

ONTOLOG ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:003015 extracellular matrix	127/1638	368/18670	3.45E-44	9.98E-41	7.65E-41	A2M/AEBF	127
BP	GO:004306 extracellular matrix	137/1638	422/18670	3.78E-44	9.98E-41	7.65E-41	A2M/AEBF	137
BP	GO:000695 humoral immune response	88/1638	356/18670	1.36E-19	2.38E-16	1.83E-16	A2M/BPI/S	88
BP	GO:007237 protein activation	57/1638	198/18670	2.72E-16	3.59E-13	2.75E-13	A2M/APOI	57
BP	GO:007026 cornification	41/1638	112/18670	4.14E-16	4.37E-13	3.35E-13	CSTA/DSC	41
BP	GO:000693 muscle contraction	79/1638	360/18670	1.33E-14	1.17E-11	8.97E-12	ACTA2/AC	79
BP	GO:000695 complement activation	50/1638	175/18670	2.56E-14	1.93E-11	1.48E-11	A2M/SERP	50
BP	GO:000252 acute inflammation	57/1638	220/18670	4.34E-14	2.86E-11	2.20E-11	A2M/ADC	57
BP	GO:004358 skin development	86/1638	419/18670	5.24E-14	3.07E-11	2.35E-11	COL1A1/C	86
BP	GO:003563 multicellular organismal process	54/1638	204/18670	7.81E-14	4.12E-11	3.16E-11	ANK2/ATP	54
BP	GO:000301 muscle system process	91/1638	465/18670	1.81E-13	8.67E-11	6.65E-11	ACTA2/AC	91
BP	GO:005148 regulation of gene expression	76/1638	357/18670	2.25E-13	9.87E-11	7.57E-11	ADCY5/AC	76
BP	GO:003142 keratinization	56/1638	224/18670	3.65E-13	1.48E-10	1.14E-10	CSTA/DSC	56
BP	GO:003021 keratinocyte differentiation	68/1638	305/18670	4.27E-13	1.53E-10	1.17E-10	CSTA/CTSI	68
BP	GO:000720 positive regulation of gene expression	70/1638	319/18670	4.35E-13	1.53E-10	1.17E-10	ADCY5/AC	70
BP	GO:000150 ossification	81/1638	398/18670	4.63E-13	1.53E-10	1.17E-10	AHSG/BMI	81
BP	GO:003158 cell-substrate adhesion	74/1638	354/18670	1.21E-12	3.76E-10	2.88E-10	ACTN2/AP	74
BP	GO:006142 connective tissue	62/1638	273/18670	1.98E-12	5.81E-10	4.46E-10	ACTA2/AN	62
BP	GO:000292 regulation of gene expression	40/1638	134/18670	2.10E-12	5.83E-10	4.47E-10	A2M/SERP	40
BP	GO:000751 muscle organ process	81/1638	410/18670	2.37E-12	6.25E-10	4.80E-10	ACTC1/AD	81
BP	GO:000267 regulation of gene expression	44/1638	159/18670	3.04E-12	7.40E-10	5.67E-10	A2M/ADC	44
BP	GO:005121 cartilage development	52/1638	209/18670	3.09E-12	7.40E-10	5.67E-10	ANXA6/NH	52
BP	GO:000687 cellular calcium ion transport	87/1638	458/18670	3.41E-12	7.83E-10	6.01E-10	ADCY5/AC	87
BP	GO:000695 complement activation	40/1638	137/18670	4.59E-12	9.83E-10	7.54E-10	SERPING1/	40
BP	GO:005090 leukocyte chemotaxis	92/1638	499/18670	4.66E-12	9.83E-10	7.54E-10	ADD2/APC	92
BP	GO:007250 cellular division	91/1638	493/18670	5.71E-12	1.16E-09	8.88E-10	ADCY5/AC	91
BP	GO:000991 epidermal cell differentiation	73/1638	358/18670	6.07E-12	1.17E-09	8.95E-10	CSTA/CTSI	73
BP	GO:000245 humoral immune response	42/1638	150/18670	6.20E-12	1.17E-09	8.95E-10	SERPING1/	42
BP	GO:005507 calcium ion transport	88/1638	471/18670	6.53E-12	1.19E-09	9.11E-10	ADCY5/AC	88
BP	GO:190352 regulation of gene expression	64/1638	297/18670	1.02E-11	1.80E-09	1.38E-09	AGTR1/AG	64
BP	GO:000854 epidermis	86/1638	464/18670	1.77E-11	3.01E-09	2.31E-09	CSTA/CCN	86
BP	GO:003042 regulation of gene expression	35/1638	115/18670	2.71E-11	4.46E-09	3.42E-09	A2M/SERP	35
BP	GO:003015 collagen fibrillogenesis	23/1638	54/18670	3.18E-11	5.09E-09	3.90E-09	AEBP1/CO	23
