/200424/4297/8473/8731/1786/3720/55870/7
BP	G0:00016 49	osteoblast differentiation	15/579	223/188 62	0.00383 22	0.04157 49	0.0325099	10413/1969/3082/651/90/4090/7480/6497/4088/89
BP	G0:00019 67	suckling behavior	3/579	11/1886 2	0.00394 91	0.04244 13	0.0331874	55585/130507/5194

BP	G0:00349 75	protein folding in endoplasmic reticulum	3/579	11/1886 2	0.00394 91	0.04244 13	0.0331874	821/2923/7184
BP	G0:00354 04	histone-serine phosphorylation	3/579	11/1886 2	0.00394 91	0.04244 13	0.0331874	5562/9252/8091
BP	G0:00608 37	blood vessel endothelial cell differentiation	3/579	11/1886 2	0.00394 91	0.04244 13	0.0331874	8829/3516/55273
BP	G0:00000 83	regulation of transcription involved in G1/S transition of mitotic cell cycle	5/579	35/1886 2	0.00405 9	0.04321 77	0.0337946	5128/7029/8462/144455/898
BP	G0:00480 09	insulin-like growth factor receptor signaling pathway	5/579	35/1886 2	0.00405 9	0.04321 77	0.0337946	7471/51232/3482/55023/5295
BP	G0:19010 30	positive regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	5/579	35/1886 2	0.00405 9	0.04321 77	0.0337946	7532/7029/7529/7533/10971
BP	G0:19052 07	regulation of cardiocyte differentiation	5/579	35/1886 2	0.00405 9	0.04321 77	0.0337946	7042/1956/1948/55553/89780
BP	G0:00704 82	response to oxygen levels	22/579	385/188 62	0.00407	0.04323 48	0.0338079	7042/5562/5715/5728/7184/4194/10197/3516/2340

BP	G0:00511 46	striated muscle cell differentiation	17/579	269/188 62	0.00408 96	0.04334 17	0.0338916	56603/150094/5915/90/1073/1147/1760/1948/7471
BP	G0:00099 52	anterior/posterior pattern specification	14/579	203/188 62	0.00410 85	0.04336 2	0.0339074	57534/3215/4087/7471/3516/6497/4088/89780/92/
BP	G0:00032 29	ventricular cardiac muscle tissue development	6/579	50/1886 2	0.00411 62	0.04336 2	0.0339074	7042/2280/23414/3516/4092/7049
BP	G0:00991 73	postsynapse organization	12/579	161/188 62	0.00412 45	0.04336 2	0.0339074	7074/9378/5789/2045/5621/5728/8976/6712/10097
BP	G0:00032 83	atrial septum development	4/579	22/1886 2	0.00413 87	0.04336 2	0.0339074	7042/90/4194/4853
BP	G0:00725 76	liver morphogenesis	4/579	22/1886 2	0.00413 87	0.04336 2	0.0339074	8452/89780/55294/4853
BP	G0:00518 96	regulation of protein kinase B signaling	16/579	247/188 62	0.00415 17	0.04339 86	0.033936	23239/23035/1956/1969/3082/253260/2885/5728/5
BP	G0:00106 32	regulation of epithelial cell migration	18/579	293/188 62	0.00428 27	0.04453 69	0.0348261	7042/8829/55466/1969/6776/3146/5728/57142/906
BP	G0:00025 73	myeloid leukocyte differentiation	14/579	204/188 62	0.00429 09	0.04453 69	0.0348261	3930/1969/3696/9935/3516/7422/9770/863/2194/5
BP	G0:00508 52	T cell receptor signaling pathway	14/579	204/188 62	0.00429 09	0.04453 69	0.0348261	5144/1147/55824/5621/5715/3551/5795/10197/894
BP	G0:00070 15	actin filament organization	24/579	435/188 62	0.00429 94	0.04453 69	0.0348261	23607/7456/8829/8452/10395/253260/2885/1073/1
BP	G0:00024 95	antigen processing and presentation of	9/579	103/188 62	0.00442 2	0.04560 11	0.0356583	163/821/10802/140735/6712/830/9493/9371/3798

