Table S2 Gene Ontology (GO) terms enriched in immune-related differentially expressed genes (DEGs)

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust
GO:0019814	immunoglobulin complex	132/659	167/19520	3.32E-165	1.21E-162
GO:0006959	humoral immune response	143/655	380/18862	2.13E-111	9.95E-108
GO:0006956	complement activation	106/655	178/18862	3.62E-109	8.44E-106
GO:0006958	complement activation, classical pathway	95/655	141/18862	1.88E-105	2.93E-102
GO:0002455	humoral immune response mediated by circulating immunoglobulin	96/655	156/18862	1.00E-100	1.17E-97
GO:0030546	signaling receptor activator activity	144/606	492/18337	6.80E-98	4.21E-95
GO:0019724	B cell mediated immunity	108/655	226/18862	4.15E-97	3.87E-94
GO:0048018	receptor ligand activity	142/606	486/18337	2.42E-96	7.49E-94
GO:0016064	immunoglobulin mediated immune response	107/655	223/18862	1.96E-96	1.52E-93
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	129/655	367/18862	1.27E-95	8.47E-93
GO:0003823	antigen binding	89/606	165/18337	4.41E-88	9.11E-86
GO:0002449	lymphocyte mediated immunity	121/655	360/18862	8.24E-87	4.81E-84
GO:0006909	phagocytosis	122/655	381/18862	1.13E-84	5.88E-82
GO:0002377	immunoglobulin production	90/655	198/18862	3.53E-78	1.65E-75
GO:0030449	regulation of complement activation	72/655	115/18862	3.49E-76	1.48E-73
GO:0002440	production of molecular mediator of immune response	101/655	286/18862	1.39E-74	5.41E-72
GO:0002920	regulation of humoral immune response	75/655	138/18862	9.99E-73	3.58E-70
GO:0009897	external side of plasma membrane	107/659	402/19520	6.79E-66	1.24E-63
GO:0002697	regulation of immune effector process	114/655	465/18862	7.70E-65	2.57E-62
GO:0006910	phagocytosis, recognition	61/655	98/18862	2.46E-64	7.66E-62
GO:0002429	immune response-activating cell surface receptor signaling pathway	115/655	481/18862	3.81E-64	1.04E-61
GO:0002757	immune response-activating signal transduction	115/655	481/18862	3.81E-64	1.04E-61
GO:0042742	defense response to bacterium	99/655	344/18862	2.49E-63	6.46E-61

GO:0002696	positive regulation of leukocyte activation	105/655	401/18862	1.09E-62	2.67E-60
GO:0050867	positive regulation of cell activation	106/655	412/18862	1.85E-62	4.32E-60
GO:0042571	immunoglobulin complex, circulating	54/659	77/19520	4.70E-62	5.71E-60
GO:0034987	immunoglobulin receptor binding	54/606	79/18337	1.21E-61	1.87E-59
GO:0002431	Fc receptor mediated stimulatory signaling pathway	65/655	145/18862	6.39E-56	1.42E-53
GO:0038094	Fc-gamma receptor signaling pathway	64/655	140/18862	9.48E-56	2.01E-53
GO:0050871	positive regulation of B cell activation	65/655	150/18862	9.84E-55	2.00E-52
GO:0002433	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	63/655	139/18862	1.37E-54	2.56E-52
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	63/655	139/18862	1.37E-54	2.56E-52
GO:0006898	receptor-mediated endocytosis	89/655	328/18862	1.97E-54	3.53E-52
GO:0051251	positive regulation of lymphocyte activation	92/655	356/18862	2.98E-54	5.14E-52
GO:0050864	regulation of B cell activation	71/655	193/18862	9.80E-54	1.63E-51
GO:0006911	phagocytosis, engulfment	59/655	126/18862	3.29E-52	5.28E-50
GO:0050853	B cell receptor signaling pathway	59/655	134/18862	3.15E-50	4.89E-48
GO:0099024	plasma membrane invagination	59/655	135/18862	5.42E-50	8.15E-48
GO:0010324	membrane invagination	59/655	143/18862	3.42E-48	4.99E-46
GO:0005125	cytokine activity	68/606	235/18337	4.67E-45	5.79E-43
GO:0038095	Fc-epsilon receptor signaling pathway	60/655	169/18862	2.09E-44	2.95E-42
GO:0042113	B cell activation	79/655	326/18862	2.80E-44	3.84E-42
GO:0038093	Fc receptor signaling pathway	69/655	239/18862	3.69E-44	4.92E-42
GO:0008037	cell recognition	68/655	232/18862	5.30E-44	6.87E-42
GO:0060326	cell chemotaxis	71/655	306/18862	1.83E-38	2.30E-36
GO:0008083	growth factor activity	51/606	162/18337	5.74E-36	5.93E-34
GO:0005126	cytokine receptor binding	62/606	270/18337	1.18E-34	1.05E-32
GO:0097529	myeloid leukocyte migration	55/655	218/18862	5.83E-32	7.16E-30

GO:0030595	leukocyte chemotaxis	55/655	226/18862	4.38E-31	5.23E-29
GO:0019955	cytokine binding	43/606	136/18337	1.46E-30	1.13E-28
GO:0050851	antigen receptor-mediated signaling pathway	64/655	323/18862	1.93E-30	2.25E-28
GO:0050920	regulation of chemotaxis	52/655	224/18862	2.28E-28	2.59E-26
GO:0005179	hormone activity	39/606	122/18337	5.05E-28	3.48E-26
GO:0072562	blood microparticle	42/659	146/19520	1.32E-27	1.20E-25
GO:0001819	positive regulation of cytokine production	68/655	437/18862	9.27E-26	1.03E-23
GO:1990868	response to chemokine	34/655	97/18862	2.19E-25	2.32E-23
GO:1990869	cellular response to chemokine	34/655	97/18862	2.19E-25	2.32E-23
GO:0001664	G protein-coupled receptor binding	53/606	289/18337	1.03E-24	6.39E-23
GO:0071621	granulocyte chemotaxis	37/655	124/18862	1.14E-24	1.18E-22
GO:0070098	chemokine-mediated signaling pathway	32/655	88/18862	1.52E-24	1.54E-22
GO:0030593	neutrophil chemotaxis	34/655	103/18862	2.15E-24	2.13E-22
GO:0097530	granulocyte migration	39/655	148/18862	1.01E-23	9.77E-22
GO:0032496	response to lipopolysaccharide	56/655	326/18862	1.66E-23	1.58E-21
GO:1990266	neutrophil migration	35/655	123/18862	1.24E-22	1.15E-20
GO:0002237	response to molecule of bacterial origin	56/655	346/18862	3.34E-22	3.05E-20
GO:0050727	regulation of inflammatory response	57/655	366/18862	9.69E-22	8.70E-20
GO:0004896	cytokine receptor activity	30/606	97/18337	2.32E-21	1.31E-19
GO:0031349	positive regulation of defense response	56/655	361/18862	2.73E-21	2.40E-19
GO:0140375	immune receptor activity	34/606	136/18337	9.94E-21	5.13E-19
GO:0050921	positive regulation of chemotaxis	35/655	139/18862	1.05E-20	9.03E-19
GO:0008009	chemokine activity	22/606	49/18337	3.91E-20	1.87E-18
GO:0008528	G protein-coupled peptide receptor activity	34/606	148/18337	1.81E-19	8.02E-18
GO:0070374	positive regulation of ERK1 and ERK2 cascade	41/655	210/18862	1.31E-19	1.11E-17

GO:0071674	mononuclear cell migration	39/655	190/18862	1.62E-19	1.35E-17
GO:0032102	negative regulation of response to external stimulus	56/655	394/18862	1.88E-19	1.54E-17
GO:0001653	peptide receptor activity	34/606	152/18337	4.46E-19	1.84E-17
GO:0070371	ERK1 and ERK2 cascade	50/655	320/18862	2.95E-19	2.37E-17
GO:0002685	regulation of leukocyte migration	40/655	205/18862	3.78E-19	2.99E-17
GO:0019730	antimicrobial humoral response	33/655	142/18862	1.93E-18	1.50E-16
GO:0002548	monocyte chemotaxis	24/655	68/18862	2.24E-18	1.71E-16
GO:0070372	regulation of ERK1 and ERK2 cascade	47/655	301/18862	3.72E-18	2.80E-16
GO:0042379	chemokine receptor binding	23/606	69/18337	1.68E-17	6.49E-16
GO:0050673	epithelial cell proliferation	56/655	428/18862	9.10E-18	6.73E-16
GO:0001935	endothelial cell proliferation	37/655	191/18862	1.07E-17	7.82E-16
GO:0007204	positive regulation of cytosolic calcium ion concentration	47/655	310/18862	1.25E-17	8.95E-16
GO:0055074	calcium ion homeostasis	57/655	454/18862	3.12E-17	2.21E-15
GO:0001936	regulation of endothelial cell proliferation	35/655	177/18862	4.21E-17	2.93E-15
GO:0002688	regulation of leukocyte chemotaxis	29/655	119/18862	5.83E-17	4.00E-15
GO:0051480	regulation of cytosolic calcium ion concentration	48/655	344/18862	1.68E-16	1.13E-14
GO:0050729	positive regulation of inflammatory response	30/655	133/18862	1.69E-16	1.13E-14
GO:0002683	negative regulation of immune system process	52/655	403/18862	2.58E-16	1.69E-14
GO:0001938	positive regulation of endothelial cell proliferation	27/655	108/18862	3.48E-16	2.26E-14
GO:0050679	positive regulation of epithelial cell proliferation	36/655	203/18862	5.68E-16	3.61E-14
GO:0072507	divalent inorganic cation homeostasis	58/655	499/18862	5.73E-16	3.61E-14
GO:0006874	cellular calcium ion homeostasis	54/655	442/18862	7.28E-16	4.53E-14
GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	38/655	230/18862	9.84E-16	6.04E-14
GO:0050678	regulation of epithelial cell proliferation	49/655	374/18862	1.05E-15	6.37E-14
GO:0002687	positive regulation of leukocyte migration	29/655	133/18862	1.42E-15	8.49E-14

GO:0018108	peptidyl-tyrosine phosphorylation	48/655	369/18862	2.77E-15	1.63E-13
GO:0018212	peptidyl-tyrosine modification	48/655	372/18862	3.80E-15	2.22E-13
GO:0019838	growth factor binding	28/606	137/18337	7.24E-15	2.64E-13
GO:0050918	positive chemotaxis	21/655	67/18862	4.78E-15	2.75E-13
GO:0072503	cellular divalent inorganic cation homeostasis	55/655	480/18862	6.27E-15	3.57E-13
GO:0071222	cellular response to lipopolysaccharide	34/655	197/18862	8.62E-15	4.84E-13
GO:0005539	glycosaminoglycan binding	35/606	228/18337	3.02E-14	1.04E-12
GO:0002690	positive regulation of leukocyte chemotaxis	23/655	91/18862	4.27E-14	2.37E-12
GO:0071216	cellular response to biotic stimulus	36/655	233/18862	4.78E-14	2.62E-12
GO:0070661	leukocyte proliferation	42/655	312/18862	4.87E-14	2.64E-12
GO:0071219	cellular response to molecule of bacterial origin	34/655	209/18862	5.23E-14	2.80E-12
GO:0045785	positive regulation of cell adhesion	49/655	425/18862	1.59E-13	8.43E-12
GO:0001818	negative regulation of cytokine production	45/655	367/18862	1.82E-13	9.52E-12
GO:0050922	negative regulation of chemotaxis	19/655	64/18862	2.92E-13	1.52E-11
GO:0034341	response to interferon-gamma	32/655	197/18862	3.05E-13	1.56E-11
GO:0051897	positive regulation of protein kinase B signaling	30/655	175/18862	3.99E-13	2.02E-11
GO:0048846	axon extension involved in axon guidance	15/655	37/18862	5.07E-13	2.51E-11
GO:1902284	neuron projection extension involved in neuron projection guidance	15/655	37/18862	5.07E-13	2.51E-11
GO:0008217	regulation of blood pressure	30/655	177/18862	5.42E-13	2.66E-11
GO:0042116	macrophage activation	23/655	102/18862	5.88E-13	2.86E-11
GO:0007159	leukocyte cell-cell adhesion	44/655	366/18862	6.79E-13	3.26E-11
GO:0001667	ameboidal-type cell migration	51/655	473/18862	6.85E-13	3.26E-11
GO:0051047	positive regulation of secretion	39/655	295/18862	7.16E-13	3.37E-11
GO:0048841	regulation of axon extension involved in axon guidance	14/655	32/18862	8.55E-13	3.99E-11
GO:0090066	regulation of anatomical structure size	52/655	493/18862	9.52E-13	4.40E-11

GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	31/655	193/18862	9.78E-13	4.47E-11
GO:0050919	negative chemotaxis	16/655	46/18862	1.40E-12	6.35E-11
GO:1903037	regulation of leukocyte cell-cell adhesion	41/655	330/18862	1.44E-12	6.42E-11
GO:0048660	regulation of smooth muscle cell proliferation	28/655	160/18862	1.44E-12	6.42E-11
GO:0002831	regulation of response to biotic stimulus	47/655	420/18862	1.50E-12	6.61E-11
GO:0033002	muscle cell proliferation	33/655	222/18862	1.67E-12	7.26E-11
GO:0048659	smooth muscle cell proliferation	28/655	162/18862	1.98E-12	8.55E-11
GO:0034612	response to tumor necrosis factor	40/655	320/18862	2.24E-12	9.58E-11
GO:1902105	regulation of leukocyte differentiation	37/655	279/18862	2.56E-12	1.09E-10
GO:0048247	lymphocyte chemotaxis	18/655	64/18862	3.47E-12	1.46E-10
GO:0071356	cellular response to tumor necrosis factor	38/655	296/18862	3.54E-12	1.47E-10
GO:1903706	regulation of hemopoiesis	46/655	415/18862	3.67E-12	1.51E-10
GO:0070851	growth factor receptor binding	25/606	141/18337	5.81E-12	1.89E-10
GO:1903532	positive regulation of secretion by cell	36/655	271/18862	4.83E-12	1.98E-10
GO:1903039	positive regulation of leukocyte cell-cell adhesion	33/655	234/18862	7.32E-12	2.97E-10
GO:0001659	temperature homeostasis	28/655	171/18862	7.70E-12	3.10E-10
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	35/655	262/18862	8.18E-12	3.26E-10
GO:0048638	regulation of developmental growth	39/655	319/18862	8.49E-12	3.36E-10
GO:0051091	positive regulation of DNA-binding transcription factor activity	35/655	266/18862	1.27E-11	4.96E-10
GO:0045499	chemorepellent activity	12/606	27/18337	1.68E-11	5.22E-10
GO:0048640	negative regulation of developmental growth	22/655	107/18862	1.34E-11	5.22E-10
GO:0050886	endocrine process	19/655	78/18862	1.43E-11	5.50E-10
GO:0070663	regulation of leukocyte proliferation	33/655	241/18862	1.65E-11	6.33E-10
GO:0048843	negative regulation of axon extension involved in axon guidance	12/655	26/18862	1.72E-11	6.53E-10
GO:0051896	regulation of protein kinase B signaling	33/655	247/18862	3.25E-11	1.21E-09

GO:0071526	semaphorin-plexin signaling pathway	14/655	40/18862	3.25E-11	1.21E-09
GO:1903131	mononuclear cell differentiation	44/655	411/18862	3.50E-11	1.29E-09
GO:0022409	positive regulation of cell-cell adhesion	35/655	276/18862	3.63E-11	1.33E-09
GO:0051092	positive regulation of NF-kappaB transcription factor activity	26/655	159/18862	4.46E-11	1.63E-09
GO:0046651	lymphocyte proliferation	35/655	282/18862	6.66E-11	2.41E-09
GO:0060284	regulation of cell development	48/655	485/18862	7.00E-11	2.51E-09
GO:0048771	tissue remodeling	27/655	175/18862	7.50E-11	2.67E-09
GO:0062023	collagen-containing extracellular matrix	44/659	423/19520	3.70E-11	2.69E-09
GO:0022407	regulation of cell-cell adhesion	45/655	437/18862	7.64E-11	2.70E-09
GO:0032147	activation of protein kinase activity	38/655	328/18862	7.92E-11	2.78E-09
GO:0032943	mononuclear cell proliferation	35/655	285/18862	8.95E-11	3.12E-09
GO:0071346	cellular response to interferon-gamma	27/655	177/18862	9.79E-11	3.38E-09
GO:0072676	lymphocyte migration	22/655	118/18862	1.02E-10	3.49E-09
GO:0043406	positive regulation of MAP kinase activity	31/655	230/18862	1.03E-10	3.51E-09
GO:0043491	protein kinase B signaling	34/655	273/18862	1.14E-10	3.85E-09
GO:0048020	CCR chemokine receptor binding	14/606	46/18337	1.44E-10	4.26E-09
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	18/655	78/18862	1.30E-10	4.36E-09
GO:0002699	positive regulation of immune effector process	30/655	219/18862	1.38E-10	4.60E-09
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	25/655	155/18862	1.43E-10	4.73E-09
GO:0043405	regulation of MAP kinase activity	36/655	307/18862	1.79E-10	5.88E-09
GO:0002446	neutrophil mediated immunity	48/655	499/18862	1.86E-10	6.08E-09
GO:0002819	regulation of adaptive immune response	26/655	170/18862	2.06E-10	6.66E-09
GO:0032609	interferon-gamma production	21/655	112/18862	2.43E-10	7.81E-09
GO:1901342	regulation of vasculature development	38/655	341/18862	2.48E-10	7.91E-09
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	14/655	46/18862	2.77E-10	8.80E-09

GO:0050870	positive regulation of T cell activation	29/655	212/18862	2.90E-10	9.15E-09
GO:0009615	response to virus	39/655	359/18862	3.05E-10	9.54E-09
GO:0042110	T cell activation	46/655	474/18862	3.38E-10	1.05E-08
GO:0045088	regulation of innate immune response	36/655	315/18862	3.68E-10	1.14E-08
GO:0032612	interleukin-1 production	22/655	126/18862	3.82E-10	1.17E-08
GO:0045766	positive regulation of angiogenesis	26/655	175/18862	3.94E-10	1.19E-08
GO:1904018	positive regulation of vasculature development	26/655	175/18862	3.94E-10	1.19E-08
GO:0061387	regulation of extent of cell growth	20/655	104/18862	4.05E-10	1.22E-08
GO:0002833	positive regulation of response to biotic stimulus	32/655	258/18862	4.49E-10	1.34E-08
GO:0060389	pathway-restricted SMAD protein phosphorylation	16/655	65/18862	4.96E-10	1.47E-08
GO:0051607	defense response to virus	32/655	260/18862	5.47E-10	1.61E-08
GO:0140546	defense response to symbiont	32/655	260/18862	5.47E-10	1.61E-08
GO:0045765	regulation of angiogenesis	37/655	335/18862	5.51E-10	1.61E-08
GO:0042119	neutrophil activation	47/655	500/18862	6.24E-10	1.81E-08
GO:0032649	regulation of interferon-gamma production	20/655	107/18862	6.89E-10	1.98E-08
GO:0043312	neutrophil degranulation	46/655	485/18862	7.15E-10	2.05E-08
GO:0043434	response to peptide hormone	43/655	435/18862	7.35E-10	2.09E-08
GO:0050670	regulation of lymphocyte proliferation	29/655	221/18862	7.87E-10	2.22E-08
GO:0002283	neutrophil activation involved in immune response	46/655	488/18862	8.74E-10	2.45E-08
GO:0010631	epithelial cell migration	38/655	357/18862	9.26E-10	2.59E-08
GO:0008201	heparin binding	24/606	164/18337	9.49E-10	2.67E-08
GO:0032944	regulation of mononuclear cell proliferation	29/655	223/18862	9.75E-10	2.71E-08
GO:0071902	positive regulation of protein serine/threonine kinase activity	35/655	311/18862	9.82E-10	2.71E-08
GO:0072593	reactive oxygen species metabolic process	33/655	281/18862	9.98E-10	2.74E-08
GO:0050863	regulation of T cell activation	36/655	327/18862	1.03E-09	2.82E-08