BP	GO:200025 regulation of gene expression	35/1638	116/18670	3.55E-11	5.51E-09	4.23E-09	A2M/SERP	35
BP	GO:006133 cardiac conduction	40/1638	146/18670	4.12E-11	6.21E-09	4.76E-09	ANK2/ATP	40
BP	GO:009872 cell-cell adhesion	59/1638	273/18670	5.81E-11	8.51E-09	6.53E-09	APOA1/CE	59
BP	GO:009917 regulation of gene expression	81/1638	437/18670	6.88E-11	9.81E-09	7.52E-09	ADCYAP1/	81
BP	GO:006053 muscle tissue	77/1638	408/18670	8.42E-11	1.17E-08	8.97E-09	ACTC1/AC	77
BP	GO:009028 regulation of gene expression	61/1638	292/18670	1.20E-10	1.62E-08	1.24E-08	AGTR2/CA	61
BP	GO:000801 regulation of gene expression	55/1638	251/18670	1.49E-10	1.89E-08	1.45E-08	AGTR2/AN	55
BP	GO:005080 modulation of gene expression	80/1638	436/18670	1.51E-10	1.89E-08	1.45E-08	ADCYAP1/	80
BP	GO:004272 defense response	66/1638	330/18670	1.51E-10	1.89E-08	1.45E-08	ADGRB1/B	66
BP	GO:006002 heart contraction	59/1638	280/18670	1.69E-10	2.07E-08	1.59E-08	ACTC1/AG	59
BP	GO:000301 heart process	60/1638	290/18670	2.55E-10	3.05E-08	2.34E-08	ACTC1/AG	60
BP	GO:001812 peptide catabolism	23/1638	60/18670	4.08E-10	4.79E-08	3.67E-08	BGN/COL3	23
BP	GO:000716 cell-matrix adhesion	50/1638	225/18670	6.08E-10	6.97E-08	5.35E-08	ACTN2/AP	50
BP	GO:004239 regulation of gene expression	78/1638	434/18670	6.99E-10	7.82E-08	6.00E-08	ACTN2/AC	78
BP	GO:000257 platelet degranulation	35/1638	128/18670	7.12E-10	7.82E-08	6.00E-08	A2M/ACTI	35
BP	GO:001046 negative regulation of gene expression	55/1638	262/18670	8.09E-10	8.69E-08	6.66E-08	A2M/AHSC	55
BP	GO:001648 protein processing	64/1638	328/18670	8.24E-10	8.69E-08	6.66E-08	A2M/AEBF	64
BP	GO:000150 action potential	35/1638	133/18670	2.18E-09	2.25E-07	1.73E-07	ANK2/ATP	35
BP	GO:001470 striated muscle tissue	71/1638	390/18670	2.32E-09	2.35E-07	1.80E-07	ACTC1/AC	71
BP	GO:001993 second-messenger signaling	77/1638	439/18670	2.81E-09	2.79E-07	2.14E-07	ADCY2/AC	77
BP	GO:005080 synapse organization	73/1638	408/18670	3.01E-09	2.92E-07	2.24E-07	ADD2/ADG	73
BP	GO:007061 regulation of gene expression	42/1638	180/18670	3.05E-09	2.92E-07	2.24E-07	A2M/SERP	42
BP	GO:001095 negative regulation of gene expression	52/1638	250/18670	3.26E-09	3.07E-07	2.35E-07	A2M/AHSC	52
BP	GO:001095 regulation of gene expression	71/1638	394/18670	3.63E-09	3.36E-07	2.58E-07	ACTN2/AC	71
BP	GO:190331 regulation of gene expression	42/1638	182/18670	4.33E-09	3.94E-07	3.02E-07	A2M/SERP	42
BP	GO:004576 regulation of gene expression	69/1638	383/18670	6.09E-09	5.44E-07	4.18E-07	AGTR1/AP	69
BP	GO:000691 phagocytosis	26/1638	84/18670	6.35E-09	5.59E-07	4.28E-07	ADGRB1/C	26
BP	GO:001081 regulation of gene expression	46/1638	215/18670	1.04E-08	8.97E-07	6.88E-07	APOA1/AF	46

BP	GO:005072	regulation	81/1638	485/18670	1.11E-08	9.40E-07	7.21E-07	A2M/ADC	81
BP	GO:001973	antimicrob	32/1638	122/18670	1.15E-08	9.61E-07	7.37E-07	BPI/CTSG/	32
BP	GO:000206	chondrocy	32/1638	123/18670	1.42E-08	1.17E-06	8.99E-07	ANXA6/NH	32
BP	GO:004269	muscle cel	68/1638	385/18670	1.78E-08	1.45E-06	1.11E-06	ACTC1/AC	68
BP	GO:000761	learning or	51/1638	256/18670	2.09E-08	1.67E-06	1.28E-06	ATP1A2/A	51