		peptide antigen via MHC class II						
BP	G0:00325 26	response to retinoic acid	9/579	103/188 62	0.00442 2	0.04560 11	0.0356583	10413/27/171023/56603/7480/6532/89780/3482/46
BP	G0:00432 81	regulation of cysteine-type endopeptidase activity involved in apoptotic process	14/579	205/188 62	0.00447 98	0.04609 41	0.0360438	8795/10395/2045/3082/3146/10018/23204/6197/40
BP	G0:00464 74	glycerophospholipid biosynthetic process	15/579	227/188 62	0.00451 66	0.04621 64	0.0361395	55500/57678/22908/8897/66036/5728/51552/8867/
BP	G0:00107 18	positive regulation of epithelial to mesenchymal transition	6/579	51/1886 2	0.00454 66	0.04621 64	0.0361395	7042/7074/90/4087/4088/8313
BP	G0:00305 14	negative regulation of BMP signaling pathway	6/579	51/1886 2	0.00454 66	0.04621 64	0.0361395	5494/7471/6497/4092/57154/51232
BP	G0:00480 41	focal adhesion assembly	8/579	85/1886 2	0.00455 09	0.04621 64	0.0361395	8829/10395/5728/5795/4088/7414/7422/3673
BP	G0:19001 82	positive regulation of protein localization to nucleus	8/579	85/1886 2	0.00455 09	0.04621 64	0.0361395	23607/10413/3843/908/983/4088/29775/5295
BP	G0:00511 70	import into nucleus	12/579	163/188 62	0.00455 22	0.04621 64	0.0361395	3842/10628/11261/3839/1871/3843/51715/4088/10

BP	G0:19037 25	regulation of phospholipid metabolic process	5/579	36/1886 2	0.00459 68	0.04656 72	0.0364137	11261/8897/66036/3949/9110
BP	G0:00068 88	endoplasmic reticulum to Golgi vesicle- mediated transport	14/579	206/188 62	0.00467 55	0.04725 92	0.0369549	64764/8452/10802/140735/22870/51014/6712/5501
BP	G0:00025 04	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	9/579	104/188 62	0.00471 29	0.04742 89	0.0370876	163/821/10802/140735/6712/830/9493/9371/3798
BP	G0:00069 06	vesicle fusion	9/579	104/188 62	0.00471 29	0.04742 89	0.0370876	11261/8675/10228/51762/83871/23557/55014/2718
BP	G0:00330 44	regulation of chromosome organization	17/579	273/188 62	0.00473 69	0.04756 59	0.0371947	80351/80312/4297/8473/8452/6421/908/1786/9252
BP	G0:00017 07	mesoderm formation	7/579	68/1886 2	0.00475 82	0.04760 49	0.0372252	1969/90/4087/4088/89780/8091/3673
BP	G0:00380 61	NIK/NF-kappaB signaling	13/579	185/188 62	0.00477 19	0.04760 49	0.0372252	8795/5494/1956/3146/1147/23405/5715/10197/977
BP	G0:00512 16	cartilage development	13/579	185/188 62	0.00477 19	0.04760 49	0.0372252	64764/3696/5915/651/4090/7480/4088/4092/55553
BP	G0:00451 65	cell fate commitment	16/579	251/188 62	0.00484 17	0.04805 3	0.0375756	8829/56603/10890/90/4087/4090/7471/7480/3516/

BP	G0:00480 13	ephrin receptor signaling pathway	8/579	86/1886 2	0.00488 65	0.04805 3	0.0375756	163/7074/1969/2045/1948/8976/3516/10097
BP	G0:00600 21	roof of mouth development	8/579	86/1886 2	0.00488 65	0.04805 3	0.0375756	7020/7042/3696/4087/6497/7049/89780/59338
BP	G0:00066 22	protein targeting to lysosome	4/579	23/1886 2	0.00489 01	0.04805 3	0.0375756	3920/64089/27183/23163
BP	G0:00486 68	collateral sprouting	4/579	23/1886 2	0.00489 01	0.04805 3	0.0375756	2045/89780/627/51199
BP	G0:00603 84	innervation	4/579	23/1886 2	0.00489 01	0.04805 3	0.0375756	104/8829/4884/9860
BP	G0:19024 10	mitotic cytokinetic process	4/579	23/1886 2	0.00489 01	0.04805 3	0.0375756	55165/128866/27183/10015
BP	G0:19028 07	negative regulation of cell cycle G1/S phase transition	10/579	124/188 62	0.00491 17	0.04816 19	0.0376608	7029/123879/983/144455/5728/4194/7465/7832/10
BP	G0:00313 46	positive regulation of cell projection organization	20/579	344/188 62	0.00497 3	0.04865 89	0.0380494	27/7074/57498/8829/5789/64764/3082/51762/8976
BP	G0:00351 96	production of miRNAs involved in gene silencing by miRNA	6/579	52/1886 2	0.00500 92	0.04889 6	0.0382348	1956/192670/23405/4087/4088/6895
BP	G0:00622 07	regulation of pattern recognition receptor signaling pathway	9/579	105/188 62	0.00501 85	0.04889 6	0.0382348	85364/3146/8780/54726/57142/9958/1654/3304/36
BP	G0:20001 16	regulation of cysteine-type	15/579	230/188 62	0.00509 26	0.04951 24	0.0387168	8795/444/10395/2045/3082/3146/10018/23204/619