GO:0030215	semaphorin receptor binding	10/606	23/18337	1.12E-09	2.89E-08
GO:0038187	pattern recognition receptor activity	10/606	23/18337	1.12E-09	2.89E-08
GO:0090132	epithelium migration	38/655	360/18862	1.17E-09	3.18E-08
GO:0040013	negative regulation of locomotion	39/655	377/18862	1.27E-09	3.42E-08
GO:0051090	regulation of DNA-binding transcription factor activity	43/655	444/18862	1.38E-09	3.70E-08
GO:0008361	regulation of cell size	25/655	173/18862	1.55E-09	4.13E-08
GO:0003073	regulation of systemic arterial blood pressure	18/655	90/18862	1.57E-09	4.16E-08
GO:0001990	regulation of systemic arterial blood pressure by hormone	12/655	36/18862	1.62E-09	4.27E-08
GO:0090130	tissue migration	38/655	365/18862	1.73E-09	4.54E-08
GO:1905952	regulation of lipid localization	26/655	189/18862	2.15E-09	5.54E-08
GO:0003018	vascular process in circulatory system	30/655	245/18862	2.15E-09	5.54E-08
GO:0045926	negative regulation of growth	30/655	245/18862	2.15E-09	5.54E-08
GO:0001503	ossification	40/655	401/18862	2.25E-09	5.73E-08
GO:0032613	interleukin-10 production	15/655	62/18862	2.25E-09	5.73E-08
GO:0070482	response to oxygen levels	39/655	385/18862	2.31E-09	5.85E-08
GO:0007200	phospholipase C-activating G protein-coupled receptor signaling pathway	19/655	103/18862	2.32E-09	5.85E-08
GO:0050770	regulation of axonogenesis	23/655	151/18862	2.47E-09	6.20E-08
GO:0030099	myeloid cell differentiation	41/655	419/18862	2.49E-09	6.21E-08
GO:0002573	myeloid leukocyte differentiation	27/655	204/18862	2.50E-09	6.21E-08
GO:0019932	second-messenger-mediated signaling	34/655	307/18862	2.59E-09	6.40E-08
GO:0007631	feeding behavior	18/655	93/18862	2.74E-09	6.71E-08
GO:0034774	secretory granule lumen	35/659	322/19520	1.21E-09	7.33E-08
GO:0001558	regulation of cell growth	40/655	406/18862	3.21E-09	7.85E-08
GO:0050764	regulation of phagocytosis	18/655	94/18862	3.28E-09	7.96E-08
GO:0071900	regulation of protein serine/threonine kinase activity	45/655	492/18862	3.45E-09	8.33E-08

GO:0023061	signal release	44/655	475/18862	3.51E-09	8.45E-08
GO:1902107	positive regulation of leukocyte differentiation	23/655	154/18862	3.66E-09	8.70E-08
GO:1903708	positive regulation of hemopoiesis	23/655	154/18862	3.66E-09	8.70E-08
GO:0060205	cytoplasmic vesicle lumen	35/659	326/19520	1.68E-09	8.74E-08
GO:0031983	vesicle lumen	35/659	328/19520	1.98E-09	8.99E-08
GO:0048588	developmental cell growth	28/655	222/18862	3.81E-09	9.01E-08
GO:0002221	pattern recognition receptor signaling pathway	27/655	208/18862	3.85E-09	9.06E-08
GO:0045089	positive regulation of innate immune response	28/655	223/18862	4.21E-09	9.87E-08
GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	22/655	143/18862	4.54E-09	1.06E-07
GO:0032652	regulation of interleukin-1 production	20/655	119/18862	4.79E-09	1.11E-07
GO:0019956	chemokine binding	11/606	33/18337	4.69E-09	1.16E-07
GO:0060560	developmental growth involved in morphogenesis	28/655	225/18862	5.15E-09	1.19E-07
GO:0002224	toll-like receptor signaling pathway	23/655	157/18862	5.35E-09	1.23E-07
GO:0098801	regulation of renal system process	11/655	32/18862	5.41E-09	1.24E-07
GO:0042277	peptide binding	33/606	315/18337	5.25E-09	1.25E-07
GO:0050767	regulation of neurogenesis	36/655	348/18862	5.54E-09	1.26E-07
GO:0002700	regulation of production of molecular mediator of immune response	22/655	146/18862	6.75E-09	1.53E-07
GO:0016049	cell growth	43/655	470/18862	7.70E-09	1.73E-07
GO:0032680	regulation of tumor necrosis factor production	23/655	160/18862	7.76E-09	1.74E-07
GO:0070665	positive regulation of leukocyte proliferation	22/655	148/18862	8.74E-09	1.95E-07
GO:0010634	positive regulation of epithelial cell migration	24/655	175/18862	9.49E-09	2.09E-07
GO:0045619	regulation of lymphocyte differentiation	24/655	175/18862	9.49E-09	2.09E-07
GO:0097696	receptor signaling pathway via STAT	24/655	175/18862	9.49E-09	2.09E-07
GO:0060759	regulation of response to cytokine stimulus	25/655	189/18862	9.87E-09	2.15E-07
GO:0032640	tumor necrosis factor production	23/655	162/18862	9.88E-09	2.15E-07

GO:0010632	regulation of epithelial cell migration	32/655	293/18862	1.07E-08	2.33E-07
GO:0097305	response to alcohol	28/655	233/18862	1.12E-08	2.41E-07
GO:0044060	regulation of endocrine process	11/655	34/18862	1.13E-08	2.41E-07
GO:0050777	negative regulation of immune response	22/655	150/18862	1.13E-08	2.41E-07
GO:0030098	lymphocyte differentiation	36/655	358/18862	1.17E-08	2.49E-07
GO:0002825	regulation of T-helper 1 type immune response	10/655	27/18862	1.18E-08	2.50E-07
GO:0001959	regulation of cytokine-mediated signaling pathway	24/655	177/18862	1.19E-08	2.51E-07
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	23/655	164/18862	1.25E-08	2.63E-07
GO:0036293	response to decreased oxygen levels	36/655	360/18862	1.35E-08	2.83E-07
GO:0030517	negative regulation of axon extension	12/655	43/18862	1.59E-08	3.31E-07
GO:1990845	adaptive thermogenesis	22/655	153/18862	1.63E-08	3.38E-07
GO:0032306	regulation of prostaglandin secretion	7/655	11/18862	1.72E-08	3.54E-07
GO:0032308	positive regulation of prostaglandin secretion	7/655	11/18862	1.72E-08	3.54E-07
GO:0071706	tumor necrosis factor superfamily cytokine production	23/655	167/18862	1.78E-08	3.64E-07
GO:0001666	response to hypoxia	35/655	348/18862	1.86E-08	3.79E-07
GO:0060393	regulation of pathway-restricted SMAD protein phosphorylation	14/655	62/18862	2.01E-08	4.08E-07
GO:0042056	chemoattractant activity	11/606	37/18337	1.84E-08	4.22E-07
GO:0048754	branching morphogenesis of an epithelial tube	21/655	143/18862	2.37E-08	4.78E-07
GO:0030308	negative regulation of cell growth	24/655	185/18862	2.86E-08	5.74E-07
GO:0032675	regulation of interleukin-6 production	22/655	158/18862	2.97E-08	5.94E-07
GO:0042100	B cell proliferation	17/655	96/18862	3.05E-08	6.06E-07
GO:0048661	positive regulation of smooth muscle cell proliferation	17/655	96/18862	3.05E-08	6.06E-07
GO:0001763	morphogenesis of a branching structure	24/655	186/18862	3.17E-08	6.27E-07
GO:0032611	interleukin-1 beta production	18/655	108/18862	3.22E-08	6.33E-07
GO:0061138	morphogenesis of a branching epithelium	23/655	173/18862	3.49E-08	6.84E-07

GO:0001755	neural crest cell migration	13/655	55/18862	3.59E-08	7.01E-07
GO:0032755	positive regulation of interleukin-6 production	16/655	86/18862	3.76E-08	7.27E-07
GO:0034103	regulation of tissue remodeling	16/655	86/18862	3.76E-08	7.27E-07
GO:0034694	response to prostaglandin	10/655	30/18862	3.82E-08	7.35E-07
GO:0043542	endothelial cell migration	30/655	278/18862	4.07E-08	7.81E-07
GO:0002285	lymphocyte activation involved in immune response	24/655	189/18862	4.33E-08	8.28E-07
GO:0050671	positive regulation of lymphocyte proliferation	20/655	135/18862	4.38E-08	8.34E-07
GO:0032635	interleukin-6 production	22/655	162/18862	4.69E-08	8.89E-07
GO:0050771	negative regulation of axonogenesis	14/655	66/18862	4.71E-08	8.89E-07
GO:0001774	microglial cell activation	12/655	47/18862	4.77E-08	8.97E-07
GO:0002702	positive regulation of production of molecular mediator of immune response	17/655	99/18862	4.91E-08	9.19E-07
GO:0032946	positive regulation of mononuclear cell proliferation	20/655	136/18862	4.97E-08	9.27E-07
GO:0071675	regulation of mononuclear cell migration	18/655	111/18862	4.99E-08	9.27E-07
GO:0045236	CXCR chemokine receptor binding	8/606	18/18337	4.44E-08	9.83E-07
GO:0019199	transmembrane receptor protein kinase activity	15/606	80/18337	4.69E-08	1.00E-06
GO:0046887	positive regulation of hormone secretion	19/655	124/18862	5.47E-08	1.01E-06
GO:0032660	regulation of interleukin-17 production	11/655	39/18862	5.63E-08	1.04E-06
GO:0050766	positive regulation of phagocytosis	14/655	67/18862	5.76E-08	1.06E-06
GO:0010862	positive regulation of pathway-restricted SMAD protein phosphorylation	12/655	48/18862	6.16E-08	1.13E-06
GO:0001906	cell killing	23/655	179/18862	6.64E-08	1.21E-06
GO:2000379	positive regulation of reactive oxygen species metabolic process	17/655	101/18862	6.66E-08	1.21E-06
GO:0002703	regulation of leukocyte mediated immunity	25/655	209/18862	7.50E-08	1.36E-06
GO:0035296	regulation of tube diameter	19/655	127/18862	8.10E-08	1.45E-06
GO:0097746	blood vessel diameter maintenance	19/655	127/18862	8.10E-08	1.45E-06
GO:0070820	tertiary granule	22/659	164/19520	3.60E-08	1.46E-06

GO:0060485	mesenchyme development	30/655	287/18862	8.31E-08	1.48E-06
GO:0007171	activation of transmembrane receptor protein tyrosine kinase activity	7/655	13/18862	8.44E-08	1.50E-06
GO:0001823	mesonephros development	16/655	91/18862	8.62E-08	1.52E-06
GO:0050927	positive regulation of positive chemotaxis	9/655	25/18862	8.63E-08	1.52E-06
GO:0032535	regulation of cellular component size	35/655	370/18862	8.64E-08	1.52E-06
GO:0051960	regulation of nervous system development	38/655	422/18862	8.81E-08	1.54E-06
GO:0014032	neural crest cell development	15/655	80/18862	8.98E-08	1.57E-06
GO:0002695	negative regulation of leukocyte activation	23/655	182/18862	9.05E-08	1.57E-06
GO:0035150	regulation of tube size	19/655	128/18862	9.21E-08	1.60E-06
GO:0042088	T-helper 1 type immune response	11/655	41/18862	9.95E-08	1.72E-06
GO:0032874	positive regulation of stress-activated MAPK cascade	18/655	116/18862	1.00E-07	1.73E-06
GO:0030516	regulation of axon extension	16/655	92/18862	1.01E-07	1.73E-06
GO:0045637	regulation of myeloid cell differentiation	28/655	258/18862	1.02E-07	1.74E-06
GO:0010720	positive regulation of cell development	30/655	290/18862	1.05E-07	1.78E-06
GO:0140353	lipid export from cell	15/655	81/18862	1.07E-07	1.81E-06
GO:0032615	interleukin-12 production	13/655	60/18862	1.09E-07	1.82E-06
GO:0032653	regulation of interleukin-10 production	13/655	60/18862	1.09E-07	1.82E-06
GO:0032655	regulation of interleukin-12 production	13/655	60/18862	1.09E-07	1.82E-06
GO:0032303	regulation of icosanoid secretion	8/655	19/18862	1.09E-07	1.82E-06
GO:0032368	regulation of lipid transport	21/655	156/18862	1.10E-07	1.84E-06
GO:0033218	amide binding	35/606	391/18337	9.96E-08	2.06E-06
GO:0030198	extracellular matrix organization	36/655	393/18862	1.26E-07	2.10E-06
GO:0050926	regulation of positive chemotaxis	9/655	26/18862	1.28E-07	2.11E-06
GO:0050866	negative regulation of cell activation	24/655	200/18862	1.28E-07	2.12E-06
GO:0003014	renal system process	18/655	118/18862	1.31E-07	2.13E-06

GO:0070304	positive regulation of stress-activated protein kinase signaling cascade	18/655	118/18862	1.31E-07	2.13E-06
GO:0106106	cold-induced thermogenesis	20/655	144/18862	1.31E-07	2.13E-06
GO:0120161	regulation of cold-induced thermogenesis	20/655	144/18862	1.31E-07	2.13E-06
GO:0019731	antibacterial humoral response	13/655	61/18862	1.34E-07	2.17E-06
GO:0043062	extracellular structure organization	36/655	394/18862	1.35E-07	2.17E-06
GO:0048864	stem cell development	15/655	83/18862	1.50E-07	2.40E-06
GO:0045229	external encapsulating structure organization	36/655	396/18862	1.53E-07	2.45E-06
GO:0002526	acute inflammatory response	17/655	107/18862	1.59E-07	2.54E-06
GO:0033138	positive regulation of peptidyl-serine phosphorylation	17/655	107/18862	1.59E-07	2.54E-06
GO:0032602	chemokine production	16/655	95/18862	1.60E-07	2.55E-06
GO:0032310	prostaglandin secretion	7/655	14/18862	1.64E-07	2.57E-06
GO:0050930	induction of positive chemotaxis	7/655	14/18862	1.64E-07	2.57E-06
GO:0002437	inflammatory response to antigenic stimulus	13/655	62/18862	1.64E-07	2.57E-06
GO:0042698	ovulation cycle	13/655	62/18862	1.64E-07	2.57E-06
GO:0032620	interleukin-17 production	11/655	43/18862	1.70E-07	2.65E-06
GO:0002718	regulation of cytokine production involved in immune response	15/655	84/18862	1.76E-07	2.73E-06
GO:0014031	mesenchymal cell development	15/655	84/18862	1.76E-07	2.73E-06
GO:0042554	superoxide anion generation	10/655	35/18862	1.99E-07	3.08E-06
GO:1901681	sulfur compound binding	27/606	260/18337	1.57E-07	3.13E-06
GO:0050829	defense response to Gram-negative bacterium	15/655	85/18862	2.07E-07	3.19E-06
GO:0031348	negative regulation of defense response	26/655	236/18862	2.17E-07	3.32E-06
GO:0070555	response to interleukin-1	24/655	206/18862	2.24E-07	3.43E-06
GO:0050830	defense response to Gram-positive bacterium	16/655	98/18862	2.50E-07	3.81E-06
GO:0046879	hormone secretion	30/655	302/18862	2.54E-07	3.86E-06
GO:0002286	T cell activation involved in immune response	17/655	111/18862	2.75E-07	4.15E-06

GO:0031623	receptor internalization	17/655	111/18862	2.75E-07	4.15E-06
GO:0032760	positive regulation of tumor necrosis factor production	15/655	87/18862	2.84E-07	4.28E-06
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	16/655	99/18862	2.89E-07	4.33E-06
GO:0007259	receptor signaling pathway via JAK-STAT	21/655	166/18862	3.21E-07	4.80E-06
GO:1901653	cellular response to peptide	35/655	391/18862	3.29E-07	4.91E-06
GO:0007260	tyrosine phosphorylation of STAT protein	15/655	88/18862	3.32E-07	4.93E-06
GO:0002686	negative regulation of leukocyte migration	11/655	46/18862	3.59E-07	5.31E-06
GO:0043032	positive regulation of macrophage activation	9/655	29/18862	3.73E-07	5.51E-06
GO:0045621	positive regulation of lymphocyte differentiation	16/655	101/18862	3.83E-07	5.64E-06
GO:0032642	regulation of chemokine production	15/655	89/18862	3.87E-07	5.66E-06
GO:0046849	bone remodeling	15/655	89/18862	3.87E-07	5.66E-06
GO:0000187	activation of MAPK activity	20/655	154/18862	3.99E-07	5.81E-06
GO:0048675	axon extension	17/655	114/18862	4.07E-07	5.92E-06
GO:0001894	tissue homeostasis	27/655	260/18862	4.20E-07	6.08E-06
GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	8/655	22/18862	4.21E-07	6.08E-06
GO:0031640	killing of cells of other organism	13/655	67/18862	4.28E-07	6.16E-06
GO:0045639	positive regulation of myeloid cell differentiation	16/655	102/18862	4.40E-07	6.32E-06
GO:0014033	neural crest cell differentiation	15/655	90/18862	4.50E-07	6.41E-06
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	15/655	90/18862	4.50E-07	6.41E-06
GO:0005184	neuropeptide hormone activity	9/606	30/18337	3.41E-07	6.60E-06
GO:0032651	regulation of interleukin-1 beta production	16/655	103/18862	5.05E-07	7.18E-06
GO:0009914	hormone transport	30/655	312/18862	5.12E-07	7.23E-06
GO:0007599	hemostasis	32/655	346/18862	5.13E-07	7.23E-06
GO:0031649	heat generation	7/655	16/18862	5.13E-07	7.23E-06