BP	GO:000717	transmemt	63/1638	349/18670	2.57E-08	2.02E-06	1.55E-06	AFP/BMP3	63
BP	GO:000758	digestion	34/1638	139/18670	2.73E-08	2.12E-06	1.63E-06	APOA1/AF	34
BP	GO:005089	cognition	56/1638	296/18670	2.89E-08	2.21E-06	1.69E-06	ATP1A2/A	56
BP	GO:006032	cell chemo	57/1638	304/18670	3.02E-08	2.28E-06	1.74E-06	AGTR1/CX	57
BP	GO:001081	positive re	31/1638	121/18670	3.51E-08	2.61E-06	2.00E-06	APOA1/CI	31
BP	GO:000164	osteoblast	46/1638	225/18670	4.50E-08	3.30E-06	2.53E-06	BMP3/COI	46
BP	GO:007025	actin-med	30/1638	116/18670	4.62E-08	3.32E-06	2.54E-06	ACTC1/AC	30
BP	GO:001606	immunogk	45/1638	218/18670	4.66E-08	3.32E-06	2.54E-06	SERPING1,	45
BP	GO:000681	potassium	48/1638	240/18670	4.75E-08	3.32E-06	2.54E-06	ACTN2/AC	48
BP	GO:005085	B cell rece	32/1638	129/18670	4.87E-08	3.32E-06	2.54E-06	BLK/CD19,	32
BP	GO:000740	axonogen	77/1638	468/18670	4.88E-08	3.32E-06	2.54E-06	APBB1/AD	77
BP	GO:003526	organ grov	43/1638	204/18670	4.90E-08	3.32E-06	2.54E-06	AGTR2/AN	43
BP	GO:006048	mesenchyr	53/1638	278/18670	5.18E-08	3.46E-06	2.65E-06	ACTA2/AC	53
BP	GO:190134	regulation	71/1638	422/18670	6.60E-08	4.35E-06	3.34E-06	AGTR1/AP	71
BP	GO:000691	phagocyto	30/1638	118/18670	7.01E-08	4.56E-06	3.50E-06	ADGRB1/C	30
BP	GO:001972	B cell med	45/1638	221/18670	7.13E-08	4.58E-06	3.52E-06	SERPING1,	45
BP	GO:000720	phospholi	27/1638	100/18670	8.19E-08	5.20E-06	3.99E-06	ACTN2/AC	27
BP	GO:000800	cell recogn	44/1638	215/18670	8.52E-08	5.35E-06	4.10E-06	ADGRB1/C	44
BP	GO:004327	positive re	52/1638	275/18670	9.10E-08	5.64E-06	4.33E-06	ACTN2/AC	52
BP	GO:007180	cellular po	44/1638	217/18670	1.13E-07	6.83E-06	5.24E-06	ACTN2/AN	44
BP	GO:007180	potassium	44/1638	217/18670	1.13E-07	6.83E-06	5.24E-06	ACTN2/AN	44
BP	GO:009752	myeloid le	43/1638	210/18670	1.17E-07	7.02E-06	5.38E-06	CALCA/CC	43
BP	GO:000176	morphoge	41/1638	196/18670	1.24E-07	7.33E-06	5.62E-06	AGTR2/AR	41
BP	GO:005114	striated m	54/1638	293/18670	1.25E-07	7.33E-06	5.62E-06	ACTC1/AC	54
BP	GO:000715	neuron cel	10/1638	16/18670	1.29E-07	7.46E-06	5.72E-06	CEL/NCAM	10
BP	GO:009009	regulation	47/1638	241/18670	1.44E-07	8.28E-06	6.35E-06	BMP3/CAV	47
BP	GO:190371	regulation	22/1638	73/18670	1.56E-07	8.85E-06	6.79E-06	ANK2/ATP	22
BP	GO:003433	cell junctio	53/1638	290/18670	2.16E-07	1.21E-05	9.28E-06	ACTN2/AN	53
BP	GO:000761	learning	33/1638	145/18670	2.71E-07	1.50E-05	1.15E-05	ATP1A2/A	33
BP	GO:000301	vascular pr	37/1638	173/18670	2.82E-07	1.54E-05	1.18E-05	ACTA2/AD	37
BP	GO:009028	negative re	36/1638	166/18670	2.83E-07	1.54E-05	1.18E-05	AGTR2/CA	36
BP	GO:005160	protein m	66/1638	397/18670	2.99E-07	1.61E-05	1.23E-05	A2M/AEBF	66
BP	GO:004566	regulation	30/1638	126/18670	3.32E-07	1.77E-05	1.36E-05	GDF10/GL	30
BP	GO:003027	regulation	41/1638	203/18670	3.37E-07	1.78E-05	1.36E-05	AHSG/COI	41
BP	GO:005090	leukocyte	112/1638	25/18670	3.52E-07	1.82E-05	1.40E-05	ADD2/CX3	12
BP	GO:009730	response t	45/1638	233/18670	3.53E-07	1.82E-05	1.40E-05	ACTC1/AD	45
BP	GO:190406	regulation	59/1638	342/18670	3.56E-07	1.82E-05	1.40E-05	ACTN2/AP	59
BP	GO:006111	morphoge	38/1638	182/18670	3.73E-07	1.89E-05	1.45E-05	AGTR2/AR	38
BP	GO:003476	regulation	76/1638	483/18670	3.79E-07	1.91E-05	1.46E-05	ACTN2/AP	76