		endopeptidase activity						
BP	G0:00488 20	hair follicle maturation	3/579	12/1886 2	0.00514 63	0.04992 94	0.0390428	7042/7480/3516
BP	G0:00482 84	organelle fusion	11/579	145/188 62	0.00517 26	0.04997 25	0.0390766	11261/8675/10228/51762/983/83871/23557/55014/
BP	G0:00719 01	negative regulation of protein serine/threonine kinase activity	11/579	145/188 62	0.00517 26	0.04997 25	0.0390766	7532/3843/5728/5795/161742/11329/26973/10527/
BP	G0:00448 18	mitotic G2/M transition checkpoint	5/579	37/1886 2	0.00518 35	0.04997 25	0.0390766	63967/983/57551/1111/8091
CC	G0:00550 37	recycling endosome	22/593	190/195 20	8.18E- 08	2.58E- 05	2.12E-05	29126/57826/10890/22841/51762/2923/55041/2014
CC	G0:19029 11	protein kinase complex	16/593	104/195 20	9.61E- 08	2.58E- 05	2.12E-05	894/9134/90/983/1147/5562/2965/3551/92/595/89
CC	G0:00616 95	transferase complex, transferring phosphorus-containing groups	24/593	253/195 20	8.95E- 07	0.00015 99	0.0001319	894/9134/9655/22863/90/983/1147/5562/6908/296
CC	G0:00059 25	focal adhesion	32/593	416/195 20	1.61E- 06	0.00021 58	0.000178	11261/7532/8675/8462/8649/8829/10395/1956/196
CC	G0:00300 55	cell-substrate junction	32/593	423/195 20	2.30E- 06	0.00024 64	0.0002033	11261/7532/8675/8462/8649/8829/10395/1956/196

CC	G0:1902554	serine/threonine protein kinase complex	13/593	89/19520	2.79E-06	0.0002492	0.0002055	894/9134/90/983/1147/2965/3551/92/595/898/905
CC	G0:0005770	late endosome	24/593	275/19520	3.90E-06	0.0002984	0.0002461	137492/57498/3920/8649/1956/55207/128866/5155
CC	G0:0055038	recycling endosome membrane	12/593	87/19520	1.23E-05	0.0008229	0.0006787	29126/57826/10890/22841/51762/2923/55041/2014
CC	G0:0005635	nuclear envelope	32/593	462/19520	1.42E-05	0.0008429	0.0006953	80351/894/23299/3839/3930/9378/26031/23333/19
CC	G0:0098793	presynapse	32/593	487/19520	3.98E-05	0.0021331	0.0017594	7532/821/8675/10228/9378/5789/10890/51762/808
CC	G0:0005667	transcription regulator complex	28/593	409/19520	5.92E-05	0.0028847	0.0023793	10413/9575/79718/7029/1871/3146/6421/144455/8
CC	G0:0031519	PcG protein complex	8/593	47/19520	7.65E-05	0.0030264	0.0024963	171023/8314/80012/3720/84733/8535/2145/26147
CC	G0:0016442	RISC complex	5/593	16/19520	8.41E-05	0.0030264	0.0024963	192670/1656/23405/27327/6895
CC	G0:0031332	RNAi effector complex	5/593	16/19520	8.41E-05	0.0030264	0.0024963	192670/1656/23405/27327/6895
CC	G0:0042470	melanosome	12/593	106/19520	9.03E-05	0.0030264	0.0024963	526/821/10672/2923/7529/7184/6856/813/2194/46
CC	G0:0048770	pigment granule	12/593	106/19520	9.03E-05	0.0030264	0.0024963	526/821/10672/2923/7529/7184/6856/813/2194/46
CC	G0:0005774	vacuolar membrane	28/593	431/19520	0.0001446	0.004559	0.0037604	163/526/3920/8649/22863/55207/201475/51552/23