GO:0048762	mesenchymal cell differentiation	25/655	231/18862	5.18E-07	7.28E-06
GO:0002821	positive regulation of adaptive immune response	16/655	104/18862	5.78E-07	8.09E-06
GO:0050769	positive regulation of neurogenesis	24/655	217/18862	5.88E-07	8.21E-06
GO:0061041	regulation of wound healing	18/655	131/18862	6.51E-07	9.06E-06
GO:0002367	cytokine production involved in immune response	15/655	93/18862	6.96E-07	9.66E-06
GO:0043030	regulation of macrophage activation	12/655	59/18862	6.98E-07	9.66E-06
GO:0010721	negative regulation of cell development	21/655	174/18862	7.09E-07	9.75E-06
GO:0033209	tumor necrosis factor-mediated signaling pathway	21/655	174/18862	7.09E-07	9.75E-06
GO:0071622	regulation of granulocyte chemotaxis	11/655	49/18862	7.13E-07	9.78E-06
GO:1903793	positive regulation of anion transport	39/655	478/18862	7.60E-07	1.04E-05
GO:0032735	positive regulation of interleukin-12 production	10/655	40/18862	7.86E-07	1.07E-05
GO:1902895	positive regulation of pri-miRNA transcription by RNA polymerase II	10/655	40/18862	7.86E-07	1.07E-05
GO:0042562	hormone binding	14/606	84/18337	6.00E-07	1.13E-05
GO:0019957	C-C chemokine binding	8/606	24/18337	6.26E-07	1.14E-05
GO:0061098	positive regulation of protein tyrosine kinase activity	12/655	60/18862	8.45E-07	1.14E-05
GO:0015732	prostaglandin transport	7/655	17/18862	8.47E-07	1.14E-05
GO:0032305	positive regulation of icosanoid secretion	7/655	17/18862	8.47E-07	1.14E-05
GO:0060337	type I interferon signaling pathway	15/655	95/18862	9.23E-07	1.24E-05
GO:2000377	regulation of reactive oxygen species metabolic process	22/655	192/18862	9.48E-07	1.27E-05
GO:0010743	regulation of macrophage derived foam cell differentiation	9/655	32/18862	9.52E-07	1.27E-05
GO:0090022	regulation of neutrophil chemotaxis	9/655	32/18862	9.52E-07	1.27E-05
GO:1901654	response to ketone	22/655	193/18862	1.04E-06	1.38E-05
GO:0071357	cellular response to type I interferon	15/655	96/18862	1.06E-06	1.40E-05
GO:0046330	positive regulation of JNK cascade	14/655	84/18862	1.08E-06	1.43E-05
GO:0046850	regulation of bone remodeling	11/655	51/18862	1.09E-06	1.44E-05

GO:1902893	regulation of pri-miRNA transcription by RNA polymerase II	11/655	51/18862	1.09E-06	1.44E-05
GO:1903034	regulation of response to wounding	20/655	164/18862	1.10E-06	1.44E-05
GO:0031100	animal organ regeneration	13/655	73/18862	1.20E-06	1.57E-05
GO:0045807	positive regulation of endocytosis	15/655	97/18862	1.21E-06	1.58E-05
GO:0120162	positive regulation of cold-induced thermogenesis	15/655	97/18862	1.21E-06	1.58E-05
GO:1901215	negative regulation of neuron death	22/655	195/18862	1.23E-06	1.60E-05
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	14/655	85/18862	1.26E-06	1.62E-05
GO:1905332	positive regulation of morphogenesis of an epithelium	9/655	33/18862	1.27E-06	1.64E-05
GO:0001867	complement activation, lectin pathway	6/655	12/18862	1.32E-06	1.70E-05
GO:0032656	regulation of interleukin-13 production	7/655	18/18862	1.34E-06	1.72E-05
GO:0061614	pri-miRNA transcription by RNA polymerase II	11/655	52/18862	1.34E-06	1.72E-05
GO:0042581	specific granule	20/659	160/19520	4.80E-07	1.75E-05
GO:0046883	regulation of hormone secretion	26/655	260/18862	1.41E-06	1.79E-05
GO:0001657	ureteric bud development	14/655	86/18862	1.45E-06	1.85E-05
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	21/655	182/18862	1.49E-06	1.89E-05
GO:0042102	positive regulation of T cell proliferation	15/655	99/18862	1.58E-06	2.00E-05
GO:0019722	calcium-mediated signaling	22/655	198/18862	1.60E-06	2.01E-05
GO:0042129	regulation of T cell proliferation	20/655	168/18862	1.61E-06	2.03E-05
GO:0002720	positive regulation of cytokine production involved in immune response	11/655	53/18862	1.64E-06	2.06E-05
GO:0030217	T cell differentiation	25/655	246/18862	1.67E-06	2.09E-05
GO:0072163	mesonephric epithelium development	14/655	87/18862	1.68E-06	2.09E-05
GO:0072164	mesonephric tubule development	14/655	87/18862	1.68E-06	2.09E-05
GO:0001637	G protein-coupled chemoattractant receptor activity	8/606	26/18337	1.25E-06	2.16E-05
GO:0004950	chemokine receptor activity	8/606	26/18337	1.25E-06	2.16E-05
GO:0032732	positive regulation of interleukin-1 production	12/655	64/18862	1.75E-06	2.17E-05

GO:0035710	CD4-positive, alpha-beta T cell activation	15/655	100/18862	1.80E-06	2.23E-05
GO:0010594	regulation of endothelial cell migration	24/655	231/18862	1.82E-06	2.24E-05
GO:0006968	cellular defense response	11/655	54/18862	2.00E-06	2.46E-05
GO:0034340	response to type I interferon	15/655	101/18862	2.05E-06	2.52E-05
GO:0035813	regulation of renal sodium excretion	7/655	19/18862	2.06E-06	2.53E-05
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	9/655	35/18862	2.18E-06	2.67E-05
GO:0002706	regulation of lymphocyte mediated immunity	19/655	157/18862	2.29E-06	2.78E-05
GO:0071887	leukocyte apoptotic process	15/655	102/18862	2.33E-06	2.83E-05
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	25/655	251/18862	2.41E-06	2.92E-05
GO:0051235	maintenance of location	29/655	319/18862	2.47E-06	2.98E-05
GO:0005024	transforming growth factor beta-activated receptor activity	6/606	13/18337	1.79E-06	3.00E-05
GO:0071624	positive regulation of granulocyte chemotaxis	8/655	27/18862	2.51E-06	3.01E-05
GO:0090025	regulation of monocyte chemotaxis	8/655	27/18862	2.51E-06	3.01E-05
GO:1901214	regulation of neuron death	28/655	302/18862	2.51E-06	3.01E-05
GO:0060986	endocrine hormone secretion	10/655	45/18862	2.53E-06	3.03E-05
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	14/655	90/18862	2.55E-06	3.04E-05
GO:0002709	regulation of T cell mediated immunity	13/655	78/18862	2.62E-06	3.11E-05
GO:0050772	positive regulation of axonogenesis	13/655	78/18862	2.62E-06	3.11E-05
GO:0032892	positive regulation of organic acid transport	9/655	36/18862	2.82E-06	3.34E-05
GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	12/655	67/18862	2.90E-06	3.42E-05
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	12/655	67/18862	2.90E-06	3.42E-05
GO:0060760	positive regulation of response to cytokine stimulus	11/655	56/18862	2.92E-06	3.43E-05
GO:0002456	T cell mediated immunity	15/655	104/18862	2.99E-06	3.50E-05
GO:0050728	negative regulation of inflammatory response	19/655	160/18862	3.04E-06	3.54E-05
GO:0051048	negative regulation of secretion	19/655	160/18862	3.04E-06	3.54E-05

GO:0032616	interleukin-13 production	7/655	20/18862	3.08E-06	3.56E-05
GO:0051767	nitric-oxide synthase biosynthetic process	7/655	20/18862	3.08E-06	3.56E-05
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	7/655	20/18862	3.08E-06	3.56E-05
GO:0006953	acute-phase response	10/655	46/18862	3.13E-06	3.62E-05
GO:0045580	regulation of T cell differentiation	18/655	146/18862	3.22E-06	3.70E-05
GO:0002761	regulation of myeloid leukocyte differentiation	16/655	118/18862	3.23E-06	3.70E-05
GO:0051928	positive regulation of calcium ion transport	16/655	118/18862	3.23E-06	3.70E-05
GO:0010595	positive regulation of endothelial cell migration	17/655	132/18862	3.30E-06	3.77E-05
GO:0055017	cardiac muscle tissue growth	14/655	92/18862	3.33E-06	3.80E-05
GO:0001649	osteoblast differentiation	23/655	223/18862	3.36E-06	3.82E-05
GO:0070997	neuron death	30/655	342/18862	3.44E-06	3.90E-05
GO:0071855	neuropeptide receptor binding	9/606	37/18337	2.41E-06	3.93E-05
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	12/655	69/18862	4.00E-06	4.53E-05
GO:0061097	regulation of protein tyrosine kinase activity	14/655	94/18862	4.33E-06	4.89E-05
GO:1990138	neuron projection extension	19/655	164/18862	4.39E-06	4.95E-05
GO:0051051	negative regulation of transport	35/655	438/18862	4.47E-06	5.03E-05
GO:0035812	renal sodium excretion	7/655	21/18862	4.48E-06	5.03E-05
GO:0042098	T cell proliferation	21/655	195/18862	4.52E-06	5.04E-05
GO:0048511	rhythmic process	27/655	294/18862	4.52E-06	5.04E-05
GO:0010742	macrophage derived foam cell differentiation	9/655	38/18862	4.59E-06	5.06E-05
GO:0032733	positive regulation of interleukin-10 production	9/655	38/18862	4.59E-06	5.06E-05
GO:0048246	macrophage chemotaxis	9/655	38/18862	4.59E-06	5.06E-05
GO:0048286	lung alveolus development	9/655	38/18862	4.59E-06	5.06E-05
GO:0090077	foam cell differentiation	9/655	38/18862	4.59E-06	5.06E-05
GO:0045123	cellular extravasation	12/655	70/18862	4.68E-06	5.15E-05

GO:0071347	cellular response to interleukin-1	20/655	180/18862	4.72E-06	5.17E-05
GO:0002673	regulation of acute inflammatory response	10/655	48/18862	4.72E-06	5.17E-05
GO:0045834	positive regulation of lipid metabolic process	18/655	150/18862	4.74E-06	5.17E-05
GO:0019216	regulation of lipid metabolic process	33/655	402/18862	4.74E-06	5.17E-05
GO:0032872	regulation of stress-activated MAPK cascade	20/655	181/18862	5.14E-06	5.58E-05
GO:0051962	positive regulation of nervous system development	25/655	263/18862	5.55E-06	6.02E-05
GO:0001961	positive regulation of cytokine-mediated signaling pathway	10/655	49/18862	5.75E-06	6.22E-05
GO:1990782	protein tyrosine kinase binding	14/606	98/18337	4.04E-06	6.42E-05
GO:0051961	negative regulation of nervous system development	17/655	138/18862	6.07E-06	6.53E-05
GO:0090288	negative regulation of cellular response to growth factor stimulus	15/655	110/18862	6.08E-06	6.53E-05
GO:1904892	regulation of receptor signaling pathway via STAT	15/655	110/18862	6.08E-06	6.53E-05
GO:0051250	negative regulation of lymphocyte activation	18/655	153/18862	6.28E-06	6.74E-05
GO:0007249	I-kappaB kinase/NF-kappaB signaling	26/655	282/18862	6.30E-06	6.74E-05
GO:0032700	negative regulation of interleukin-17 production	7/655	22/18862	6.38E-06	6.79E-05
GO:0044062	regulation of excretion	7/655	22/18862	6.38E-06	6.79E-05
GO:0044406	adhesion of symbiont to host	6/655	15/18862	6.56E-06	6.95E-05
GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	6/655	15/18862	6.56E-06	6.95E-05
GO:0017046	peptide hormone binding	10/606	50/18337	4.49E-06	6.97E-05
GO:0070302	regulation of stress-activated protein kinase signaling cascade	20/655	184/18862	6.60E-06	6.97E-05
GO:1905954	positive regulation of lipid localization	15/655	111/18862	6.80E-06	7.18E-05
GO:0002705	positive regulation of leukocyte mediated immunity	16/655	125/18862	6.91E-06	7.27E-05
GO:0019229	regulation of vasoconstriction	11/655	61/18862	7.01E-06	7.33E-05
GO:0030888	regulation of B cell proliferation	11/655	61/18862	7.01E-06	7.33E-05
GO:1905330	regulation of morphogenesis of an epithelium	11/655	61/18862	7.01E-06	7.33E-05
GO:0048639	positive regulation of developmental growth	19/655	170/18862	7.45E-06	7.77E-05

GO:0001655	urogenital system development	28/655	320/18862	7.60E-06	7.91E-05
GO:0005164	tumor necrosis factor receptor binding	8/606	31/18337	5.47E-06	8.27E-05
GO:0038024	cargo receptor activity	12/606	75/18337	5.94E-06	8.76E-05
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	30/655	358/18862	8.54E-06	8.88E-05
GO:0016493	C-C chemokine receptor activity	7/606	23/18337	6.43E-06	8.99E-05
GO:0004879	nuclear receptor activity	10/606	52/18337	6.52E-06	8.99E-05
GO:0098531	ligand-activated transcription factor activity	10/606	52/18337	6.52E-06	8.99E-05
GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	7/655	23/18862	8.89E-06	9.18E-05
GO:0034695	response to prostaglandin E	7/655	23/18862	8.89E-06	9.18E-05
GO:0072677	eosinophil migration	7/655	23/18862	8.89E-06	9.18E-05
GO:0032689	negative regulation of interferon-gamma production	9/655	41/18862	8.99E-06	9.26E-05
GO:0060419	heart growth	14/655	100/18862	9.06E-06	9.30E-05
GO:0072001	renal system development	26/655	288/18862	9.20E-06	9.43E-05
GO:0007596	blood coagulation	29/655	342/18862	9.61E-06	9.83E-05
GO:0045670	regulation of osteoclast differentiation	11/655	63/18862	9.69E-06	9.87E-05
GO:0071677	positive regulation of mononuclear cell migration	11/655	63/18862	9.69E-06	9.87E-05
GO:0033135	regulation of peptidyl-serine phosphorylation	17/655	143/18862	9.83E-06	9.99E-05
GO:0071375	cellular response to peptide hormone stimulus	28/655	325/18862	1.02E-05	0.000103032
GO:0046634	regulation of alpha-beta T cell activation	14/655	101/18862	1.02E-05	0.000103032
GO:0052547	regulation of peptidase activity	35/655	455/18862	1.03E-05	0.00010357
GO:0045582	positive regulation of T cell differentiation	13/655	88/18862	1.04E-05	0.000104563
GO:1902622	regulation of neutrophil migration	9/655	42/18862	1.11E-05	0.000111532
GO:0060395	SMAD protein signal transduction	12/655	76/18862	1.13E-05	0.000113158
GO:0050786	RAGE receptor binding	5/606	10/18337	8.51E-06	0.00011475
GO:0050431	transforming growth factor beta binding	7/606	24/18337	8.81E-06	0.00011627

GO:0048525	negative regulation of viral process	13/655	89/18862	1.18E-05	0.000117602
GO:0097306	cellular response to alcohol	13/655	89/18862	1.18E-05	0.000117602
GO:0018105	peptidyl-serine phosphorylation	27/655	310/18862	1.20E-05	0.0001194
GO:0009620	response to fungus	10/655	53/18862	1.20E-05	0.000119448
GO:1905517	macrophage migration	10/655	53/18862	1.20E-05	0.000119448
GO:0003094	glomerular filtration	7/655	24/18862	1.22E-05	0.000120118
GO:0032753	positive regulation of interleukin-4 production	7/655	24/18862	1.22E-05	0.000120118
GO:0090023	positive regulation of neutrophil chemotaxis	7/655	24/18862	1.22E-05	0.000120118
GO:0050817	coagulation	29/655	347/18862	1.27E-05	0.000124647
GO:0032729	positive regulation of interferon-gamma production	11/655	65/18862	1.32E-05	0.000129864
GO:0030336	negative regulation of cell migration	28/655	330/18862	1.35E-05	0.00013219
GO:0022602	ovulation cycle process	9/655	43/18862	1.36E-05	0.000133021
GO:0007411	axon guidance	25/655	277/18862	1.37E-05	0.000133451
GO:0010977	negative regulation of neuron projection development	16/655	132/18862	1.39E-05	0.000135738
GO:0007162	negative regulation of cell adhesion	26/655	295/18862	1.41E-05	0.000136681
GO:0097485	neuron projection guidance	25/655	278/18862	1.45E-05	0.00014106
GO:0090287	regulation of cellular response to growth factor stimulus	26/655	296/18862	1.49E-05	0.000144442
GO:0045342	MHC class II biosynthetic process	6/655	17/18862	1.53E-05	0.000147592
GO:0050768	negative regulation of neurogenesis	16/655	133/18862	1.53E-05	0.000147885
GO:0030193	regulation of blood coagulation	11/655	66/18862	1.54E-05	0.000147898
GO:0002218	activation of innate immune response	17/655	148/18862	1.55E-05	0.000149153
GO:0018209	peptidyl-serine modification	28/655	333/18862	1.59E-05	0.000152617
GO:0045121	membrane raft	28/659	323/19520	5.40E-06	0.000155038
GO:0098857	membrane microdomain	28/659	323/19520	5.40E-06	0.000155038
GO:0070821	tertiary granule membrane	12/659	73/19520	5.54E-06	0.000155038

GO:0002092	positive regulation of receptor internalization	7/655	25/18862	1.64E-05	0.000156173
GO:0003148	outflow tract septum morphogenesis	7/655	25/18862	1.64E-05	0.000156173
GO:0097205	renal filtration	7/655	25/18862	1.64E-05	0.000156173
GO:0001822	kidney development	25/655	280/18862	1.64E-05	0.000156173
GO:0002691	regulation of cellular extravasation	8/655	34/18862	1.65E-05	0.000156628
GO:0051271	negative regulation of cellular component movement	29/655	352/18862	1.66E-05	0.000156897
GO:0042310	vasoconstriction	12/655	79/18862	1.69E-05	0.000159427
GO:0048145	regulation of fibroblast proliferation	12/655	79/18862	1.69E-05	0.000159427
GO:0031345	negative regulation of cell projection organization	19/655	180/18862	1.70E-05	0.000159427
GO:0046631	alpha-beta T cell activation	17/655	149/18862	1.70E-05	0.000159427
GO:1900046	regulation of hemostasis	11/655	67/18862	1.78E-05	0.000166995
GO:0032736	positive regulation of interleukin-13 production	5/655	11/18862	1.93E-05	0.000179733
GO:0048144	fibroblast proliferation	12/655	80/18862	1.93E-05	0.000179733
GO:2000106	regulation of leukocyte apoptotic process	12/655	80/18862	1.93E-05	0.000179733
GO:0090100	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	14/655	107/18862	1.99E-05	0.000185206
GO:0032731	positive regulation of interleukin-1 beta production	10/655	56/18862	2.00E-05	0.000185206
GO:0051353	positive regulation of oxidoreductase activity	10/655	56/18862	2.00E-05	0.000185206
GO:0030414	peptidase inhibitor activity	19/606	187/18337	1.46E-05	0.000189005
GO:0016175	superoxide-generating NAD(P)H oxidase activity	5/606	11/18337	1.52E-05	0.000192119
GO:0031667	response to nutrient levels	34/655	451/18862	2.08E-05	0.000192246
GO:0071772	response to BMP	18/655	167/18862	2.12E-05	0.000194863
GO:0071773	cellular response to BMP stimulus	18/655	167/18862	2.12E-05	0.000194863
GO:0022617	extracellular matrix disassembly	12/655	81/18862	2.20E-05	0.000201609
GO:0002708	positive regulation of lymphocyte mediated immunity	14/655	108/18862	2.22E-05	0.000203347
GO:0003012	muscle system process	34/655	453/18862	2.28E-05	0.000208471