BP	GO:009902	plasma me	30/1638	127/18670	3.99E-07	1.98E-05	1.52E-05	ADGRB1/C	30
BP	GO:005254	regulation	72/1638	452/18670	4.78E-07	2.35E-05	1.81E-05	A2M/AHSC	72
BP	GO:001092	cellular cor	28/1638	115/18670	4.97E-07	2.38E-05	1.83E-05	ACTC1/AC	28
BP	GO:001032	membrane	31/1638	135/18670	5.01E-07	2.38E-05	1.83E-05	ADGRB1/C	31
BP	GO:005092	positive re	31/1638	135/18670	5.01E-07	2.38E-05	1.83E-05	CCR4/CCR	31
BP	GO:009906	postsynap	13/1638	30/18670	5.01E-07	2.38E-05	1.83E-05	CBLN1/CEI	13
BP	GO:005500	muscle cel	38/1638	186/18670	6.64E-07	3.13E-05	2.40E-05	ACTC1/AC	38
BP	GO:009748	neuron pr	50/1638	277/18670	6.93E-07	3.24E-05	2.48E-05	CSF1R/EP	50
BP	GO:003032	lung devel	36/1638	172/18670	7.05E-07	3.26E-05	2.50E-05	CRH/CCN2	36
BP	GO:008606	cell comm	18/1638	56/18670	7.18E-07	3.28E-05	2.51E-05	ANK2/ATP	18
BP	GO:003515	regulation	32/1638	144/18670	7.21E-07	3.28E-05	2.51E-05	ACTA2/AD	32
BP	GO:006040	calcium ior	34/1638	158/18670	7.27E-07	3.28E-05	2.51E-05	ADCYAP1F	34
BP	GO:003055	leukocyte	43/1638	224/18670	7.57E-07	3.38E-05	2.59E-05	CXCR5/CA	43
BP	GO:005500	striated m	36/1638	173/18670	8.17E-07	3.62E-05	2.78E-05	ACTC1/AC	36
BP	GO:002261	extracellul	22/1638	80/18670	9.04E-07	3.97E-05	3.05E-05	A2M/CMA	22
BP	GO:001972	calcium-m	42/1638	218/18670	9.17E-07	4.00E-05	3.07E-05	AGTR1/AN	42
BP	GO:003025	intestinal c	9/1638	15/18670	9.26E-07	4.00E-05	3.07E-05	APOA1/AF	9
BP	GO:000244	lymphocyt	59/1638	352/18670	9.55E-07	4.09E-05	3.14E-05	SERPING1,	59

BP	GO:000246 adaptive ir	60/1638	361/18670	1.03E-06	4.39E-05	3.37E-05	SERPING1/	60
BP	GO:005507 sodium ior	17/1638	52/18670	1.11E-06	4.69E-05	3.60E-05	AGTR1/AC	17
BP	GO:008600 cardiac m	20/1638	69/18670	1.13E-06	4.73E-05	3.63E-05	ANK2/ATP	20
BP	GO:004424 lipid diges	10/1638	19/18670	1.16E-06	4.82E-05	3.69E-05	APOA1/AF	10
BP	GO:006054 respiratory	39/1638	198/18670	1.25E-06	5.14E-05	3.94E-05	ALDH1A3/	39
BP	GO:003032 respiratory	36/1638	176/18670	1.26E-06	5.14E-05	3.94E-05	CRH/CCN2	36
BP	GO:000741 synapse as	36/1638	177/18670	1.45E-06	5.86E-05	4.50E-05	ADD2/AD	36
BP	GO:000741 axon guid	49/1638	276/18670	1.47E-06	5.91E-05	4.54E-05	CSF1R/EP	49
BP	GO:003296 collagen r	27/1638	115/18670	1.70E-06	6.78E-05	5.20E-05	COL1A1/C	27
BP	GO:006040 cytosolic c	35/1638	171/18670	1.73E-06	6.85E-05	5.26E-05	ADCYAP1F	35
BP	GO:003529 regulation	31/1638	143/18670	1.87E-06	7.27E-05	5.57E-05	ACTA2/AD	31
BP	GO:005088 regulation	31/1638	143/18670	1.87E-06	7.27E-05	5.57E-05	ACTA2/AD	31
BP	GO:009774 regulation	31/1638	143/18670	1.87E-06	7.27E-05	5.57E-05	ACTA2/AD	31
BP	GO:008609 regulation	14/1638	38/18670	1.94E-06	7.48E-05	5.74E-05	ANK2/CAC	14
BP	GO:004244 hormone r	43/1638	232/18670	2.00E-06	7.64E-05	5.86E-05	ADH1B/AL	43
BP	GO:001610 diterpenoi	26/1638	110/18670	2.29E-06	8.70E-05	6.68E-05	ADH1B/AL	26
BP	GO:199086 response t	24/1638	97/18670	2.35E-06	8.79E-05	6.74E-05	CXCR5/CC	24
BP	GO:199086 cellular res	24/1638	97/18670	2.35E-06	8.79E-05	6.74E-05	CXCR5/CC	24
BP	GO:003004 actin filam	30/1638	138/18670	2.57E-06	9.44E-05	7.24E-05	ACTC1/AC	30
BP	GO:000152 retinoid m	25/1638	104/18670	2.57E-06	9.44E-05	7.24E-05	ADH1B/AL	25