CC	G0:00301 39	endocytic vesicle	22/593	307/195 20	0.00018 9	0.00562 68	0.0046411	23607/163/10228/3920/1956/10890/51762/22863/2
CC	G0:00905 75	RNA polymerase II transcription regulator complex	15/593	170/195 20	0.00022 06	0.00622 19	0.005132	10413/9575/7029/1871/6421/144455/4087/4090/69
CC	G0:00057 69	early endosome	25/593	378/195 20	0.00024 69	0.00628 39	0.0051831	29126/10228/8829/1956/3146/57561/51552/56674/
CC	G0:00058 74	microtubule	27/593	423/195 20	0.00025 07	0.00628 39	0.0051831	7461/7074/8452/908/983/140735/57326/8867/5461
CC	G0:01201 11	neuron projection cytoplasm	10/593	86/1952 0	0.00027 61	0.00628 39	0.0051831	5813/6421/55207/23557/22906/23710/23095/9371/
CC	G0:00058 19	spindle	25/593	381/195 20	0.00027 82	0.00628 39	0.0051831	994/79718/7029/23035/8452/55207/983/54617/992
CC	G0:00304 96	midbody	16/593	193/195 20	0.00028 14	0.00628 39	0.0051831	22849/55207/983/55165/128866/23503/7184/9928/
CC	G0:00319 02	late endosome membrane	13/593	140/195 20	0.00034 79	0.00745 84	0.0061519	137492/3920/8649/55207/128866/4891/64089/2627
CC	G0:00001 51	ubiquitin ligase complex	20/593	289/195 20	0.00056 87	0.01165 25	0.0096112	9354/80012/8452/123879/84961/56929/165918/255
CC	G0:00905 43	Flemming body	6/593	35/1952 0	0.00058 7	0.01165 25	0.0096112	55165/9928/9960/27183/9493/10015
CC	G0:00364 64	cytoplasmic ribonucleoprotein granule	17/593	234/195 20	0.00084 3	0.01613 65	0.0133098	23112/9575/57532/192670/8087/1656/84271/27327
CC	G0:00059 11	cell-cell junction	28/593	485/195 20	0.00094 69	0.01750 13	0.0144355	54532/23607/23705/7074/1969/57826/2885/10890/

CC	G0:00056 43	nuclear pore	9/593	85/1952 0	0.00109 61	0.01916 32	0.0158062	23299/3839/3843/64328/81929/23039/10527/3836/
CC	G0:00016 50	fibrillar center	12/593	139/195 20	0.00110 83	0.01916 32	0.0158062	23607/1316/3215/8731/5049/55127/4092/6629/223
CC	G0:00357 70	ribonucleoprotein granule	17/593	244/195 20	0.00133 33	0.02220 44	0.0183147	23112/9575/57532/192670/8087/1656/84271/27327
CC	G0:00301 33	transport vesicle	24/593	402/195 20	0.00136 71	0.02220 44	0.0183147	11261/8675/10228/64418/10802/10890/51762/4884
CC	G0:00170 53	transcription repressor complex	8/593	74/1952 0	0.00179 07	0.02621 64	0.0216239	79718/3146/7529/3516/6497/23013/595/54815
CC	G0:00319 65	nuclear membrane	19/593	295/195 20	0.00179 1	0.02621 64	0.0216239	894/3930/9378/26031/23333/1956/9123/1760/1663
CC	G0:00003 07	cyclin-dependent protein kinase holoenzyme complex	6/593	43/1952 0	0.00179 57	0.02621 64	0.0216239	894/9134/983/595/898/905
CC	G0:19041 15	axon cytoplasm	7/593	58/1952 0	0.00180 97	0.02621 64	0.0216239	55207/23557/22906/23095/9371/3798/5048
CC	G0:00325 93	insulin-responsive compartment	3/593	10/1952 0	0.00285 35	0.03781 02	0.0311868	10890/201475/4644
CC	G0:00057 65	lysosomal membrane	22/593	378/195 20	0.00290 17	0.03781 02	0.0311868	163/526/3920/8649/55207/201475/51552/23557/56
CC	G0:00988 52	lytic vacuole membrane	22/593	378/195 20	0.00290 17	0.03781 02	0.0311868	163/526/3920/8649/55207/201475/51552/23557/56
CC	G0:00453 35	phagocytic vesicle	11/593	136/195 20	0.00294 32	0.03781 02	0.0311868	10228/3920/10890/51762/22863/2923/51552/83871