GO:0043112	receptor metabolic process	18/655	168/18862	2.30E-05	0.000209675
GO:0002040	sprouting angiogenesis	19/655	184/18862	2.32E-05	0.00021094
GO:0097191	extrinsic apoptotic signaling pathway	21/655	217/18862	2.35E-05	0.00021347
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	10/655	57/18862	2.35E-05	0.00021347
GO:0005796	Golgi lumen	14/659	102/19520	8.34E-06	0.000216922
GO:0048146	positive regulation of fibroblast proliferation	9/655	46/18862	2.42E-05	0.000218911
GO:2000107	negative regulation of leukocyte apoptotic process	9/655	46/18862	2.42E-05	0.000218911
GO:0045730	respiratory burst	8/655	36/18862	2.59E-05	0.000233645
GO:0030509	BMP signaling pathway	17/655	154/18862	2.62E-05	0.000235703
GO:0048306	calcium-dependent protein binding	12/606	84/18337	1.96E-05	0.000238739
GO:0005044	scavenger receptor activity	9/606	47/18337	1.96E-05	0.000238739
GO:0006801	superoxide metabolic process	11/655	70/18862	2.73E-05	0.000245062
GO:0055021	regulation of cardiac muscle tissue growth	11/655	70/18862	2.73E-05	0.000245062
GO:0031663	lipopolysaccharide-mediated signaling pathway	10/655	58/18862	2.76E-05	0.000246526
GO:0015850	organic hydroxy compound transport	24/655	271/18862	2.76E-05	0.000246526
GO:0009991	response to extracellular stimulus	35/655	477/18862	2.78E-05	0.000247959
GO:1904705	regulation of vascular associated smooth muscle cell proliferation	12/655	83/18862	2.82E-05	0.000250788
GO:1990874	vascular associated smooth muscle cell proliferation	12/655	83/18862	2.82E-05	0.000250788
GO:0033688	regulation of osteoblast proliferation	7/655	27/18862	2.85E-05	0.000252603
GO:0045672	positive regulation of osteoclast differentiation	7/655	27/18862	2.85E-05	0.000252603
GO:0002698	negative regulation of immune effector process	15/655	125/18862	2.90E-05	0.000256051
GO:0097028	dendritic cell differentiation	9/655	47/18862	2.90E-05	0.000256051
GO:2000146	negative regulation of cell motility	28/655	345/18862	3.03E-05	0.000266481
GO:0005501	retinoid binding	8/606	37/18337	2.25E-05	0.000267844
GO:0051924	regulation of calcium ion transport	22/655	238/18862	3.08E-05	0.000270705

GO:0031091	platelet alpha granule	13/659	91/19520	1.12E-05	0.000271908
GO:0004675	transmembrane receptor protein serine/threonine kinase activity	6/606	19/18337	2.39E-05	0.000274038
GO:0030296	protein tyrosine kinase activator activity	6/606	19/18337	2.39E-05	0.000274038
GO:0050818	regulation of coagulation	11/655	71/18862	3.13E-05	0.000274683
GO:0060562	epithelial tube morphogenesis	26/655	309/18862	3.14E-05	0.000274724
GO:0032634	interleukin-5 production	6/655	19/18862	3.16E-05	0.000274738
GO:0032674	regulation of interleukin-5 production	6/655	19/18862	3.16E-05	0.000274738
GO:0048245	eosinophil chemotaxis	6/655	19/18862	3.16E-05	0.000274738
GO:1904064	positive regulation of cation transmembrane transport	16/655	141/18862	3.20E-05	0.000277555
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	8/655	37/18862	3.20E-05	0.000277816
GO:0070493	thrombin-activated receptor signaling pathway	5/655	12/18862	3.22E-05	0.000278202
GO:0006869	lipid transport	34/655	461/18862	3.26E-05	0.000281202
GO:0030278	regulation of ossification	14/655	112/18862	3.36E-05	0.000289591
GO:0045778	positive regulation of ossification	9/655	48/18862	3.47E-05	0.000296564
GO:0060688	regulation of morphogenesis of a branching structure	9/655	48/18862	3.47E-05	0.000296564
GO:2000191	regulation of fatty acid transport	9/655	48/18862	3.47E-05	0.000296564
GO:2001238	positive regulation of extrinsic apoptotic signaling pathway	9/655	48/18862	3.47E-05	0.000296564
GO:0033612	receptor serine/threonine kinase binding	7/606	28/18337	2.69E-05	0.000298415
GO:0061134	peptidase regulator activity	21/606	230/18337	2.70E-05	0.000298415
GO:0019840	isoprenoid binding	8/606	38/18337	2.76E-05	0.000298415
GO:0032813	tumor necrosis factor receptor superfamily binding	9/606	49/18337	2.79E-05	0.000298415
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	15/655	127/18862	3.50E-05	0.000299039
GO:0030246	carbohydrate binding	23/606	267/18337	2.88E-05	0.000303001
GO:0007193	adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway	12/655	85/18862	3.60E-05	0.000306405
GO:0032370	positive regulation of lipid transport	12/655	85/18862	3.60E-05	0.000306405

GO:0031093	platelet alpha granule lumen	11/659	67/19520	1.37E-05	0.000312717
GO:0031098	stress-activated protein kinase signaling cascade	24/655	276/18862	3.71E-05	0.000314316
GO:0030282	bone mineralization	14/655	113/18862	3.71E-05	0.000314316
GO:0034764	positive regulation of transmembrane transport	20/655	207/18862	3.74E-05	0.000314316
GO:0034767	positive regulation of ion transmembrane transport	20/655	207/18862	3.74E-05	0.000314316
GO:0007588	excretion	10/655	60/18862	3.74E-05	0.000314316
GO:0032722	positive regulation of chemokine production	10/655	60/18862	3.74E-05	0.000314316
GO:0032890	regulation of organic acid transport	10/655	60/18862	3.74E-05	0.000314316
GO:0045823	positive regulation of heart contraction	8/655	38/18862	3.94E-05	0.000330235
GO:0030667	secretory granule membrane	26/659	305/19520	1.56E-05	0.000334166
GO:0048738	cardiac muscle tissue development	20/655	208/18862	4.00E-05	0.00033535
GO:0007589	body fluid secretion	12/655	86/18862	4.05E-05	0.000338842
GO:0002292	T cell differentiation involved in immune response	11/655	73/18862	4.09E-05	0.000340573
GO:0006809	nitric oxide biosynthetic process	11/655	73/18862	4.09E-05	0.000340573
GO:0046328	regulation of JNK cascade	15/655	129/18862	4.21E-05	0.000349968
GO:0051651	maintenance of location in cell	20/655	209/18862	4.29E-05	0.000355856
GO:0004857	enzyme inhibitor activity	29/606	385/18337	3.49E-05	0.000360142
GO:0071379	cellular response to prostaglandin stimulus	6/655	20/18862	4.38E-05	0.000362724
GO:0009755	hormone-mediated signaling pathway	19/655	193/18862	4.50E-05	0.00037157
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	22/655	244/18862	4.50E-05	0.00037157
GO:0003206	cardiac chamber morphogenesis	14/655	115/18862	4.52E-05	0.000372743
GO:1902624	positive regulation of neutrophil migration	7/655	29/18862	4.72E-05	0.000388437
GO:0045933	positive regulation of muscle contraction	8/655	39/18862	4.80E-05	0.000393721
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	8/655	39/18862	4.80E-05	0.000393721
GO:1904019	epithelial cell apoptotic process	14/655	116/18862	4.98E-05	0.000407743

GO:0045453	bone resorption	10/655	62/18862	5.01E-05	0.000409339
GO:0031650	regulation of heat generation	5/655	13/18862	5.08E-05	0.000412389
GO:0035815	positive regulation of renal sodium excretion	5/655	13/18862	5.08E-05	0.000412389
GO:0060340	positive regulation of type I interferon-mediated signaling pathway	5/655	13/18862	5.08E-05	0.000412389
GO:0004713	protein tyrosine kinase activity	15/606	135/18337	4.08E-05	0.000414201
GO:0070664	negative regulation of leukocyte proliferation	12/655	88/18862	5.11E-05	0.000414645
GO:0010959	regulation of metal ion transport	22/655	247/18862	5.41E-05	0.000437305
GO:0030072	peptide hormone secretion	22/655	247/18862	5.41E-05	0.000437305
GO:0051098	regulation of binding	28/655	357/18862	5.55E-05	0.000447642
GO:0043277	apoptotic cell clearance	9/655	51/18862	5.73E-05	0.00046071
GO:0043900	regulation of multi-organism process	9/655	51/18862	5.73E-05	0.00046071
GO:0048662	negative regulation of smooth muscle cell proliferation	10/655	63/18862	5.77E-05	0.000463468
GO:0071774	response to fibroblast growth factor	16/655	148/18862	5.79E-05	0.000463468
GO:0045776	negative regulation of blood pressure	8/655	40/18862	5.82E-05	0.000463468
GO:0098760	response to interleukin-7	8/655	40/18862	5.82E-05	0.000463468
GO:0098761	cellular response to interleukin-7	8/655	40/18862	5.82E-05	0.000463468
GO:1903524	positive regulation of blood circulation	8/655	40/18862	5.82E-05	0.000463468
GO:0043903	regulation of biological process involved in symbiotic interaction	19/655	197/18862	5.95E-05	0.000472655
GO:0001960	negative regulation of cytokine-mediated signaling pathway	11/655	76/18862	5.99E-05	0.00047512
GO:1903035	negative regulation of response to wounding	12/655	90/18862	6.40E-05	0.000506844
GO:0007568	aging	25/655	304/18862	6.44E-05	0.000509207
GO:0060411	cardiac septum morphogenesis	10/655	64/18862	6.63E-05	0.000523492
GO:0002711	positive regulation of T cell mediated immunity	9/655	52/18862	6.72E-05	0.000529229
GO:0046209	nitric oxide metabolic process	11/655	77/18862	6.77E-05	0.000531762
GO:0060420	regulation of heart growth	11/655	77/18862	6.77E-05	0.000531762

GO:0035265	organ growth	17/655	166/18862	6.83E-05	0.000535325
GO:0048863	stem cell differentiation	22/655	251/18862	6.88E-05	0.000538063
GO:1903707	negative regulation of hemopoiesis	13/655	105/18862	7.04E-05	0.000549838
GO:0043524	negative regulation of neuron apoptotic process	15/655	135/18862	7.15E-05	0.00055748
GO:0002790	peptide secretion	30/655	401/18862	7.25E-05	0.000564171
GO:0043020	NADPH oxidase complex	5/659	12/19520	2.81E-05	0.000567932
GO:0002793	positive regulation of peptide secretion	16/655	151/18862	7.38E-05	0.000573571
GO:0001516	prostaglandin biosynthetic process	7/655	31/18862	7.49E-05	0.000579293
GO:0046457	prostanoid biosynthetic process	7/655	31/18862	7.49E-05	0.000579293
GO:2000193	positive regulation of fatty acid transport	7/655	31/18862	7.49E-05	0.000579293
GO:2001057	reactive nitrogen species metabolic process	11/655	78/18862	7.64E-05	0.000590021
GO:0033691	sialic acid binding	6/606	22/18337	6.03E-05	0.000603078
GO:0014821	phasic smooth muscle contraction	6/655	22/18862	7.94E-05	0.000612329
GO:0030316	osteoclast differentiation	12/655	92/18862	7.96E-05	0.000612689
GO:1903522	regulation of blood circulation	24/655	290/18862	8.13E-05	0.000624469
GO:0009612	response to mechanical stimulus	19/655	202/18862	8.34E-05	0.000639862
GO:0014002	astrocyte development	8/655	42/18862	8.41E-05	0.00064383
GO:0046632	alpha-beta T cell differentiation	13/655	107/18862	8.57E-05	0.00065531
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	10/655	66/18862	8.68E-05	0.000661601
GO:0046635	positive regulation of alpha-beta T cell activation	10/655	66/18862	8.68E-05	0.000661601
GO:0005581	collagen trimer	12/659	87/19520	3.47E-05	0.000665531
GO:0045071	negative regulation of viral genome replication	9/655	54/18862	9.13E-05	0.000693372
GO:0061756	leukocyte adhesion to vascular endothelial cell	9/655	54/18862	9.13E-05	0.000693372
GO:0052548	regulation of endopeptidase activity	31/655	426/18862	9.20E-05	0.000697631
GO:0061135	endopeptidase regulator activity	18/606	192/18337	7.09E-05	0.00069823

GO:0001501	skeletal system development	34/655	486/18862	9.26E-05	0.000700768
GO:0016486	peptide hormone processing	7/655	32/18862	9.30E-05	0.000700856
GO:0032673	regulation of interleukin-4 production	7/655	32/18862	9.30E-05	0.000700856
GO:0033687	osteoblast proliferation	7/655	32/18862	9.30E-05	0.000700856
GO:0014065	phosphatidylinositol 3-kinase signaling	16/655	154/18862	9.34E-05	0.000701262
GO:2001236	regulation of extrinsic apoptotic signaling pathway	16/655	154/18862	9.34E-05	0.000701262
GO:1903409	reactive oxygen species biosynthetic process	14/655	123/18862	9.51E-05	0.000712904
GO:0002287	alpha-beta T cell activation involved in immune response	10/655	67/18862	9.89E-05	0.000735797
GO:0002293	alpha-beta T cell differentiation involved in immune response	10/655	67/18862	9.89E-05	0.000735797
GO:0002637	regulation of immunoglobulin production	10/655	67/18862	9.89E-05	0.000735797
GO:0046637	regulation of alpha-beta T cell differentiation	10/655	67/18862	9.89E-05	0.000735797
GO:1901224	positive regulation of NIK/NF-kappaB signaling	10/655	67/18862	9.89E-05	0.000735797
GO:1903531	negative regulation of secretion by cell	15/655	139/18862	9.99E-05	0.000740428
GO:0032309	icosanoid secretion	8/655	43/18862	0.000100174	0.000740428
GO:0061383	trabecula morphogenesis	8/655	43/18862	0.000100174	0.000740428
GO:2000273	positive regulation of signaling receptor activity	8/655	43/18862	0.000100174	0.000740428
GO:0006816	calcium ion transport	30/655	409/18862	0.000103254	0.000761986
GO:0032963	collagen metabolic process	13/655	109/18862	0.000103842	0.000765119
GO:0002021	response to dietary excess	6/655	23/18862	0.000104324	0.000766249
GO:0032693	negative regulation of interleukin-10 production	6/655	23/18862	0.000104324	0.000766249
GO:0017134	fibroblast growth factor binding	6/606	23/18337	7.93E-05	0.000768461
GO:0030100	regulation of endocytosis	19/655	206/18862	0.000108316	0.000792488
GO:0043367	CD4-positive, alpha-beta T cell differentiation	11/655	81/18862	0.000108406	0.000792488
GO:0060761	negative regulation of response to cytokine stimulus	11/655	81/18862	0.000108406	0.000792488
GO:0090277	positive regulation of peptide hormone secretion	12/655	95/18862	0.000109107	0.000796359

GO:0002827	positive regulation of T-helper 1 type immune response	5/655	15/18862	0.000111764	0.000814477
GO:0000302	response to reactive oxygen species	20/655	224/18862	0.000112767	0.00082051
GO:0032355	response to estradiol	14/655	125/18862	0.00011326	0.00082281
GO:0032633	interleukin-4 production	7/655	33/18862	0.000114552	0.000825765
GO:0032814	regulation of natural killer cell activation	7/655	33/18862	0.000114552	0.000825765
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	7/655	33/18862	0.000114552	0.000825765
GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway	7/655	33/18862	0.000114552	0.000825765
GO:0140448	signaling receptor ligand precursor processing	7/655	33/18862	0.000114552	0.000825765
GO:0030168	platelet activation	16/655	157/18862	0.000117366	0.000844745
GO:0002639	positive regulation of immunoglobulin production	8/655	44/18862	0.00011875	0.000852076
GO:0045124	regulation of bone resorption	8/655	44/18862	0.00011875	0.000852076
GO:0051403	stress-activated MAPK cascade	22/655	261/18862	0.000121982	0.000873924
GO:0045471	response to ethanol	14/655	126/18862	0.000123433	0.000882963
GO:0046660	female sex differentiation	13/655	111/18862	0.0001252	0.00089423
GO:0044344	cellular response to fibroblast growth factor stimulus	15/655	142/18862	0.00012719	0.000907055
GO:0043550	regulation of lipid kinase activity	10/655	69/18862	0.000127442	0.000907467
GO:0034599	cellular response to oxidative stress	24/655	299/18862	0.000130284	0.000926285
GO:0031099	regeneration	18/655	192/18862	0.000132654	0.00094027
GO:0048015	phosphatidylinositol-mediated signaling	18/655	192/18862	0.000132654	0.00094027
GO:0098581	detection of external biotic stimulus	6/655	24/18862	0.000135038	0.000955719
GO:0004866	endopeptidase inhibitor activity	17/606	180/18337	0.00010212	0.000965966
GO:0005160	transforming growth factor beta receptor binding	6/606	24/18337	0.000102829	0.000965966
GO:0002576	platelet degranulation	14/655	128/18862	0.000146175	0.001029853
GO:0032479	regulation of type I interferon production	14/655	128/18862	0.000146175	0.001029853
GO:0045667	regulation of osteoblast differentiation	14/655	128/18862	0.000146175	0.001029853

GO:0031214	biomineral tissue development	16/655	160/18862	0.000146582	0.001031162
GO:0031341	regulation of cell killing	12/655	98/18862	0.000147534	0.001036294
GO:0042063	gliogenesis	23/655	283/18862	0.000148782	0.001043489
GO:0030101	natural killer cell activation	11/655	84/18862	0.000151185	0.001058747
GO:0003953	NAD+ nucleosidase activity	5/606	16/18337	0.000125096	0.001092385
GO:0019841	retinol binding	5/606	16/18337	0.000125096	0.001092385
GO:0050135	NAD(P)+ nucleosidase activity	5/606	16/18337	0.000125096	0.001092385
GO:0050664	oxidoreductase activity, acting on NAD(P)H, oxygen as acceptor	5/606	16/18337	0.000125096	0.001092385
GO:0061809	NAD+ nucleotidase, cyclic ADP-ribose generating	5/606	16/18337	0.000125096	0.001092385
GO:0045346	regulation of MHC class II biosynthetic process	5/655	16/18862	0.000157934	0.001104354
GO:0032606	type I interferon production	14/655	129/18862	0.000158846	0.001109069
GO:0002763	positive regulation of myeloid leukocyte differentiation	9/655	58/18862	0.000161557	0.001126309
GO:0019233	sensory perception of pain	12/655	99/18862	0.000162681	0.001132457
GO:0005104	fibroblast growth factor receptor binding	6/606	25/18337	0.000131545	0.001132747
GO:0007409	axonogenesis	32/655	460/18862	0.000163696	0.001137825
GO:0019207	kinase regulator activity	19/606	220/18337	0.000135286	0.001149003
GO:0110148	biomineralization	16/655	162/18862	0.000169413	0.001175809
GO:0048872	homeostasis of number of cells	21/655	249/18862	0.000171354	0.001187509
GO:0043393	regulation of protein binding	18/655	196/18862	0.000172044	0.00118838
GO:0048017	inositol lipid-mediated signaling	18/655	196/18862	0.000172044	0.00118838
GO:0048143	astrocyte activation	6/655	25/18862	0.000172499	0.00118838
GO:0060259	regulation of feeding behavior	6/655	25/18862	0.000172499	0.00118838
GO:0006939	smooth muscle contraction	12/655	100/18862	0.000179138	0.001232301
GO:0035924	cellular response to vascular endothelial growth factor stimulus	10/655	72/18862	0.000183069	0.001255638
GO:0048708	astrocyte differentiation	10/655	72/18862	0.000183069	0.001255638