BP	GO:004888 sensory sy	60/1638	371/18670	2.58E-06	9.44E-05	7.24E-05	ALDH1A3/	60
BP	GO:000694 striated m	35/1638	174/18670	2.63E-06	9.44E-05	7.24E-05	ACTC1/AN	35
BP	GO:000165 urogenital	55/1638	330/18670	2.64E-06	9.44E-05	7.24E-05	ACTA2/AG	55
BP	GO:004876 mesenchyr	41/1638	219/18670	2.64E-06	9.44E-05	7.24E-05	ANXA6/CC	41
BP	GO:004586 negative r	59/1638	363/18670	2.65E-06	9.44E-05	7.24E-05	A2M/AHSC	59
BP	GO:009030 positive re	18/1638	61/18670	2.90E-06	0.000103	7.87E-05	APOH/CD	18
BP	GO:000715 homophilic	34/1638	168/18670	3.15E-06	0.000111	8.49E-05	CDH9/CD	34
BP	GO:009010 negative r	28/1638	126/18670	3.49E-06	0.000122	9.35E-05	CAV1/CIDI	28
BP	GO:008600 cardiac m	17/1638	56/18670	3.54E-06	0.000123	9.42E-05	ANK2/CAC	17
BP	GO:000681 calcium ior	67/1638	434/18670	3.60E-06	0.000123	9.46E-05	ADCYAP1F	67
BP	GO:005067 epithelial c	67/1638	434/18670	3.60E-06	0.000123	9.46E-05	AGTR1/AP	67
BP	GO:003103 actomyosin	38/1638	199/18670	3.72E-06	0.000126	9.65E-05	ACTC1/AC	38
BP	GO:005196 regulation	25/1638	106/18670	3.72E-06	0.000126	9.65E-05	ADGRB1/A	25
BP	GO:008600 cardiac m	20/1638	74/18670	3.76E-06	0.000126	9.69E-05	ANK2/ATP	20
BP	GO:009885 intestinal li	9/1638	17/18670	3.82E-06	0.000128	9.78E-05	APOA1/AF	9
BP	GO:006103 negative r	12/1638	30/18670	3.86E-06	0.000128	9.82E-05	NKX3-2/C	12
BP	GO:002261 gland mor	27/1638	120/18670	4.04E-06	0.000133	0.000102	AR/CAV1/	27
BP	GO:007171 response t	34/1638	170/18670	4.14E-06	0.000135	0.000103	COMP/NK	34
BP	GO:007171 cellular res	34/1638	170/18670	4.14E-06	0.000135	0.000103	COMP/NK	34
BP	GO:004516 cell fate co	47/1638	270/18670	4.17E-06	0.000135	0.000104	AR/NKX2-	47
BP	GO:000690 phagocyto	59/1638	369/18670	4.50E-06	0.000145	0.000111	AHSG/APC	59
BP	GO:000693 regulation	34/1638	171/18670	4.74E-06	0.000152	0.000116	ANK2/AN	34
BP	GO:000202 regulation	24/1638	101/18670	5.03E-06	0.00016	0.000123	AGTR2/AN	24
BP	GO:007009 chemokine	22/1638	88/18670	5.10E-06	0.000161	0.000124	CXCR5/CC	22
BP	GO:004876 cardiac m	42/1638	233/18670	5.44E-06	0.000171	0.000131	ACTC1/AC	42
BP	GO:003432 cell junctio	43/1638	241/18670	5.54E-06	0.000173	0.000133	ACTN2/AN	43
BP	GO:190406 positive re	30/1638	144/18670	6.39E-06	0.000198	0.000152	ACTN2/AP	30
BP	GO:009886 bone grow	15/1638	47/18670	6.64E-06	0.000205	0.000157	ANXA6/CC	15
BP	GO:003476 positive re	38/1638	204/18670	6.83E-06	0.000209	0.000161	ACTN2/AP	38
BP	GO:000300 heart mor	45/1638	259/18670	6.97E-06	0.000211	0.000162	ACTC1/CC	45
BP	GO:009025 regulation	45/1638	259/18670	6.97E-06	0.000211	0.000162	ANK2/AN	45
BP	GO:015006 visual syste	58/1638	366/18670	7.15E-06	0.000215	0.000165	ALDH1A3/	58
BP	GO:000693 smooth m	25/1638	110/18670	7.53E-06	0.000226	0.000173	ACTA2/AT	25
BP	GO:005105 positive re	19/1638	71/18670	7.65E-06	0.000228	0.000175	ADCYAP1F	19
BP	GO:007200 renal syste	49/1638	293/18670	8.26E-06	0.000245	0.000188	ACTA2/AG	49
BP	GO:001923 sensory pe	24/1638	104/18670	8.62E-06	0.000254	0.000195	ADCYAP1/	24
BP	GO:006015 positive re	19/1638	72/18670	9.55E-06	0.000278	0.000213	ADCYAP1F	19
BP	GO:006103 regulation	19/1638	72/18670	9.55E-06	0.000278	0.000213	NKX3-2/C	19
BP	GO:001052 positive re	16/1638	54/18670	9.66E-06	0.00028	0.000215	ADCYAP1F	16