CC	G0:00057 76	autophagosome	9/593	98/1952 0	0.00296 27	0.03781 02	0.0311868	3920/22863/201475/81671/51715/55014/79065/237
CC	G0:00726 86	mitotic spindle	12/593	157/195 20	0.00310 08	0.03865 18	0.0318809	79718/7029/23035/8452/983/8555/996/1729/20116
CC	G0:00319 01	early endosome membrane	12/593	162/195 20	0.00399 81	0.04870 37	0.040172	29126/1956/51552/56674/10479/64089/26276/1049
MF	G0:00463 32	SMAD binding	16/585	77/1833 7	2.12E- 09	1.54E- 06	1.30E-06	5494/5813/2280/90/4087/4090/6497/4088/4092/57
MF	G0:00046 74	protein serine/threonine kinase activity	36/585	430/183 37	1.45E- 07	5.26E- 05	4.46E-05	5128/23097/25778/1956/150094/8780/90/983/1147
MF	G0:00704 11	I-SMAD binding	6/585	14/1833 7	2.48E- 06	0.00060 03	0.0005091	4087/4090/4088/4092/57154/8313
MF	G0:00481 85	activin binding	6/585	15/1833 7	4.02E- 06	0.00073 01	0.0006193	2280/90/4092/57154/7049/92
MF	G0:00044 38	phosphatidylinositol- 3-phosphatase activity	6/585	16/1833 7	6.26E- 06	0.00084 68	0.0007182	22908/8897/66036/5728/8867/9110
MF	G0:00051 60	transforming growth factor beta receptor binding	7/585	24/1833 7	7.00E- 06	0.00084 68	0.0007182	7042/2280/4087/4088/4092/7049/9958
MF	G0:00527 44	phosphatidylinositol monophosphate phosphatase activity	6/585	17/1833 7	9.42E- 06	0.00097 68	0.0008285	22908/8897/66036/5728/8867/9110
MF	G0:00199 02	phosphatase binding	19/585	193/183 37	1.40E- 05	0.00127 45	0.001081	11215/1956/2885/8897/66036/22870/4087/7184/61

MF	G0:0019903	protein phosphatase binding	16/585	148/18337	2.09E-05	0.0016849	0.0014292	11215/1956/2885/8897/66036/22870/7184/6198/80
MF	G0:0019207	kinase regulator activity	20/585	220/18337	2.71E-05	0.0019653	0.001667	894/9134/11261/7532/11215/9655/57498/8649/314
MF	G0:0030165	PDZ domain binding	11/585	83/18337	6.39E-05	0.0042144	0.0035747	23705/57498/5728/9928/6198/7049/51/92/440193/
MF	G0:0008013	beta-catenin binding	11/585	85/18337	7.97E-05	0.0048211	0.0040892	23607/79718/139285/5795/6299/4088/4092/7414/8
MF	G0:0042393	histone binding	20/585	241/18337	9.76E-05	0.0051216	0.0043441	8019/79718/4297/80012/165918/54617/55206/6749
MF	G0:0051219	phosphoprotein binding	11/585	87/18337	9.88E-05	0.0051216	0.0043441	27/2885/7529/5774/8945/8535/1399/55294/3482/5
MF	G0:0019003	GDP binding	10/585	75/18337	0.0001298	0.0061373	0.0052057	57826/10890/51762/55207/201475/51552/51209/15
MF	G0:0015631	tubulin binding	26/585	368/18337	0.0001401	0.0061373	0.0052057	11261/7461/7074/10018/55207/5621/54617/9928/5
MF	G0:0106311	protein threonine kinase activity	20/585	248/18337	0.0001441	0.0061373	0.0052057	150094/8780/1760/5562/9252/3551/5681/6197/619
MF	G0:0106310	protein serine kinase activity	20/585	249/18337	0.0001522	0.0061373	0.0052057	150094/8780/1760/5562/9252/3551/5681/6197/619
MF	G0:0004721	phosphoprotein phosphatase activity	16/585	179/18337	0.0002052	0.0078397	0.0066496	994/23239/23035/5494/5789/8897/5728/5795/5774
MF	G0:0019199	transmembrane receptor protein kinase activity	10/585	80/18337	0.0002236	0.0081156	0.0068836	8829/1956/1969/2045/90/7049/92/51232/2260/348