GO:0045428	regulation of nitric oxide biosynthetic process	9/655	59/18862	0.000184849	0.001265983
GO:0051781	positive regulation of cell division	11/655	86/18862	0.000187046	0.001277361
GO:0072073	kidney epithelium development	14/655	131/18862	0.000187058	0.001277361
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	8/655	47/18862	0.000192254	0.001307102
GO:0009409	response to cold	8/655	47/18862	0.000192254	0.001307102
GO:1904707	positive regulation of vascular associated smooth muscle cell proliferation	8/655	47/18862	0.000192254	0.001307102
GO:0006979	response to oxidative stress	31/655	444/18862	0.000193318	0.001312421
GO:0046425	regulation of receptor signaling pathway via JAK-STAT	12/655	101/18862	0.000196995	0.001333505
GO:1902106	negative regulation of leukocyte differentiation	12/655	101/18862	0.000196995	0.001333505
GO:0048608	reproductive structure development	29/655	405/18862	0.000201991	0.001365345
GO:0003015	heart process	23/655	289/18862	0.000202432	0.001366275
GO:0030879	mammary gland development	14/655	132/18862	0.000202715	0.001366275
GO:0042311	vasodilation	7/655	36/18862	0.000204492	0.001376266
GO:0004714	transmembrane receptor protein tyrosine kinase activity	9/606	61/18337	0.00016568	0.001388126
GO:0062197	cellular response to chemical stress	26/655	347/18862	0.000210365	0.001413747
GO:0045576	mast cell activation	9/655	60/18862	0.000210869	0.001415095
GO:0045927	positive regulation of growth	21/655	253/18862	0.000213451	0.001430369
GO:0017171	serine hydrolase activity	17/606	188/18337	0.000173502	0.00143428
GO:0034393	positive regulation of smooth muscle cell apoptotic process	5/655	17/18862	0.000217371	0.001450385
GO:0048670	regulation of collateral sprouting	5/655	17/18862	0.000217371	0.001450385
GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	5/655	17/18862	0.000217371	0.001450385
GO:1901623	regulation of lymphocyte chemotaxis	6/655	26/18862	0.00021771	0.001450574
GO:2001233	regulation of apoptotic signaling pathway	26/655	348/18862	0.000220089	0.001464328
GO:0001913	T cell mediated cytotoxicity	8/655	48/18862	0.000223774	0.001480398

GO:0030195	negative regulation of blood coagulation	8/655	48/18862	0.000223774	0.001480398
GO:0038084	vascular endothelial growth factor signaling pathway	8/655	48/18862	0.000223774	0.001480398
GO:1904894	positive regulation of receptor signaling pathway via STAT	8/655	48/18862	0.000223774	0.001480398
GO:0071695	anatomical structure maturation	19/655	218/18862	0.000226615	0.001497073
GO:0061458	reproductive system development	29/655	408/18862	0.000228689	0.001508634
GO:0061045	negative regulation of wound healing	10/655	74/18862	0.000230495	0.001518399
GO:0048545	response to steroid hormone	25/655	330/18862	0.000233968	0.001537042
GO:0015908	fatty acid transport	15/655	150/18862	0.000233984	0.001537042
GO:0032526	response to retinoic acid	12/655	103/18862	0.000237296	0.00155661
GO:0080164	regulation of nitric oxide metabolic process	9/655	61/18862	0.00023986	0.001571218
GO:0090218	positive regulation of lipid kinase activity	7/655	37/18862	0.00024473	0.001598627
GO:2000403	positive regulation of lymphocyte migration	7/655	37/18862	0.00024473	0.001598627
GO:0019887	protein kinase regulator activity	17/606	190/18337	0.000197029	0.001607345
GO:0051208	sequestering of calcium ion	13/655	119/18862	0.000252823	0.001649183
GO:0001660	fever generation	4/655	10/18862	0.00025599	0.001658247
GO:0002024	diet induced thermogenesis	4/655	10/18862	0.00025599	0.001658247
GO:0003093	regulation of glomerular filtration	4/655	10/18862	0.00025599	0.001658247
GO:0032754	positive regulation of interleukin-5 production	4/655	10/18862	0.00025599	0.001658247
GO:0040015	negative regulation of multicellular organism growth	4/655	10/18862	0.00025599	0.001658247
GO:0046638	positive regulation of alpha-beta T cell differentiation	8/655	49/18862	0.000259406	0.001673402
GO:0060043	regulation of cardiac muscle cell proliferation	8/655	49/18862	0.000259406	0.001673402
GO:1900047	negative regulation of hemostasis	8/655	49/18862	0.000259406	0.001673402
GO:0031960	response to corticosteroid	15/655	152/18862	0.000270461	0.001742304
GO:0002675	positive regulation of acute inflammatory response	6/655	27/18862	0.000271759	0.001748251
GO:0048732	gland development	29/655	413/18862	0.000280215	0.001800172

GO:0044706	multi-multicellular organism process	18/655	204/18862	0.000282496	0.001812325
GO:0001914	regulation of T cell mediated cytotoxicity	7/655	38/18862	0.000291102	0.001858077
GO:0009595	detection of biotic stimulus	7/655	38/18862	0.000291102	0.001858077
GO:0001991	regulation of systemic arterial blood pressure by circulatory renin-angiotensin	5/655	18/18862	0.000292416	0.001858077
GO:0002281	macrophage activation involved in immune response	5/655	18/18862	0.000292416	0.001858077
GO:0006957	complement activation, alternative pathway	5/655	18/18862	0.000292416	0.001858077
GO:0032740	positive regulation of interleukin-17 production	5/655	18/18862	0.000292416	0.001858077
GO:2000831	regulation of steroid hormone secretion	5/655	18/18862	0.000292416	0.001858077
GO:0042834	peptidoglycan binding	5/606	18/18337	0.000232273	0.001870248
GO:0030183	B cell differentiation	14/655	137/18862	0.000299079	0.001895643
GO:0048260	positive regulation of receptor-mediated endocytosis	8/655	50/18862	0.000299547	0.001895643
GO:1904036	negative regulation of epithelial cell apoptotic process	8/655	50/18862	0.000299547	0.001895643
GO:0031343	positive regulation of cell killing	9/655	63/18862	0.000307804	0.001945257
GO:0060047	heart contraction	22/655	279/18862	0.000314087	0.001982274
GO:0032481	positive regulation of type I interferon production	10/655	77/18862	0.00032066	0.002018295
GO:0034121	regulation of toll-like receptor signaling pathway	10/655	77/18862	0.00032066	0.002018295
GO:0007254	JNK cascade	17/655	189/18862	0.000330049	0.002074593
GO:1901655	cellular response to ketone	11/655	92/18862	0.000340682	0.002138547
GO:0007190	activation of adenylate cyclase activity	7/655	39/18862	0.000344273	0.002145927
GO:0030501	positive regulation of bone mineralization	7/655	39/18862	0.000344273	0.002145927
GO:0050832	defense response to fungus	7/655	39/18862	0.000344273	0.002145927
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	8/655	51/18862	0.000344618	0.002145927
GO:0071715	icosanoid transport	8/655	51/18862	0.000344618	0.002145927
GO:1904645	response to amyloid-beta	8/655	51/18862	0.000344618	0.002145927
GO:0042093	T-helper cell differentiation	9/655	64/18862	0.000347318	0.002156976

GO:0072577	endothelial cell apoptotic process	9/655	64/18862	0.000347318	0.002156976
GO:0008016	regulation of heart contraction	20/655	245/18862	0.000371681	0.002305216
GO:0008585	female gonad development	11/655	93/18862	0.000374503	0.002316551
GO:0051591	response to cAMP	11/655	93/18862	0.000374503	0.002316551
GO:0030139	endocytic vesicle	24/659	307/19520	0.000128066	0.002330798
GO:0002689	negative regulation of leukocyte chemotaxis	5/655	19/18862	0.000385574	0.002375584
GO:0010744	positive regulation of macrophage derived foam cell differentiation	5/655	19/18862	0.000385574	0.002375584
GO:0098543	detection of other organism	5/655	19/18862	0.000385574	0.002375584
GO:0050795	regulation of behavior	9/655	65/18862	0.000390924	0.002394664
GO:0008228	opsonization	4/655	11/18862	0.000391238	0.002394664
GO:0033212	iron import into cell	4/655	11/18862	0.000391238	0.002394664
GO:0033690	positive regulation of osteoblast proliferation	4/655	11/18862	0.000391238	0.002394664
GO:0034975	protein folding in endoplasmic reticulum	4/655	11/18862	0.000391238	0.002394664
GO:0002820	negative regulation of adaptive immune response	8/655	52/18862	0.000395062	0.002411742
GO:0050819	negative regulation of coagulation	8/655	52/18862	0.000395062	0.002411742
GO:0030890	positive regulation of B cell proliferation	7/655	40/18862	0.000404949	0.00246564
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	7/655	40/18862	0.000404949	0.00246564
GO:0061036	positive regulation of cartilage development	6/655	29/18862	0.000411087	0.002496561
GO:1904035	regulation of epithelial cell apoptotic process	11/655	94/18862	0.000411098	0.002496561
GO:0061035	regulation of cartilage development	9/655	66/18862	0.000438941	0.002658729
GO:0072678	T cell migration	9/655	66/18862	0.000438941	0.002658729
GO:2001235	positive regulation of apoptotic signaling pathway	13/655	126/18862	0.000443152	0.002680755
GO:2000116	regulation of cysteine-type endopeptidase activity	19/655	230/18862	0.000445465	0.002691254
GO:0003179	heart valve morphogenesis	8/655	53/18862	0.000451348	0.002719753
GO:0010524	positive regulation of calcium ion transport into cytosol	8/655	53/18862	0.000451348	0.002719753

GO:0007565	female pregnancy	16/655	177/18862	0.000462856	0.0027855
GO:0022612	gland morphogenesis	12/655	111/18862	0.000475999	0.002860903
GO:0050672	negative regulation of lymphocyte proliferation	10/655	81/18862	0.000485016	0.002911342
GO:0014074	response to purine-containing compound	14/655	144/18862	0.000498266	0.002960209
GO:0045577	regulation of B cell differentiation	6/655	30/18862	0.000498918	0.002960209
GO:0061384	heart trabecula morphogenesis	6/655	30/18862	0.000498918	0.002960209
GO:0110110	positive regulation of animal organ morphogenesis	6/655	30/18862	0.000498918	0.002960209
GO:0007252	I-kappaB phosphorylation	5/655	20/18862	0.000499504	0.002960209
GO:0032816	positive regulation of natural killer cell activation	5/655	20/18862	0.000499504	0.002960209
GO:0070233	negative regulation of T cell apoptotic process	5/655	20/18862	0.000499504	0.002960209
GO:0090026	positive regulation of monocyte chemotaxis	5/655	20/18862	0.000499504	0.002960209
GO:0090189	regulation of branching involved in ureteric bud morphogenesis	5/655	20/18862	0.000499504	0.002960209
GO:0090280	positive regulation of calcium ion import	5/655	20/18862	0.000499504	0.002960209
GO:0002791	regulation of peptide secretion	23/655	308/18862	0.000501396	0.002967101
GO:0010975	regulation of neuron projection development	29/655	428/18862	0.000501939	0.002967101
GO:0002043	blood vessel endothelial cell proliferation involved in sprouting angiogenesis	8/655	54/18862	0.000513969	0.003030533
GO:0055078	sodium ion homeostasis	8/655	54/18862	0.000513969	0.003030533
GO:0051209	release of sequestered calcium ion into cytosol	12/655	112/18862	0.000516652	0.003042505
GO:0032945	negative regulation of mononuclear cell proliferation	10/655	82/18862	0.000535526	0.003149676
GO:0046545	development of primary female sexual characteristics	11/655	97/18862	0.000539336	0.003164107
GO:0060191	regulation of lipase activity	11/655	97/18862	0.000539336	0.003164107
GO:0032965	regulation of collagen biosynthetic process	7/655	42/18862	0.000551835	0.003229309
GO:0043114	regulation of vascular permeability	7/655	42/18862	0.000551835	0.003229309
GO:0001909	leukocyte mediated cytotoxicity	12/655	113/18862	0.000560186	0.003265883
GO:0008543	fibroblast growth factor receptor signaling pathway	12/655	113/18862	0.000560186	0.003265883

GO:0051283	negative regulation of sequestering of calcium ion	12/655	113/18862	0.000560186	0.003265883
GO:0010455	positive regulation of cell fate commitment	4/655	12/18862	0.000570782	0.003311101
GO:0044650	adhesion of symbiont to host cell	4/655	12/18862	0.000570782	0.003311101
GO:0044849	estrous cycle	4/655	12/18862	0.000570782	0.003311101
GO:0061469	regulation of type B pancreatic cell proliferation	4/655	12/18862	0.000570782	0.003311101
GO:0101003	ficolin-1-rich granule membrane	9/659	61/19520	0.000194737	0.003375439
GO:0014706	striated muscle tissue development	25/655	351/18862	0.000586527	0.003398212
GO:0045069	regulation of viral genome replication	10/655	83/18862	0.000590315	0.003415918
GO:0019835	cytolysis	6/655	31/18862	0.000600684	0.003463028
GO:0034390	smooth muscle cell apoptotic process	6/655	31/18862	0.000600684	0.003463028
GO:0034391	regulation of smooth muscle cell apoptotic process	6/655	31/18862	0.000600684	0.003463028
GO:0006936	muscle contraction	25/655	352/18862	0.000611254	0.003519616
GO:0010952	positive regulation of peptidase activity	17/655	200/18862	0.000633555	0.003636452
GO:0001759	organ induction	5/655	21/18862	0.000637003	0.003636452
GO:0035809	regulation of urine volume	5/655	21/18862	0.000637003	0.003636452
GO:0035929	steroid hormone secretion	5/655	21/18862	0.000637003	0.003636452
GO:0046641	positive regulation of alpha-beta T cell proliferation	5/655	21/18862	0.000637003	0.003636452
GO:1903429	regulation of cell maturation	5/655	21/18862	0.000637003	0.003636452
GO:1905209	positive regulation of cardiocyte differentiation	5/655	21/18862	0.000637003	0.003636452
GO:0035580	specific granule lumen	9/659	62/19520	0.000221084	0.003657941
GO:1903426	regulation of reactive oxygen species biosynthetic process	11/655	99/18862	0.000642149	0.003661348
GO:0008236	serine-type peptidase activity	16/606	186/18337	0.000466929	0.003689128
GO:0004252	serine-type endopeptidase activity	15/606	168/18337	0.000470066	0.003689128
GO:0004869	cysteine-type endopeptidase inhibitor activity	8/606	56/18337	0.000476216	0.003690674
GO:0051346	negative regulation of hydrolase activity	30/655	456/18862	0.000655531	0.00372973

GO:1903900	regulation of viral life cycle	14/655	148/18862	0.00065613	0.00372973
GO:0051282	regulation of sequestering of calcium ion	12/655	115/18862	0.000656541	0.00372973
GO:0043388	positive regulation of DNA binding	8/655	56/18862	0.000660306	0.003746553
GO:0035579	specific granule membrane	11/659	91/19520	0.000243586	0.003855006
GO:0006879	cellular iron ion homeostasis	9/655	70/18862	0.000682039	0.003860471
GO:0010517	regulation of phospholipase activity	9/655	70/18862	0.000682039	0.003860471
GO:0002832	negative regulation of response to biotic stimulus	11/655	100/18862	0.000699375	0.0039538
GO:0002861	regulation of inflammatory response to antigenic stimulus	6/655	32/18862	0.000717838	0.004038595
GO:0010661	positive regulation of muscle cell apoptotic process	6/655	32/18862	0.000717838	0.004038595
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	6/655	32/18862	0.000717838	0.004038595
GO:0051385	response to mineralocorticoid	6/655	32/18862	0.000717838	0.004038595
GO:0045444	fat cell differentiation	18/655	221/18862	0.000735753	0.004134401
GO:0150076	neuroinflammatory response	7/655	44/18862	0.000738208	0.004143205
GO:0031295	T cell costimulation	8/655	57/18862	0.000745129	0.004172008
GO:0032757	positive regulation of interleukin-8 production	8/655	57/18862	0.000745129	0.004172008
GO:0051216	cartilage development	16/655	185/18862	0.000750699	0.004198154
GO:0070227	lymphocyte apoptotic process	9/655	71/18862	0.000757438	0.004230767
GO:0001530	lipopolysaccharide binding	6/606	32/18337	0.000552975	0.004232648
GO:0097553	calcium ion transmembrane import into cytosol	13/655	134/18862	0.000797604	0.004394932
GO:0003205	cardiac chamber development	14/655	151/18862	0.00080067	0.004394932
GO:2001056	positive regulation of cysteine-type endopeptidase activity	14/655	151/18862	0.00080067	0.004394932
GO:0032727	positive regulation of interferon-alpha production	5/655	22/18862	0.000800995	0.004394932
GO:0055093	response to hyperoxia	5/655	22/18862	0.000800995	0.004394932
GO:0060343	trabecula formation	5/655	22/18862	0.000800995	0.004394932
GO:1904996	positive regulation of leukocyte adhesion to vascular endothelial cell	5/655	22/18862	0.000800995	0.004394932