BP	GO:009755 calcium ior	29/1638	140/18670	1.02E-05	0.000293	0.000225	APLNR/AN	29
BP	GO:004870 skeletal sy	42/1638	239/18670	1.04E-05	0.000299	0.00023	ANXA6/N	42
BP	GO:005128 negative r	27/1638	126/18670	1.06E-05	0.000302	0.000232	APLNR/AN	27

BP	GO:200125 regulation	34/1638	178/18670	1.17E-05	0.000333	0.000255	ACTN2/AN	34
BP	GO:003023 myofibril a	19/1638	73/18670	1.19E-05	0.000334	0.000256	ACTC1/AC	19
BP	GO:005123 maintenanc	53/1638	330/18670	1.19E-05	0.000334	0.000256	APLNR/AN	53
BP	GO:004856 digestive ti	28/1638	134/18670	1.21E-05	0.000338	0.000259	NKX3-2/C	28
BP	GO:003090 forebrain c	59/1638	381/18670	1.23E-05	0.000341	0.000261	ADCYAP1/	59
BP	GO:000672 terpenoid	26/1638	120/18670	1.25E-05	0.000344	0.000264	ADH1B/AL	26
BP	GO:004512 cellular ext	17/1638	61/18670	1.27E-05	0.000349	0.000268	ADD2/CX3	17
BP	GO:005254 regulation	64/1638	425/18670	1.33E-05	0.000364	0.000279	A2M/AHSC	64
BP	GO:190004 regulation	20/1638	80/18670	1.35E-05	0.000368	0.000282	APOH/SER	20
BP	GO:000341 endochonch	14/1638	44/18670	1.40E-05	0.000378	0.00029	ANXA6/CC	14
BP	GO:000268 positive re	27/1638	128/18670	1.44E-05	0.000383	0.000294	CCR7/ELAI	27
BP	GO:005128 regulation	27/1638	128/18670	1.44E-05	0.000383	0.000294	APLNR/AN	27
BP	GO:200014 negative re	55/1638	349/18670	1.44E-05	0.000383	0.000294	AGTR2/AP	55
BP	GO:190303 positive re	19/1638	74/18670	1.47E-05	0.000388	0.000298	APOH/CD3	19
BP	GO:000689 receptor-n	51/1638	316/18670	1.50E-05	0.000397	0.000304	APOA1/AF	51
BP	GO:000170 endoderm	15/1638	50/18670	1.54E-05	0.000405	0.000311	COL4A2/C	15
BP	GO:005196 positive re	18/1638	68/18670	1.55E-05	0.000406	0.000311	ADGRB1/A	18
BP	GO:000341 growth pla	10/1638	24/18670	1.63E-05	0.000425	0.000326	ANXA6/CC	10
BP	GO:003033 negative re	53/1638	334/18670	1.68E-05	0.000435	0.000333	AGTR2/AP	53
BP	GO:000300 regionaliza	55/1638	351/18670	1.70E-05	0.000437	0.000335	AR/C3/NK	55
BP	GO:006053 cartilage m	11/1638	29/18670	1.79E-05	0.000458	0.000351	COL6A1/C	11
BP	GO:003598 endoderm	14/1638	45/18670	1.87E-05	0.000474	0.000363	COL4A2/C	14
BP	GO:006004 cardiac m	28/1638	137/18670	1.87E-05	0.000474	0.000363	ACTC1/AN	28
BP	GO:005196 regulation	22/1638	95/18670	1.90E-05	0.00048	0.000368	AGTR2/AT	22
BP	GO:000821 regulation	34/1638	182/18670	1.91E-05	0.000481	0.000369	ACTA2/AC	34
BP	GO:000718 adenylate	39/1638	221/18670	1.93E-05	0.000482	0.00037	ADCY2/AC	39
BP	GO:005076 positive re	69/1638	474/18670	1.96E-05	0.000483	0.00037	ADCYAP1/	69
BP	GO:001052 regulation	23/1638	102/18670	1.97E-05	0.000483	0.00037	ADCYAP1F	23
BP	GO:001583 amine tran	23/1638	102/18670	1.97E-05	0.000483	0.00037	AGTR2/AT	23
BP	GO:005192 positive re	26/1638	123/18670	1.98E-05	0.000483	0.00037	ADCYAP1F	26
BP	GO:007162 granulocyt	26/1638	123/18670	1.98E-05	0.000483	0.00037	CCR7/ITGA	26
BP	GO:000758 excretion	17/1638	63/18670	2.02E-05	0.000492	0.000377	AGTR1/AC	17
BP	GO:000182 kidney dev	46/1638	278/18670	2.04E-05	0.000493	0.000378	ACTA2/AC	46
BP	GO:009869 postsynapt	19/1638	20/18670	2.07E-05	0.000497	0.000381	CBLN1/GA	9
BP	GO:005134 negative re	68/1638	466/18670	2.07E-05	0.000497	0.000381	A2M/ADC	68