MF	G0:00616 59	ubiquitin-like protein ligase activity	22/585	305/183 37	0.00033 65	0.01163 17	0.009866	9354/8452/152006/147339/286827/84937/84461/51
MF	G0:00453 09	protein phosphorylated amino acid binding	8/585	56/1833 7	0.00037 67	0.01208 98	0.0102545	27/2885/7529/5774/8945/1399/55294/5295
MF	G0:01401 42	nucleocytoplasmic carrier activity	6/585	31/1833 7	0.00038 3	0.01208 98	0.0102545	3842/3839/3843/64328/23039/3836
MF	G0:00198 87	protein kinase regulator activity	16/585	190/183 37	0.00040 25	0.01217 71	0.0103285	894/9134/11261/7532/57498/3146/253260/9052/75
MF	G0:00616 30	ubiquitin protein ligase activity	21/585	294/183 37	0.00051 8	0.01504 23	0.0127588	9354/8452/152006/147339/286827/84937/84461/51
MF	G0:00528 66	phosphatidylinositol phosphate phosphatase activity	6/585	33/1833 7	0.00054 58	0.01524 1	0.0129274	22908/8897/66036/5728/8867/9110
MF	G0:00048 42	ubiquitin-protein transferase activity	27/585	429/183 37	0.00065 72	0.01712 11	0.0145221	9354/57534/8452/165918/152006/147339/286827/8
MF	G0:00197 87	ubiquitin-like protein transferase activity	28/585	452/183 37	0.00067 3	0.01712 11	0.0145221	9354/57534/8452/165918/152006/147339/286827/8
MF	G0:00037 25	double-stranded RNA binding	9/585	76/1833 7	0.00068 39	0.01712 11	0.0145221	104/3146/192670/8087/23405/51092/6895/1654/19
MF	G0:00452 96	cadherin binding	22/585	332/183 37	0.00104 54	0.02475 56	0.0209976	23607/1956/1969/10890/90/128866/1656/9052/571

MF	G0:00051 61	platelet-derived growth factor receptor binding	4/585	15/1833 7	0.00105 71	0.02475 56	0.0209976	5728/3678/5795/7422
MF	G0:00316 25	ubiquitin protein ligase binding	20/585	293/183 37	0.00121 73	0.02761 85	0.0234259	10628/8452/1956/57142/4087/4090/6497/4088/409
MF	G0:00047 22	protein serine/threonine phosphatase activity	10/585	101/183 37	0.00143 79	0.03090 88	0.0262167	23239/23035/5494/8897/5728/8555/9110/8493/551
MF	G0:00167 91	phosphatase activity	19/585	276/183 37	0.00144 75	0.03090 88	0.0262167	994/23239/23035/5494/5789/22908/8897/66036/57
MF	G0:00047 25	protein tyrosine phosphatase activity	10/585	102/183 37	0.00154 98	0.03214 64	0.0272664	994/5789/8897/5728/5795/5774/5775/8555/993/91
MF	G0:00085 74	ATP-dependent microtubule motor activity, plus-end- directed	4/585	17/1833 7	0.00175 19	0.03437 57	0.0291573	9928/23095/9371/3798
MF	G0:00430 24	ribosomal small subunit binding	4/585	17/1833 7	0.00175 19	0.03437 57	0.0291573	132864/1654/1975/5292
MF	G0:00037 14	transcription corepressor activity	14/585	182/183 37	0.00215 18	0.04111 02	0.0348694	10413/79718/57326/23414/862/23013/7091/7832/8
MF	G0:00443 89	ubiquitin-like protein ligase binding	20/585	312/183 37	0.00255 24	0.04751 41	0.0403012	10628/8452/1956/57142/4087/4090/6497/4088/409