GO:0010745	negative regulation of macrophage derived foam cell differentiation	4/655	13/18862	0.000801906	0.004394932
GO:0016264	gap junction assembly	4/655	13/18862	0.000801906	0.004394932
GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	4/655	13/18862	0.000801906	0.004394932
GO:0033605	positive regulation of catecholamine secretion	4/655	13/18862	0.000801906	0.004394932
GO:0035810	positive regulation of urine volume	4/655	13/18862	0.000801906	0.004394932
GO:0060100	positive regulation of phagocytosis, engulfment	4/655	13/18862	0.000801906	0.004394932
GO:0060732	positive regulation of inositol phosphate biosynthetic process	4/655	13/18862	0.000801906	0.004394932
GO:1903236	regulation of leukocyte tethering or rolling	4/655	13/18862	0.000801906	0.004394932
GO:1905155	positive regulation of membrane invagination	4/655	13/18862	0.000801906	0.004394932
GO:0031589	cell-substrate adhesion	25/655	359/18862	0.000811311	0.004441261
GO:0030971	receptor tyrosine kinase binding	9/606	72/18337	0.00058952	0.004457345
GO:0046620	regulation of organ growth	11/655	102/18862	0.000826587	0.00451958
GO:0060038	cardiac muscle cell proliferation	8/655	58/18862	0.000838501	0.004573998
GO:2000351	regulation of endothelial cell apoptotic process	8/655	58/18862	0.000838501	0.004573998
GO:0014855	striated muscle cell proliferation	9/655	72/18862	0.000839491	0.004574047
GO:0001974	blood vessel remodeling	7/655	45/18862	0.00084839	0.004608172
GO:0014911	positive regulation of smooth muscle cell migration	7/655	45/18862	0.00084839	0.004608172
GO:1904062	regulation of cation transmembrane transport	24/655	340/18862	0.000848718	0.004608172
GO:0045589	regulation of regulatory T cell differentiation	6/655	33/18862	0.000851901	0.004609359
GO:0050869	negative regulation of B cell activation	6/655	33/18862	0.000851901	0.004609359
GO:0051954	positive regulation of amine transport	6/655	33/18862	0.000851901	0.004609359
GO:0060402	calcium ion transport into cytosol	14/655	152/18862	0.000854459	0.004617843
GO:0061448	connective tissue development	19/655	243/18862	0.000870184	0.004691949
GO:0090257	regulation of muscle system process	19/655	243/18862	0.000870184	0.004691949
GO:0051099	positive regulation of binding	15/655	170/18862	0.000884433	0.004763277

GO:0002758	innate immune response-activating signal transduction	12/655	119/18862	0.000891241	0.004793508
GO:0030001	metal ion transport	31/655	486/18862	0.000892102	0.004793508
GO:0002062	chondrocyte differentiation	11/655	103/18862	0.000897046	0.004814524
GO:0039706	co-receptor binding	4/606	13/18337	0.000665469	0.004911793
GO:0070700	BMP receptor binding	4/606	13/18337	0.000665469	0.004911793
GO:0006940	regulation of smooth muscle contraction	8/655	59/18862	0.000941035	0.005039019
GO:0031294	lymphocyte costimulation	8/655	59/18862	0.000941035	0.005039019
GO:0046777	protein autophosphorylation	18/655	226/18862	0.000953201	0.005098313
GO:0003158	endothelium development	13/655	137/18862	0.000981059	0.005241303
GO:0003181	atrioventricular valve morphogenesis	5/655	23/18862	0.000994515	0.005294995
GO:0048668	collateral sprouting	5/655	23/18862	0.000994515	0.005294995
GO:1902932	positive regulation of alcohol biosynthetic process	5/655	23/18862	0.000994515	0.005294995
GO:0010092	specification of animal organ identity	6/655	34/18862	0.001004459	0.005317588
GO:0010543	regulation of platelet activation	6/655	34/18862	0.001004459	0.005317588
GO:0046640	regulation of alpha-beta T cell proliferation	6/655	34/18862	0.001004459	0.005317588
GO:0070232	regulation of T cell apoptotic process	6/655	34/18862	0.001004459	0.005317588
GO:2000352	negative regulation of endothelial cell apoptotic process	6/655	34/18862	0.001004459	0.005317588
GO:0005901	caveola	10/659	80/19520	0.000351734	0.005334632
GO:1903038	negative regulation of leukocyte cell-cell adhesion	13/655	138/18862	0.001049553	0.005550016
GO:0062207	regulation of pattern recognition receptor signaling pathway	11/655	105/18862	0.001052912	0.005561473
GO:0060401	cytosolic calcium ion transport	15/655	173/18862	0.001057417	0.00557895
GO:0034349	glial cell apoptotic process	4/655	14/18862	0.001091989	0.005736358
GO:0038166	angiotensin-activated signaling pathway	4/655	14/18862	0.001091989	0.005736358
GO:0072540	T-helper 17 cell lineage commitment	4/655	14/18862	0.001091989	0.005736358
GO:0010001	glial cell differentiation	17/655	210/18862	0.001092171	0.005736358

GO:0010712	regulation of collagen metabolic process	7/655	47/18862	0.00110745	0.005784765
GO:0030225	macrophage differentiation	7/655	47/18862	0.00110745	0.005784765
GO:0070169	positive regulation of biomineral tissue development	7/655	47/18862	0.00110745	0.005784765
GO:1903053	regulation of extracellular matrix organization	7/655	47/18862	0.00110745	0.005784765
GO:0045862	positive regulation of proteolysis	25/655	367/18862	0.001107589	0.005784765
GO:0007218	neuropeptide signaling pathway	11/655	106/18862	0.001138842	0.005941339
GO:0021700	developmental maturation	20/655	268/18862	0.001145475	0.005969269
GO:0051402	neuron apoptotic process	18/655	230/18862	0.001164644	0.006062388
GO:0032970	regulation of actin filament-based process	26/655	389/18862	0.001169094	0.006078767
GO:0003170	heart valve development	8/655	61/18862	0.001176161	0.006093501
GO:0048645	animal organ formation	8/655	61/18862	0.001176161	0.006093501
GO:0060338	regulation of type I interferon-mediated signaling pathway	6/655	35/18862	0.001177154	0.006093501
GO:1905207	regulation of cardiocyte differentiation	6/655	35/18862	0.001177154	0.006093501
GO:0060348	bone development	16/655	193/18862	0.001178905	0.006095801
GO:0060333	interferon-gamma-mediated signaling pathway	10/655	91/18862	0.001217908	0.006284007
GO:0002407	dendritic cell chemotaxis	5/655	24/18862	0.001220693	0.006284007
GO:0044321	response to leptin	5/655	24/18862	0.001220693	0.006284007
GO:1903901	negative regulation of viral life cycle	5/655	24/18862	0.001220693	0.006284007
GO:2000278	regulation of DNA biosynthetic process	11/655	107/18862	0.001230464	0.006327328
GO:0005178	integrin binding	13/606	142/18337	0.000870992	0.00635312
GO:0030500	regulation of bone mineralization	9/655	76/18862	0.001243068	0.006378074
GO:0051279	regulation of release of sequestered calcium ion into cytosol	9/655	76/18862	0.001243068	0.006378074
GO:0006692	prostanoid metabolic process	7/655	48/18862	0.001258321	0.006428051
GO:0006693	prostaglandin metabolic process	7/655	48/18862	0.001258321	0.006428051
GO:0052372	modulation by symbiont of entry into host	7/655	48/18862	0.001258321	0.006428051

GO:0110151	positive regulation of biomineralization	7/655	48/18862	0.001258321	0.006428051
GO:0060537	muscle tissue development	25/655	371/18862	0.001288	0.006572466
GO:0034614	cellular response to reactive oxygen species	14/655	159/18862	0.001323101	0.006744201
GO:0010038	response to metal ion	24/655	352/18862	0.001363197	0.006933425
GO:0032956	regulation of actin cytoskeleton organization	24/655	352/18862	0.001363197	0.006933425
GO:0003176	aortic valve development	6/655	36/18862	0.001371686	0.006953851
GO:0045066	regulatory T cell differentiation	6/655	36/18862	0.001371686	0.006953851
GO:0051930	regulation of sensory perception of pain	6/655	36/18862	0.001371686	0.006953851
GO:0070696	transmembrane receptor protein serine/threonine kinase binding	5/606	24/18337	0.000977834	0.007049503
GO:1904724	tertiary granule lumen	8/659	55/19520	0.000484833	0.007059175
GO:0070231	T cell apoptotic process	7/655	49/18862	0.001424807	0.00721531
GO:0001977	renal system process involved in regulation of blood volume	4/655	15/18862	0.001448435	0.0072718
GO:0010919	regulation of inositol phosphate biosynthetic process	4/655	15/18862	0.001448435	0.0072718
GO:0032645	regulation of granulocyte macrophage colony-stimulating factor production	4/655	15/18862	0.001448435	0.0072718
GO:0035635	entry of bacterium into host cell	4/655	15/18862	0.001448435	0.0072718
GO:0042976	activation of Janus kinase activity	4/655	15/18862	0.001448435	0.0072718
GO:0060099	regulation of phagocytosis, engulfment	4/655	15/18862	0.001448435	0.0072718
GO:0071380	cellular response to prostaglandin E stimulus	4/655	15/18862	0.001448435	0.0072718
GO:2000846	regulation of corticosteroid hormone secretion	4/655	15/18862	0.001448435	0.0072718
GO:0014015	positive regulation of gliogenesis	8/655	63/18862	0.001455888	0.007293512
GO:2000401	regulation of lymphocyte migration	8/655	63/18862	0.001455888	0.007293512
GO:0043523	regulation of neuron apoptotic process	16/655	197/18862	0.001460882	0.00731068
GO:0003171	atrioventricular valve development	5/655	25/18862	0.001482741	0.007387479
GO:0021884	forebrain neuron development	5/655	25/18862	0.001482741	0.007387479
GO:0032682	negative regulation of chemokine production	5/655	25/18862	0.001482741	0.007387479

GO:1990776	response to angiotensin	5/655	25/18862	0.001482741	0.007387479
GO:0071241	cellular response to inorganic substance	17/655	216/18862	0.001484148	0.007387479
GO:0006937	regulation of muscle contraction	14/655	161/18862	0.00149096	0.00740558
GO:0030307	positive regulation of cell growth	14/655	161/18862	0.00149096	0.00740558
GO:0030522	intracellular receptor signaling pathway	20/655	274/18862	0.001495503	0.007410435
GO:0001570	vasculogenesis	9/655	78/18862	0.001496704	0.007410435
GO:0045913	positive regulation of carbohydrate metabolic process	9/655	78/18862	0.001496704	0.007410435
GO:0051341	regulation of oxidoreductase activity	11/655	110/18862	0.001542354	0.007628357
GO:0035051	cardiocyte differentiation	13/655	144/18862	0.001549801	0.007657067
GO:0015837	amine transport	10/655	94/18862	0.001561807	0.00770007
GO:0070167	regulation of biomineral tissue development	10/655	94/18862	0.001561807	0.00770007
GO:0101002	ficolin-1-rich granule	16/659	185/19520	0.000556768	0.007794749
GO:0046633	alpha-beta T cell proliferation	6/655	37/18862	0.001589806	0.007813338
GO:0051931	regulation of sensory perception	6/655	37/18862	0.001589806	0.007813338
GO:0060412	ventricular septum morphogenesis	6/655	37/18862	0.001589806	0.007813338
GO:0003281	ventricular septum development	8/655	64/18862	0.001614255	0.007925141
GO:0001910	regulation of leukocyte mediated cytotoxicity	9/655	79/18862	0.001638251	0.008028367
GO:0042445	hormone metabolic process	17/655	218/18862	0.001638723	0.008028367
GO:0030900	forebrain development	24/655	357/18862	0.001646195	0.008056511
GO:0002262	myeloid cell homeostasis	13/655	145/18862	0.001649809	0.008065734
GO:0030324	lung development	14/655	163/18862	0.001676218	0.008183328
GO:0010466	negative regulation of peptidase activity	19/655	257/18862	0.001677372	0.008183328
GO:0010522	regulation of calcium ion transport into cytosol	10/655	95/18862	0.001692532	0.008248661
GO:0042923	neuropeptide binding	5/606	25/18337	0.001189407	0.008396146
GO:0031406	carboxylic acid binding	15/606	184/18337	0.001203349	0.008396146

GO:0048185	activin binding	4/606	15/18337	0.001205253	0.008396146
GO:0010950	positive regulation of endopeptidase activity	15/655	182/18862	0.001756463	0.008551298
GO:0002026	regulation of the force of heart contraction	5/655	26/18862	0.001783939	0.008657951
GO:0003156	regulation of animal organ formation	5/655	26/18862	0.001783939	0.008657951
GO:0061082	myeloid leukocyte cytokine production	5/655	26/18862	0.001783939	0.008657951
GO:0010660	regulation of muscle cell apoptotic process	9/655	80/18862	0.001790329	0.008679933
GO:0019079	viral genome replication	12/655	129/18862	0.001797271	0.00870454
GO:0006636	unsaturated fatty acid biosynthetic process	7/655	51/18862	0.00180898	0.00874309
GO:0032964	collagen biosynthetic process	7/655	51/18862	0.00180898	0.00874309
GO:0003279	cardiac septum development	10/655	96/18862	0.001831974	0.008805947
GO:0110149	regulation of biomineralization	10/655	96/18862	0.001831974	0.008805947
GO:0002714	positive regulation of B cell mediated immunity	6/655	38/18862	0.001833314	0.008805947
GO:0002891	positive regulation of immunoglobulin mediated immune response	6/655	38/18862	0.001833314	0.008805947
GO:0045429	positive regulation of nitric oxide biosynthetic process	6/655	38/18862	0.001833314	0.008805947
GO:2000249	regulation of actin cytoskeleton reorganization	6/655	38/18862	0.001833314	0.008805947
GO:0060249	anatomical structure homeostasis	29/655	466/18862	0.001867373	0.008940613
GO:0032604	granulocyte macrophage colony-stimulating factor production	4/655	16/18862	0.001878602	0.008940613
GO:0035930	corticosteroid hormone secretion	4/655	16/18862	0.001878602	0.008940613
GO:0044546	NLRP3 inflammasome complex assembly	4/655	16/18862	0.001878602	0.008940613
GO:0060263	regulation of respiratory burst	4/655	16/18862	0.001878602	0.008940613
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	4/655	16/18862	0.001878602	0.008940613
GO:0071361	cellular response to ethanol	4/655	16/18862	0.001878602	0.008940613
GO:1900747	negative regulation of vascular endothelial growth factor signaling pathway	4/655	16/18862	0.001878602	0.008940613
GO:1905153	regulation of membrane invagination	4/655	16/18862	0.001878602	0.008940613
GO:0009743	response to carbohydrate	17/655	221/18862	0.001895885	0.009013666

GO:0046683	response to organophosphorus	12/655	130/18862	0.001919176	0.009115109
GO:0014910	regulation of smooth muscle cell migration	9/655	81/18862	0.001953493	0.009268661
GO:0001933	negative regulation of protein phosphorylation	24/655	362/18862	0.001978115	0.009366427
GO:0042692	muscle cell differentiation	24/655	362/18862	0.001978115	0.009366427
GO:0001658	branching involved in ureteric bud morphogenesis	7/655	52/18862	0.002028922	0.009587532
GO:0050433	regulation of catecholamine secretion	7/655	52/18862	0.002028922	0.009587532
GO:0055007	cardiac muscle cell differentiation	11/655	114/18862	0.00205597	0.009705508
GO:0007548	sex differentiation	19/655	262/18862	0.002089146	0.009852151
GO:0045622	regulation of T-helper cell differentiation	6/655	39/18862	0.002104048	0.009864421
GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	6/655	39/18862	0.002104048	0.009864421
GO:0045773	positive regulation of axon extension	6/655	39/18862	0.002104048	0.009864421
GO:1904407	positive regulation of nitric oxide metabolic process	6/655	39/18862	0.002104048	0.009864421
GO:2000279	negative regulation of DNA biosynthetic process	6/655	39/18862	0.002104048	0.009864421
GO:0030323	respiratory tube development	14/655	167/18862	0.002104438	0.009864421
GO:0002360	T cell lineage commitment	5/655	27/18862	0.002127616	0.009933135
GO:0007263	nitric oxide mediated signal transduction	5/655	27/18862	0.002127616	0.009933135
GO:0032958	inositol phosphate biosynthetic process	5/655	27/18862	0.002127616	0.009933135
GO:0045987	positive regulation of smooth muscle contraction	5/655	27/18862	0.002127616	0.009933135
GO:0045669	positive regulation of osteoblast differentiation	8/655	67/18862	0.002172428	0.010132206
GO:0005788	endoplasmic reticulum lumen	22/659	306/19520	0.000754875	0.010176834
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	16/655	205/18862	0.002197001	0.010236574
GO:0002090	regulation of receptor internalization	7/655	53/18862	0.002268988	0.010540399
GO:0002704	negative regulation of leukocyte mediated immunity	7/655	53/18862	0.002268988	0.010540399
GO:0050432	catecholamine secretion	7/655	53/18862	0.002268988	0.010540399
GO:0022600	digestive system process	10/655	99/18862	0.00230685	0.010705622

GO:0001946	lymphangiogenesis	4/655	17/18862	0.00238975	0.010959484
GO:0002076	osteoblast development	4/655	17/18862	0.00238975	0.010959484
GO:0002295	T-helper cell lineage commitment	4/655	17/18862	0.00238975	0.010959484
GO:0002888	positive regulation of myeloid leukocyte mediated immunity	4/655	17/18862	0.00238975	0.010959484
GO:0016045	detection of bacterium	4/655	17/18862	0.00238975	0.010959484
GO:0030889	negative regulation of B cell proliferation	4/655	17/18862	0.00238975	0.010959484
GO:0034374	low-density lipoprotein particle remodeling	4/655	17/18862	0.00238975	0.010959484
GO:0043116	negative regulation of vascular permeability	4/655	17/18862	0.00238975	0.010959484
GO:0060457	negative regulation of digestive system process	4/655	17/18862	0.00238975	0.010959484
GO:0060749	mammary gland alveolus development	4/655	17/18862	0.00238975	0.010959484
GO:0061377	mammary gland lobule development	4/655	17/18862	0.00238975	0.010959484
GO:0150078	positive regulation of neuroinflammatory response	4/655	17/18862	0.00238975	0.010959484
GO:0055023	positive regulation of cardiac muscle tissue growth	6/655	40/18862	0.002403889	0.011002689
GO:0060443	mammary gland morphogenesis	6/655	40/18862	0.002403889	0.011002689
GO:0010469	regulation of signaling receptor activity	15/655	188/18862	0.002409817	0.011019005
GO:0010657	muscle cell apoptotic process	9/655	84/18862	0.00251525	0.011453603
GO:0010039	response to iron ion	5/655	28/18862	0.00251714	0.011453603
GO:0021988	olfactory lobe development	5/655	28/18862	0.00251714	0.011453603
GO:0032607	interferon-alpha production	5/655	28/18862	0.00251714	0.011453603
GO:0032647	regulation of interferon-alpha production	5/655	28/18862	0.00251714	0.011453603
GO:0002712	regulation of B cell mediated immunity	7/655	54/18862	0.002530374	0.011480218
GO:0002889	regulation of immunoglobulin mediated immune response	7/655	54/18862	0.002530374	0.011480218
GO:0070228	regulation of lymphocyte apoptotic process	7/655	54/18862	0.002530374	0.011480218
GO:0022408	negative regulation of cell-cell adhesion	15/655	189/18862	0.002536148	0.011484072
GO:0071248	cellular response to metal ion	15/655	189/18862	0.002536148	0.011484072