BP	GO:009710 postsynapt	7/1638	12/18670	2.11E-05	0.000503	0.000386	CEL/NRXN	7
BP	GO:190401 positive re	40/1638	230/18670	2.16E-05	0.00051	0.000391	AGTR1/AP	40
BP	GO:002195 central ner	34/1638	183/18670	2.16E-05	0.00051	0.000391	PHOX2A/C	34
BP	GO:005120 sequester	27/1638	131/18670	2.23E-05	0.000526	0.000403	APLNR/AN	27
BP	GO:005124 regulation	70/1638	485/18670	2.27E-05	0.000532	0.000408	AXL/CAV1	70
BP	GO:005120 release of	26/1638	124/18670	2.30E-05	0.000536	0.000411	APLNR/AN	26
BP	GO:000722 integrin-m	23/1638	103/18670	2.33E-05	0.00054	0.000414	APOA1/CC	23
BP	GO:006055 morphoge	8/1638	16/18670	2.34E-05	0.00054	0.000414	AR/FGF10/	8
BP	GO:005512 digestive s	29/1638	146/18670	2.35E-05	0.000542	0.000416	NKX3-2/C	29
BP	GO:001993 cyclic-nucl	38/1638	215/18670	2.37E-05	0.000543	0.000416	ADCY2/AC	38
BP	GO:003300 muscle cel	41/1638	239/18670	2.39E-05	0.000543	0.000417	APOD/CNI	41
BP	GO:200125 positive re	18/1638	70/18670	2.39E-05	0.000543	0.000417	ACTN2/AN	18
BP	GO:002260 ovulation c	14/1638	46/18670	2.47E-05	0.000556	0.000426	AFP/ESR1/	14
BP	GO:009917 presynaps	14/1638	46/18670	2.47E-05	0.000556	0.000426	CBLN1/CE	14
BP	GO:005092 positive re	10/1638	25/18670	2.51E-05	0.000563	0.000432	CCR4/S1P	10
BP	GO:000718 G protein-	43/1638	256/18670	2.59E-05	0.000577	0.000442	ADCY2/AC	43
BP	GO:003051 negative re	15/1638	52/18670	2.60E-05	0.000577	0.000442	DLX1/FBN	15
BP	GO:000341 chondrocy	11/1638	30/18670	2.60E-05	0.000577	0.000442	ANXA6/CC	11
BP	GO:004547 response t	26/1638	125/18670	2.66E-05	0.000587	0.00045	ACTC1/AD	26
BP	GO:003210 positive re	51/1638	323/18670	2.76E-05	0.000606	0.000465	AGTR1/AP	51
BP	GO:004206 gliogenesis	47/1638	290/18670	2.87E-05	0.000628	0.000482	ADCYAP1/	47
BP	GO:007156 cellular res	42/1638	249/18670	2.89E-05	0.000629	0.000483	CAV1/CIDI	42
BP	GO:005092 regulation	38/1638	217/18670	2.93E-05	0.000635	0.000487	CCR4/CCR	38
BP	GO:007251 divalent in	70/1638	489/18670	2.98E-05	0.000644	0.000494	ADCYAP1F	70
BP	GO:006104 regulation	29/1638	148/18670	3.07E-05	0.000661	0.000507	APOH/SER	29
BP	GO:003051 regulation	21/1638	91/18670	3.09E-05	0.000662	0.000508	DLX1/FBN	21
BP	GO:000602 aminoglyc	17/1638	65/18670	3.15E-05	0.000673	0.000516	BGN/VCAI	17

BP	GO:006015 regulation	22/1638	98/18670	3.19E-05	0.000678	0.00052	ADCYAP1F	22
BP	GO:009753 granulocyte	28/1638	141/18670	3.24E-05	0.000687	0.000527	CCR7/IL1R	28
BP	GO:003476 positive regulation	30/1638	156/18670	3.28E-05	0.000692	0.000531	ACTN2/AP	30
BP	GO:009021 positive regulation	12/1638	36/18670	3.39E-05	0.000713	0.000547	CD19/CCR	12
BP	GO:004578 positive regulation	60/1638	403/18670	3.45E-05	0.000722	0.000554	APOA1/CA	60
BP	GO:007083 divalent metal ion	69/1638	483/18670	3.62E-05	0.000754	0.000578	ADCYAP1F	69
BP	GO:003050 BMP signaling	30/1638	157/18670	3.72E-05	0.000762	0.000585	COMP/NK	30
BP	GO:005067 regulation	57/1638	378/18670	3.73E-05	0.000762	0.000585	AGTR1/AP	57
BP	GO:003015 positive regulation	10/1638	26/18670	3.76E-05	0.000762	0.000585	APOH/CD3	10
BP	GO:005092 regulation	10/1638	26/18670	3.76E-05	0.000762	0.000585	CCR4/S1P	10
BP	GO:006074 prostate gland	10/1638	26/18670	3.76E-05	0.000762	0.000585	AR/ESR1/F	10