GO:0009266	response to temperature stimulus	17/655	228/18862	0.002630114	0.011898012
GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	12/655	135/18862	0.002634692	0.011907173
GO:0090276	regulation of peptide hormone secretion	16/655	209/18862	0.002667824	0.012045239
GO:0002220	innate immune response activating cell surface receptor signaling pathway	11/655	118/18862	0.002700631	0.0121698
GO:0051101	regulation of DNA binding	11/655	118/18862	0.002700631	0.0121698
GO:0001540	amyloid-beta binding	9/606	84/18337	0.001798023	0.012250264
GO:0030295	protein kinase activator activity	9/606	84/18337	0.001798023	0.012250264
GO:0019915	lipid storage	9/655	85/18862	0.002728575	0.012252517
GO:0033003	regulation of mast cell activation	6/655	41/18862	0.002734749	0.012252517
GO:0090279	regulation of calcium ion import	6/655	41/18862	0.002734749	0.012252517
GO:1901186	positive regulation of ERBB signaling pathway	6/655	41/18862	0.002734749	0.012252517
GO:1904646	cellular response to amyloid-beta	6/655	41/18862	0.002734749	0.012252517
GO:1905314	semi-lunar valve development	6/655	41/18862	0.002734749	0.012252517
GO:0051427	hormone receptor binding	14/606	173/18337	0.001853755	0.0124927
GO:0007405	neuroblast proliferation	7/655	55/18862	0.002814302	0.012584758
GO:0045620	negative regulation of lymphocyte differentiation	7/655	55/18862	0.002814302	0.012584758
GO:0051145	smooth muscle cell differentiation	8/655	70/18862	0.002872001	0.012818195
GO:1904427	positive regulation of calcium ion transmembrane transport	8/655	70/18862	0.002872001	0.012818195
GO:0045446	endothelial cell differentiation	11/655	119/18862	0.002884921	0.012863547
GO:0001773	myeloid dendritic cell activation	5/655	29/18862	0.002955902	0.013105141
GO:0036296	response to increased oxygen levels	5/655	29/18862	0.002955902	0.013105141
GO:0036336	dendritic cell migration	5/655	29/18862	0.002955902	0.013105141
GO:0045940	positive regulation of steroid metabolic process	5/655	29/18862	0.002955902	0.013105141
GO:0051952	regulation of amine transport	9/655	86/18862	0.002955962	0.013105141
GO:0055072	iron ion homeostasis	9/655	86/18862	0.002955962	0.013105141

GO:0002523	leukocyte migration involved in inflammatory response	4/655	18/18862	0.002988989	0.013201367
GO:0010885	regulation of cholesterol storage	4/655	18/18862	0.002988989	0.013201367
GO:0045063	T-helper 1 cell differentiation	4/655	18/18862	0.002988989	0.013201367
GO:1902548	negative regulation of cellular response to vascular endothelial growth factor stimulus	4/655	18/18862	0.002988989	0.013201367
GO:0071453	cellular response to oxygen levels	17/655	231/18862	0.003010355	0.013283154
GO:0030169	low-density lipoprotein particle binding	4/606	17/18337	0.001993886	0.013292575
GO:0071560	cellular response to transforming growth factor beta stimulus	18/655	251/18862	0.003045439	0.013425263
GO:0031532	actin cytoskeleton reorganization	10/655	103/18862	0.003088677	0.01360301
GO:0003197	endocardial cushion development	6/655	42/18862	0.003098568	0.01362085
GO:0062208	positive regulation of pattern recognition receptor signaling pathway	6/655	42/18862	0.003098568	0.01362085
GO:0010883	regulation of lipid storage	7/655	56/18862	0.003122015	0.013698099
GO:0046456	icosanoid biosynthetic process	7/655	56/18862	0.003122015	0.013698099
GO:0043627	response to estrogen	8/655	71/18862	0.003140517	0.013766327
GO:0007586	digestion	12/655	138/18862	0.003159138	0.01383495
GO:0043178	alcohol binding	9/606	86/18337	0.002119296	0.013978334
GO:0043534	blood vessel endothelial cell migration	14/655	175/18862	0.003233913	0.01414913
GO:0038111	interleukin-7-mediated signaling pathway	5/655	30/18862	0.003447298	0.015005879
GO:0042755	eating behavior	5/655	30/18862	0.003447298	0.015005879
GO:0050901	leukocyte tethering or rolling	5/655	30/18862	0.003447298	0.015005879
GO:0090183	regulation of kidney development	5/655	30/18862	0.003447298	0.015005879
GO:2000406	positive regulation of T cell migration	5/655	30/18862	0.003447298	0.015005879
GO:0002532	production of molecular mediator involved in inflammatory response	9/655	88/18862	0.00345547	0.015005879
GO:0014909	smooth muscle cell migration	9/655	88/18862	0.00345547	0.015005879
GO:0060993	kidney morphogenesis	9/655	88/18862	0.00345547	0.015005879
GO:0033293	monocarboxylic acid binding	8/606	71/18337	0.002315376	0.015110878

GO:0034142	toll-like receptor 4 signaling pathway	6/655	43/18862	0.00349731	0.015173447
GO:0002544	chronic inflammatory response	4/655	19/18862	0.003683233	0.015891394
GO:0010002	cardioblast differentiation	4/655	19/18862	0.003683233	0.015891394
GO:0033005	positive regulation of mast cell activation	4/655	19/18862	0.003683233	0.015891394
GO:0043902	positive regulation of multi-organism process	4/655	19/18862	0.003683233	0.015891394
GO:0044320	cellular response to leptin stimulus	4/655	19/18862	0.003683233	0.015891394
GO:0045780	positive regulation of bone resorption	4/655	19/18862	0.003683233	0.015891394
GO:0016500	protein-hormone receptor activity	4/606	18/18337	0.002497204	0.015961512
GO:0016918	retinal binding	4/606	18/18337	0.002497204	0.015961512
GO:0051147	regulation of muscle cell differentiation	13/655	159/18862	0.003707223	0.015980117
GO:0042493	response to drug	23/655	359/18862	0.003714712	0.015997613
GO:0007173	epidermal growth factor receptor signaling pathway	11/655	123/18862	0.003725909	0.01602909
GO:0042058	regulation of epidermal growth factor receptor signaling pathway	9/655	89/18862	0.003728894	0.01602909
GO:0003151	outflow tract morphogenesis	8/655	73/18862	0.003735779	0.016029136
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	8/655	73/18862	0.003735779	0.016029136
GO:1901222	regulation of NIK/NF-kappaB signaling	10/655	106/18862	0.003803152	0.016303216
GO:0060675	ureteric bud morphogenesis	7/655	58/18862	0.003813876	0.016334178
GO:0071559	response to transforming growth factor beta	18/655	257/18862	0.003906989	0.016717612
GO:0060421	positive regulation of heart growth	6/655	44/18862	0.003932958	0.016797909
GO:0060976	coronary vasculature development	6/655	44/18862	0.003932958	0.016797909
GO:0070229	negative regulation of lymphocyte apoptotic process	5/655	31/18862	0.003994724	0.017046105
GO:0071813	lipoprotein particle binding	5/606	30/18337	0.002784553	0.017438618
GO:0071814	protein-lipid complex binding	5/606	30/18337	0.002784553	0.017438618
GO:0002524	hypersensitivity	3/655	10/18862	0.004166561	0.017538664
GO:0003129	heart induction	3/655	10/18862	0.004166561	0.017538664

GO:0014041	regulation of neuron maturation	3/655	10/18862	0.004166561	0.017538664
GO:0031652	positive regulation of heat generation	3/655	10/18862	0.004166561	0.017538664
GO:0032817	regulation of natural killer cell proliferation	3/655	10/18862	0.004166561	0.017538664
GO:0034350	regulation of glial cell apoptotic process	3/655	10/18862	0.004166561	0.017538664
GO:0042045	epithelial fluid transport	3/655	10/18862	0.004166561	0.017538664
GO:0043084	penile erection	3/655	10/18862	0.004166561	0.017538664
GO:0045625	regulation of T-helper 1 cell differentiation	3/655	10/18862	0.004166561	0.017538664
GO:0048672	positive regulation of collateral sprouting	3/655	10/18862	0.004166561	0.017538664
GO:0051712	positive regulation of killing of cells of other organism	3/655	10/18862	0.004166561	0.017538664
GO:0060453	regulation of gastric acid secretion	3/655	10/18862	0.004166561	0.017538664
GO:0070391	response to lipoteichoic acid	3/655	10/18862	0.004166561	0.017538664
GO:0071223	cellular response to lipoteichoic acid	3/655	10/18862	0.004166561	0.017538664
GO:2000318	positive regulation of T-helper 17 type immune response	3/655	10/18862	0.004166561	0.017538664
GO:0072171	mesonephric tubule morphogenesis	7/655	59/18862	0.004200605	0.017666025
GO:0003007	heart morphogenesis	17/655	239/18862	0.00425268	0.017868917
GO:0099177	regulation of trans-synaptic signaling	25/655	406/18862	0.00426339	0.017897796
GO:0019209	kinase activator activity	9/606	90/18337	0.002898395	0.017970049
GO:0030510	regulation of BMP signaling pathway	9/655	91/18862	0.00432642	0.018146063
GO:0042326	negative regulation of phosphorylation	25/655	407/18862	0.004398393	0.018431362
GO:0051495	positive regulation of cytoskeleton organization	16/655	220/18862	0.004410132	0.018463962
GO:0043536	positive regulation of blood vessel endothelial cell migration	8/655	75/18862	0.004414696	0.018466495
GO:0002029	desensitization of G protein-coupled receptor signaling pathway	4/655	20/18862	0.004479165	0.01855313
GO:0002726	positive regulation of T cell cytokine production	4/655	20/18862	0.004479165	0.01855313
GO:0010878	cholesterol storage	4/655	20/18862	0.004479165	0.01855313
GO:0022401	negative adaptation of signaling pathway	4/655	20/18862	0.004479165	0.01855313

GO:0034104	negative regulation of tissue remodeling	4/655	20/18862	0.004479165	0.01855313
GO:0043011	myeloid dendritic cell differentiation	4/655	20/18862	0.004479165	0.01855313
GO:0043373	CD4-positive, alpha-beta T cell lineage commitment	4/655	20/18862	0.004479165	0.01855313
GO:0043901	negative regulation of multi-organism process	4/655	20/18862	0.004479165	0.01855313
GO:0044342	type B pancreatic cell proliferation	4/655	20/18862	0.004479165	0.01855313
GO:0046597	negative regulation of viral entry into host cell	4/655	20/18862	0.004479165	0.01855313
GO:0140131	positive regulation of lymphocyte chemotaxis	4/655	20/18862	0.004479165	0.01855313
GO:0031128	developmental induction	5/655	32/18862	0.004601555	0.018992612
GO:0035767	endothelial cell chemotaxis	5/655	32/18862	0.004601555	0.018992612
GO:0045648	positive regulation of erythrocyte differentiation	5/655	32/18862	0.004601555	0.018992612
GO:0098751	bone cell development	5/655	32/18862	0.004601555	0.018992612
GO:0010518	positive regulation of phospholipase activity	7/655	60/18862	0.004616278	0.01900293
GO:0040014	regulation of multicellular organism growth	7/655	60/18862	0.004616278	0.01900293
GO:0046888	negative regulation of hormone secretion	7/655	60/18862	0.004616278	0.01900293
GO:0045638	negative regulation of myeloid cell differentiation	9/655	92/18862	0.004651887	0.01913263
GO:0038127	ERBB signaling pathway	12/655	145/18862	0.004714733	0.019374023
GO:0071496	cellular response to external stimulus	20/655	303/18862	0.004739294	0.019457804
GO:0032409	regulation of transporter activity	19/655	283/18862	0.00486534	0.019957738
GO:0101023	vascular endothelial cell proliferation	6/655	46/18862	0.004922961	0.020158641
GO:1905562	regulation of vascular endothelial cell proliferation	6/655	46/18862	0.004922961	0.020158641
GO:0051153	regulation of striated muscle cell differentiation	9/655	93/18862	0.004996083	0.020440117
GO:0070542	response to fatty acid	7/655	61/18862	0.005062219	0.020692541
GO:0003203	endocardial cushion morphogenesis	5/655	33/18862	0.005271136	0.021377893
GO:0003298	physiological muscle hypertrophy	5/655	33/18862	0.005271136	0.021377893
GO:0003301	physiological cardiac muscle hypertrophy	5/655	33/18862	0.005271136	0.021377893

GO:0032941	secretion by tissue	5/655	33/18862	0.005271136	0.021377893
GO:0034368	protein-lipid complex remodeling	5/655	33/18862	0.005271136	0.021377893
GO:0034369	plasma lipoprotein particle remodeling	5/655	33/18862	0.005271136	0.021377893
GO:0035025	positive regulation of Rho protein signal transduction	5/655	33/18862	0.005271136	0.021377893
GO:0061049	cell growth involved in cardiac muscle cell development	5/655	33/18862	0.005271136	0.021377893
GO:0072538	T-helper 17 type immune response	5/655	33/18862	0.005271136	0.021377893
GO:0050714	positive regulation of protein secretion	11/655	129/18862	0.005343306	0.021651765
GO:0002363	alpha-beta T cell lineage commitment	4/655	21/18862	0.005383203	0.02170031
GO:0003177	pulmonary valve development	4/655	21/18862	0.005383203	0.02170031
GO:0023058	adaptation of signaling pathway	4/655	21/18862	0.005383203	0.02170031
GO:0036303	lymph vessel morphogenesis	4/655	21/18862	0.005383203	0.02170031
GO:0072574	hepatocyte proliferation	4/655	21/18862	0.005383203	0.02170031
GO:0072575	epithelial cell proliferation involved in liver morphogenesis	4/655	21/18862	0.005383203	0.02170031
GO:0004955	prostaglandin receptor activity	3/606	10/18337	0.003622301	0.021804143
GO:0005031	tumor necrosis factor-activated receptor activity	3/606	10/18337	0.003622301	0.021804143
GO:0017002	activin-activated receptor activity	3/606	10/18337	0.003622301	0.021804143
GO:0010951	negative regulation of endopeptidase activity	17/655	245/18862	0.00543813	0.021902795
GO:0030574	collagen catabolic process	6/655	47/18862	0.005481329	0.02201974
GO:0045646	regulation of erythrocyte differentiation	6/655	47/18862	0.005481329	0.02201974
GO:1903587	regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	6/655	47/18862	0.005481329	0.02201974
GO:0006027	glycosaminoglycan catabolic process	7/655	62/18862	0.005539761	0.022158195
GO:0050792	regulation of viral process	14/655	186/18862	0.005552025	0.022158195
GO:0001787	natural killer cell proliferation	3/655	11/18862	0.005582307	0.022158195
GO:0010739	positive regulation of protein kinase A signaling	3/655	11/18862	0.005582307	0.022158195
GO:0030157	pancreatic juice secretion	3/655	11/18862	0.005582307	0.022158195

GO:0034145	positive regulation of toll-like receptor 4 signaling pathway	3/655	11/18862	0.005582307	0.022158195
GO:0035747	natural killer cell chemotaxis	3/655	11/18862	0.005582307	0.022158195
GO:0036363	transforming growth factor beta activation	3/655	11/18862	0.005582307	0.022158195
GO:0045348	positive regulation of MHC class II biosynthetic process	3/655	11/18862	0.005582307	0.022158195
GO:0097048	dendritic cell apoptotic process	3/655	11/18862	0.005582307	0.022158195
GO:0098883	synapse pruning	3/655	11/18862	0.005582307	0.022158195
GO:1902287	semaphorin-plexin signaling pathway involved in axon guidance	3/655	11/18862	0.005582307	0.022158195
GO:2000668	regulation of dendritic cell apoptotic process	3/655	11/18862	0.005582307	0.022158195
GO:2000826	regulation of heart morphogenesis	3/655	11/18862	0.005582307	0.022158195
GO:0001972	retinoic acid binding	4/606	20/18337	0.003752201	0.022368888
GO:0001569	branching involved in blood vessel morphogenesis	5/655	34/18862	0.00600677	0.023746142
GO:0002756	MyD88-independent toll-like receptor signaling pathway	5/655	34/18862	0.00600677	0.023746142
GO:0044319	wound healing, spreading of cells	5/655	34/18862	0.00600677	0.023746142
GO:0090505	epiboly involved in wound healing	5/655	34/18862	0.00600677	0.023746142
GO:0022898	regulation of transmembrane transporter activity	18/655	268/18862	0.006007815	0.023746142
GO:0015844	monoamine transport	8/655	79/18862	0.006053228	0.023885155
GO:0030104	water homeostasis	8/655	79/18862	0.006053228	0.023885155
GO:0002762	negative regulation of myeloid leukocyte differentiation	6/655	48/18862	0.006084616	0.023968453
GO:0014009	glial cell proliferation	6/655	48/18862	0.006084616	0.023968453
GO:0060541	respiratory system development	14/655	188/18862	0.006090175	0.023970106
GO:1901184	regulation of ERBB signaling pathway	9/655	96/18862	0.006148127	0.024177794
GO:0002223	stimulatory C-type lectin receptor signaling pathway	10/655	114/18862	0.006358315	0.024962272
GO:0003231	cardiac ventricle development	10/655	114/18862	0.006358315	0.024962272
GO:0010888	negative regulation of lipid storage	4/655	22/18862	0.006401471	0.025005413
GO:0043369	CD4-positive or CD8-positive, alpha-beta T cell lineage commitment	4/655	22/18862	0.006401471	0.025005413

GO:0045624	positive regulation of T-helper cell differentiation	4/655	22/18862	0.006401471	0.025005413
GO:0072576	liver morphogenesis	4/655	22/18862	0.006401471	0.025005413
GO:1903589	positive regulation of blood vessel endothelial cell proliferation involved in sprouting angiogenesis	4/655	22/18862	0.006401471	0.025005413
GO:2000725	regulation of cardiac muscle cell differentiation	4/655	22/18862	0.006401471	0.025005413
GO:0032677	regulation of interleukin-8 production	9/655	97/18862	0.006574356	0.025659243
GO:0007160	cell-matrix adhesion	16/655	230/18862	0.00671347	0.026180289
GO:0032330	regulation of chondrocyte differentiation	6/655	49/18862	0.006734822	0.026197839
GO:0032692	negative regulation of interleukin-1 production	6/655	49/18862	0.006734822	0.026197839
GO:0072132	mesenchyme morphogenesis	6/655	49/18862	0.006734822	0.026197839
GO:0001848	complement binding	4/606	21/18337	0.004515511	0.026411481
GO:0051428	peptide hormone receptor binding	4/606	21/18337	0.004515511	0.026411481
GO:0034367	protein-containing complex remodeling	5/655	35/18862	0.006811706	0.026430778
GO:0090504	epiboly	5/655	35/18862	0.006811706	0.026430778
GO:0097009	energy homeostasis	5/655	35/18862	0.006811706	0.026430778
GO:0045824	negative regulation of innate immune response	7/655	65/18862	0.007175421	0.027795506
GO:0044409	entry into host	12/655	153/18862	0.007184479	0.027795506
GO:0110053	regulation of actin filament organization	18/655	273/18862	0.00722827	0.027795506
GO:0002002	regulation of angiotensin levels in blood	3/655	12/18862	0.007252815	0.027795506
GO:0002003	angiotensin maturation	3/655	12/18862	0.007252815	0.027795506
GO:0002863	positive regulation of inflammatory response to antigenic stimulus	3/655	12/18862	0.007252815	0.027795506
GO:0032908	regulation of transforming growth factor beta1 production	3/655	12/18862	0.007252815	0.027795506
GO:0035630	bone mineralization involved in bone maturation	3/655	12/18862	0.007252815	0.027795506
GO:0043380	regulation of memory T cell differentiation	3/655	12/18862	0.007252815	0.027795506
GO:0045989	positive regulation of striated muscle contraction	3/655	12/18862	0.007252815	0.027795506
GO:0051549	positive regulation of keratinocyte migration	3/655	12/18862	0.007252815	0.027795506

GO:0070278	extracellular matrix constituent secretion	3/655	12/18862	0.007252815	0.027795506
GO:1900272	negative regulation of long-term synaptic potentiation	3/655	12/18862	0.007252815	0.027795506
GO:2000727	positive regulation of cardiac muscle cell differentiation	3/655	12/18862	0.007252815	0.027795506
GO:2001204	regulation of osteoclast development	3/655	12/18862	0.007252815	0.027795506
GO:0043254	regulation of protein-containing complex assembly	26/655	446/18862	0.007259775	0.027799335
GO:0004954	prostanoid receptor activity	3/606	11/18337	0.004859243	0.027895651
GO:0019864	IgG binding	3/606	11/18337	0.004859243	0.027895651
GO:0007623	circadian rhythm	15/655	212/18862	0.007328814	0.028017696
GO:0008406	gonad development	15/655	212/18862	0.007328814	0.028017696
GO:0002931	response to ischemia	6/655	50/18862	0.007433935	0.028349856
GO:0032648	regulation of interferon-beta production	6/655	50/18862	0.007433935	0.028349856
GO:0045744	negative regulation of G protein-coupled receptor signaling pathway	6/655	50/18862	0.007433935	0.028349856
GO:0051384	response to glucocorticoid	11/655	135/18862	0.007470317	0.028465325
GO:0043279	response to alkaloid	9/655	99/18862	0.007494511	0.028534204
GO:0002438	acute inflammatory response to antigenic stimulus	4/655	23/18862	0.007539778	0.028566633
GO:0010738	regulation of protein kinase A signaling	4/655	23/18862	0.007539778	0.028566633
GO:0071157	negative regulation of cell cycle arrest	4/655	23/18862	0.007539778	0.028566633
GO:0071676	negative regulation of mononuclear cell migration	4/655	23/18862	0.007539778	0.028566633
GO:1904385	cellular response to angiotensin	4/655	23/18862	0.007539778	0.028566633
GO:1904754	positive regulation of vascular associated smooth muscle cell migration	4/655	23/18862	0.007539778	0.028566633
GO:0032715	negative regulation of interleukin-6 production	7/655	66/18862	0.007792806	0.029501338
GO:0050804	modulation of chemical synaptic transmission	24/655	405/18862	0.007978652	0.030180399
GO:0043027	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	4/606	22/18337	0.005376771	0.030583468
GO:0032092	positive regulation of protein binding	8/655	83/18862	0.008116972	0.030678733
GO:0052126	movement in host environment	13/655	175/18862	0.008203966	0.030982427

GO:0034394	protein localization to cell surface	7/655	67/18862	0.008448517	0.031828662
GO:0072078	nephron tubule morphogenesis	7/655	67/18862	0.008448517	0.031828662
GO:1905953	negative regulation of lipid localization	7/655	67/18862	0.008448517	0.031828662
GO:0014812	muscle cell migration	9/655	101/18862	0.00850985	0.032033852
GO:0050868	negative regulation of T cell activation	10/655	119/18862	0.008530604	0.032086077
GO:0010737	protein kinase A signaling	5/655	37/18862	0.008642147	0.032479432
GO:0061351	neural precursor cell proliferation	11/655	138/18862	0.008755571	0.032821717
GO:0072006	nephron development	11/655	138/18862	0.008755571	0.032821717
GO:0002418	immune response to tumor cell	4/655	24/18862	0.008803595	0.032821717
GO:0003272	endocardial cushion formation	4/655	24/18862	0.008803595	0.032821717
GO:0010804	negative regulation of tumor necrosis factor-mediated signaling pathway	4/655	24/18862	0.008803595	0.032821717
GO:0014829	vascular associated smooth muscle contraction	4/655	24/18862	0.008803595	0.032821717
GO:0060396	growth hormone receptor signaling pathway	4/655	24/18862	0.008803595	0.032821717
GO:1905523	positive regulation of macrophage migration	4/655	24/18862	0.008803595	0.032821717
GO:1905564	positive regulation of vascular endothelial cell proliferation	4/655	24/18862	0.008803595	0.032821717
GO:2001026	regulation of endothelial cell chemotaxis	4/655	24/18862	0.008803595	0.032821717
GO:0016860	intramolecular oxidoreductase activity	6/606	50/18337	0.005874331	0.033109865
GO:0050708	regulation of protein secretion	18/655	279/18862	0.008949884	0.033340463
GO:0002886	regulation of myeloid leukocyte mediated immunity	6/655	52/18862	0.008986756	0.033392439
GO:0032608	interferon-beta production	6/655	52/18862	0.008986756	0.033392439
GO:0051155	positive regulation of striated muscle cell differentiation	6/655	52/18862	0.008986756	0.033392439
GO:0045137	development of primary sexual characteristics	15/655	217/18862	0.008992475	0.033392439
GO:0006026	aminoglycan catabolic process	7/655	68/18862	0.009143893	0.033584046
GO:0043507	positive regulation of JUN kinase activity	7/655	68/18862	0.009143893	0.033584046
GO:0045685	regulation of glial cell differentiation	7/655	68/18862	0.009143893	0.033584046

GO:0051937	catecholamine transport	7/655	68/18862	0.009143893	0.033584046
GO:0002430	complement receptor mediated signaling pathway	3/655	13/18862	0.009188088	0.033584046
GO:0002921	negative regulation of humoral immune response	3/655	13/18862	0.009188088	0.033584046
GO:0032274	gonadotropin secretion	3/655	13/18862	0.009188088	0.033584046
GO:0032905	transforming growth factor beta1 production	3/655	13/18862	0.009188088	0.033584046
GO:0043379	memory T cell differentiation	3/655	13/18862	0.009188088	0.033584046
GO:0045472	response to ether	3/655	13/18862	0.009188088	0.033584046
GO:0045741	positive regulation of epidermal growth factor-activated receptor activity	3/655	13/18862	0.009188088	0.033584046
GO:0050872	white fat cell differentiation	3/655	13/18862	0.009188088	0.033584046
GO:0055057	neuroblast division	3/655	13/18862	0.009188088	0.033584046
GO:0060347	heart trabecula formation	3/655	13/18862	0.009188088	0.033584046
GO:0060841	venous blood vessel development	3/655	13/18862	0.009188088	0.033584046
GO:0071285	cellular response to lithium ion	3/655	13/18862	0.009188088	0.033584046
GO:0071635	negative regulation of transforming growth factor beta production	3/655	13/18862	0.009188088	0.033584046
GO:1902285	semaphorin-plexin signaling pathway involved in neuron projection guidance	3/655	13/18862	0.009188088	0.033584046
GO:1902947	regulation of tau-protein kinase activity	3/655	13/18862	0.009188088	0.033584046
GO:1904995	negative regulation of leukocyte adhesion to vascular endothelial cell	3/655	13/18862	0.009188088	0.033584046
GO:0043394	proteoglycan binding	5/606	36/18337	0.006262175	0.033892837
GO:0004875	complement receptor activity	3/606	12/18337	0.006321315	0.033892837
GO:0005035	death receptor activity	3/606	12/18337	0.006321315	0.033892837
GO:0017154	semaphorin receptor activity	3/606	12/18337	0.006321315	0.033892837
GO:0089720	caspase binding	3/606	12/18337	0.006321315	0.033892837
GO:0009931	calcium-dependent protein serine/threonine kinase activity	4/606	23/18337	0.00634124	0.033892837
GO:0010810	regulation of cell-substrate adhesion	15/655	218/18862	0.009358558	0.034180356
GO:0009306	protein secretion	22/655	367/18862	0.009513337	0.034718468

GO:0010811	positive regulation of cell-substrate adhesion	10/655	121/18862	0.009543511	0.034774169
GO:0034101	erythrocyte homeostasis	10/655	121/18862	0.009543511	0.034774169
GO:0032637	interleukin-8 production	9/655	103/18862	0.009626322	0.035032578
GO:2000241	regulation of reproductive process	12/655	159/18862	0.009629452	0.035032578
GO:0097242	amyloid-beta clearance	5/655	38/18862	0.009673789	0.035166446
GO:0045861	negative regulation of proteolysis	21/655	346/18862	0.009763052	0.035463298
GO:0035592	establishment of protein localization to extracellular region	22/655	368/18862	0.009799929	0.035569546
GO:0007369	gastrulation	13/655	179/18862	0.009819735	0.035613719
GO:0001541	ovarian follicle development	6/655	53/18862	0.009844344	0.035647531
GO:0010332	response to gamma radiation	6/655	53/18862	0.009844344	0.035647531
GO:0072088	nephron epithelium morphogenesis	7/655	69/18862	0.009880268	0.035749859
GO:0019218	regulation of steroid metabolic process	10/655	122/18862	0.010083173	0.036455749
GO:0001562	response to protozoan	4/655	25/18862	0.010198044	0.036586485
GO:0031664	regulation of lipopolysaccharide-mediated signaling pathway	4/655	25/18862	0.010198044	0.036586485
GO:0033622	integrin activation	4/655	25/18862	0.010198044	0.036586485
GO:0035902	response to immobilization stress	4/655	25/18862	0.010198044	0.036586485
GO:0042730	fibrinolysis	4/655	25/18862	0.010198044	0.036586485
GO:0042832	defense response to protozoan	4/655	25/18862	0.010198044	0.036586485
GO:0051873	killing by host of symbiont cells	4/655	25/18862	0.010198044	0.036586485
GO:0071378	cellular response to growth hormone stimulus	4/655	25/18862	0.010198044	0.036586485
GO:0072012	glomerulus vasculature development	4/655	25/18862	0.010198044	0.036586485
GO:0072202	cell differentiation involved in metanephros development	4/655	25/18862	0.010198044	0.036586485
GO:0062013	positive regulation of small molecule metabolic process	11/655	141/18862	0.010205621	0.036586485
GO:0005504	fatty acid binding	5/606	37/18337	0.007047909	0.037060681
GO:0005518	collagen binding	7/606	68/18337	0.007053484	0.037060681

GO:0019058	viral life cycle	21/655	348/18862	0.010375879	0.037168278
GO:0055067	monovalent inorganic cation homeostasis	12/655	161/18862	0.010573909	0.03784859
GO:0007498	mesoderm development	10/655	123/18862	0.010645762	0.03807656
GO:0010676	positive regulation of cellular carbohydrate metabolic process	6/655	54/18862	0.01075859	0.038375669
GO:0046622	positive regulation of organ growth	6/655	54/18862	0.01075859	0.038375669
GO:0002701	negative regulation of production of molecular mediator of immune response	5/655	39/18862	0.010786986	0.038375669
GO:0044058	regulation of digestive system process	5/655	39/18862	0.010786986	0.038375669
GO:0072210	metanephric nephron development	5/655	39/18862	0.010786986	0.038375669
GO:1905521	regulation of macrophage migration	5/655	39/18862	0.010786986	0.038375669
GO:2001222	regulation of neuron migration	5/655	39/18862	0.010786986	0.038375669
GO:0010857	calcium-dependent protein kinase activity	4/606	24/18337	0.007413922	0.038627155
GO:0007179	transforming growth factor beta receptor signaling pathway	14/655	202/18862	0.011128641	0.039560961
GO:0002864	regulation of acute inflammatory response to antigenic stimulus	3/655	14/18862	0.011396115	0.040266273
GO:0010872	regulation of cholesterol esterification	3/655	14/18862	0.011396115	0.040266273
GO:0010935	regulation of macrophage cytokine production	3/655	14/18862	0.011396115	0.040266273
GO:0032966	negative regulation of collagen biosynthetic process	3/655	14/18862	0.011396115	0.040266273
GO:0035437	maintenance of protein localization in endoplasmic reticulum	3/655	14/18862	0.011396115	0.040266273
GO:0036295	cellular response to increased oxygen levels	3/655	14/18862	0.011396115	0.040266273
GO:0051547	regulation of keratinocyte migration	3/655	14/18862	0.011396115	0.040266273
GO:0090715	immunological memory formation process	3/655	14/18862	0.011396115	0.040266273
GO:0032024	positive regulation of insulin secretion	7/655	71/18862	0.011481294	0.040414155
GO:0032720	negative regulation of tumor necrosis factor production	7/655	71/18862	0.011481294	0.040414155
GO:0061333	renal tubule morphogenesis	7/655	71/18862	0.011481294	0.040414155
GO:0072028	nephron morphogenesis	7/655	71/18862	0.011481294	0.040414155
GO:0098586	cellular response to virus	7/655	71/18862	0.011481294	0.040414155

GO:0007229	integrin-mediated signaling pathway	9/655	106/18862	0.011503723	0.040432076
GO:0048259	regulation of receptor-mediated endocytosis	9/655	106/18862	0.011503723	0.040432076
GO:0046890	regulation of lipid biosynthetic process	14/655	203/18862	0.011585643	0.040658719
GO:1902905	positive regulation of supramolecular fiber organization	14/655	203/18862	0.011585643	0.040658719
GO:0016799	hydrolase activity, hydrolyzing N-glycosyl compounds	5/606	38/18337	0.007899952	0.040747562
GO:0036122	BMP binding	3/606	13/18337	0.008018069	0.040747562
GO:0061783	peptidoglycan muralytic activity	3/606	13/18337	0.008018069	0.040747562
GO:0001945	lymph vessel development	4/655	26/18862	0.011727881	0.040801688
GO:0010460	positive regulation of heart rate	4/655	26/18862	0.011727881	0.040801688
GO:0021772	olfactory bulb development	4/655	26/18862	0.011727881	0.040801688
GO:0042104	positive regulation of activated T cell proliferation	4/655	26/18862	0.011727881	0.040801688
GO:0048520	positive regulation of behavior	4/655	26/18862	0.011727881	0.040801688
GO:0060142	regulation of syncytium formation by plasma membrane fusion	4/655	26/18862	0.011727881	0.040801688
GO:0061437	renal system vasculature development	4/655	26/18862	0.011727881	0.040801688
GO:0061440	kidney vasculature development	4/655	26/18862	0.011727881	0.040801688
GO:0098868	bone growth	4/655	26/18862	0.011727881	0.040801688
GO:1900746	regulation of vascular endothelial growth factor signaling pathway	4/655	26/18862	0.011727881	0.040801688
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	6/655	55/18862	0.01173136	0.040801688
GO:1903428	positive regulation of reactive oxygen species biosynthetic process	6/655	55/18862	0.01173136	0.040801688
GO:0150077	regulation of neuroinflammatory response	5/655	40/18862	0.011984571	0.041651296
GO:0071692	protein localization to extracellular region	22/655	375/18862	0.0120071	0.041698522
GO:0051052	regulation of DNA metabolic process	21/655	353/18862	0.012044011	0.041795586
GO:0019935	cyclic-nucleotide-mediated signaling	8/655	89/18862	0.012146004	0.042086895
GO:0051149	positive regulation of muscle cell differentiation	8/655	89/18862	0.012146004	0.042086895
GO:1903036	positive regulation of response to wounding	7/655	72/18862	0.012348556	0.042756991

GO:1903169	regulation of calcium ion transmembrane transport	11/655	145/18862	0.012417816	0.042964907
GO:0007584	response to nutrient	12/655	165/18862	0.01267623	0.043826491
GO:0021872	forebrain generation of neurons	6/655	56/18862	0.012764481	0.044066278
GO:0060135	maternal process involved in female pregnancy	6/655	56/18862	0.012764481	0.044066278
GO:0071456	cellular response to hypoxia	14/655	206/18862	0.013044801	0.045000704
GO:0048469	cell maturation	12/655	166/18862	0.013248629	0.045640021
GO:0060193	positive regulation of lipase activity	7/655	73/18862	0.013262033	0.045640021
GO:0046596	regulation of viral entry into host cell	5/655	41/18862	0.013269269	0.045640021
GO:0050691	regulation of defense response to virus by host	5/655	41/18862	0.013269269	0.045640021
GO:0003401	axis elongation	4/655	27/18862	0.013397492	0.04584439
GO:0010758	regulation of macrophage chemotaxis	4/655	27/18862	0.013397492	0.04584439
GO:0010818	T cell chemotaxis	4/655	27/18862	0.013397492	0.04584439
GO:0032967	positive regulation of collagen biosynthetic process	4/655	27/18862	0.013397492	0.04584439
GO:0034123	positive regulation of toll-like receptor signaling pathway	4/655	27/18862	0.013397492	0.04584439
GO:0045671	negative regulation of osteoclast differentiation	4/655	27/18862	0.013397492	0.04584439
GO:0051883	killing of cells in other organism involved in symbiotic interaction	4/655	27/18862	0.013397492	0.04584439
GO:0030301	cholesterol transport	9/655	109/18862	0.013642252	0.046647699
GO:0050840	extracellular matrix binding	6/606	55/18337	0.009334619	0.047052551
GO:0055008	cardiac muscle tissue morphogenesis	6/655	57/18862	0.01385974	0.047057031
GO:0010713	negative regulation of collagen metabolic process	3/655	15/18862	0.013883035	0.047057031
GO:0010838	positive regulation of keratinocyte proliferation	3/655	15/18862	0.013883035	0.047057031
GO:0010934	macrophage cytokine production	3/655	15/18862	0.013883035	0.047057031
GO:0045579	positive regulation of B cell differentiation	3/655	15/18862	0.013883035	0.047057031
GO:0048532	anatomical structure arrangement	3/655	15/18862	0.013883035	0.047057031
GO:0055091	phospholipid homeostasis	3/655	15/18862	0.013883035	0.047057031

GO:0072224	metanephric glomerulus development	3/655	15/18862	0.013883035	0.047057031
GO:1900225	regulation of NLRP3 inflammasome complex assembly	3/655	15/18862	0.013883035	0.047057031
GO:2000345	regulation of hepatocyte proliferation	3/655	15/18862	0.013883035	0.047057031
GO:2001028	positive regulation of endothelial cell chemotaxis	3/655	15/18862	0.013883035	0.047057031
GO:2001224	positive regulation of neuron migration	3/655	15/18862	0.013883035	0.047057031
GO:0042593	glucose homeostasis	15/655	229/18862	0.014213085	0.04814076
GO:0003707	steroid hormone receptor activity	4/606	26/18337	0.009902549	0.048610611
GO:0005041	low-density lipoprotein particle receptor activity	3/606	14/18337	0.009957335	0.048610611
GO:0005172	vascular endothelial growth factor receptor binding	3/606	14/18337	0.009957335	0.048610611
GO:0044548	S100 protein binding	3/606	14/18337	0.009957335	0.048610611
GO:0045309	protein phosphorylated amino acid binding	6/606	56/18337	0.010170671	0.048886424
GO:0019903	protein phosphatase binding	11/606	148/18337	0.01017153	0.048886424
GO:0051702	biological process involved in interaction with symbiont	8/655	92/18862	0.014637297	0.049527309
GO:0045687	positive regulation of glial cell differentiation	5/655	42/18862	0.014643688	0.049527309
GO:0033500	carbohydrate homeostasis	15/655	230/18862	0.014736314	0.049804468