BP	GO:009956 synaptic transmission	10/1638	26/18670	3.76E-05	0.000762	0.000585	CDH9/SPA	10
BP	GO:190004 positive regulation	10/1638	26/18670	3.76E-05	0.000762	0.000585	APOH/CD3	10
BP	GO:001072 negative regulation	53/1638	344/18670	3.84E-05	0.000776	0.000595	ADCYAP1/	53
BP	GO:000268 regulation	35/1638	196/18670	3.91E-05	0.000788	0.000604	APOD/CCF	35
BP	GO:003015 regulation	19/1638	79/18670	3.96E-05	0.000792	0.000607	APOH/SER	19
BP	GO:004578 positive regulation	36/1638	204/18670	3.96E-05	0.000792	0.000607	AGTR1/AP	36
BP	GO:004875 branching	29/1638	150/18670	3.98E-05	0.000792	0.000607	AGTR2/AR	29
BP	GO:000688 cellular social	8/1638	17/18670	4.07E-05	0.000807	0.000619	AGTR2/AT	8
BP	GO:000165 eye development	55/1638	362/18670	4.11E-05	0.000811	0.000622	ALDH1A3/	55
BP	GO:004566 positive regulation	56/1638	371/18670	4.23E-05	0.000831	0.000638	ADCYAP1/	56
BP	GO:000170 formation	25/1638	121/18670	4.24E-05	0.000832	0.000638	COL4A2/C	25
BP	GO:003028 bone mineral	24/1638	114/18670	4.36E-05	0.000851	0.000653	AHSG/COI	24
BP	GO:000320 cardiac ventricle	18/1638	73/18670	4.40E-05	0.000856	0.000656	COL11A1/	18
BP	GO:002260 digestive system	22/1638	100/18670	4.43E-05	0.000856	0.000656	APOA1/AF	22
BP	GO:006084 artery development	22/1638	100/18670	4.43E-05	0.000856	0.000656	APOB/COI	22
BP	GO:008601 membrane	12/1638	37/18670	4.63E-05	0.00089	0.000683	ANK2/ATP	12
BP	GO:005192 regulation	42/1638	254/18670	4.66E-05	0.000893	0.000685	ADCYAP1F	42
BP	GO:007155 response to	42/1638	255/18670	5.11E-05	0.000972	0.000745	CAV1/CIDI	42
BP	GO:000602 glycosaminoglycan	16/1638	61/18670	5.15E-05	0.000972	0.000745	BGN/VCAI	16
BP	GO:003411 heterotypic cell-cell	16/1638	61/18670	5.15E-05	0.000972	0.000745	APOA1/DS	16
BP	GO:009905 presynaptic transmission	13/1638	43/18670	5.18E-05	0.000972	0.000745	CBLN1/CEI	13
BP	GO:004355 positive regulation	11/1638	32/18670	5.21E-05	0.000972	0.000745	CD19/CCR	11
BP	GO:005196 positive regulation	11/1638	32/18670	5.21E-05	0.000972	0.000745	ADCYAP1/	11
BP	GO:007125 cellular response	11/1638	32/18670	5.21E-05	0.000972	0.000745	COL1A1/F	11
BP	GO:008601 cell-cell signaling	11/1638	32/18670	5.21E-05	0.000972	0.000745	ANK2/CAC	11
BP	GO:000320 cardiac ventricle	26/1638	130/18670	5.39E-05	0.001002	0.000768	COL11A1/	26
BP	GO:005082 positive regulation	10/1638	27/18670	5.50E-05	0.001014	0.000778	APOH/CD3	10
BP	GO:007237 blood coagulation	10/1638	27/18670	5.50E-05	0.001014	0.000778	A2M/APOI	10
BP	GO:005080 positive regulation	31/1638	168/18670	5.59E-05	0.001027	0.000788	ADCYAP1/	31
BP	GO:000738 pattern specification	64/1638	446/18670	5.98E-05	0.001095	0.00084	AR/NKX3-	64
BP	GO:005089 intestinal absorption	12/1638	38/18670	6.22E-05	0.001136	0.000871	APOA1/AF	12
BP	GO:190165 response to	34/1638	193/18670	6.65E-05	0.001206	0.000925	ADCY2/AC	34
BP	GO:006034 bone development	37/1638	217/18670	6.66E-05	0.001206	0.000925	ANXA6/CC	37
BP	GO:006068 regulation	15/1638	56/18670	6.74E-05	0.001206	0.000925	AGTR2/AR	15
BP	GO:000341 chondrocyte	8/1638	18/18670	6.77E-05	0.001206	0.000925	COL6A1/C	8
BP	GO:000342 growth plate	8/1638	18/18670	6.77E-05	0.001206	0.000925	COL6A1/C	8
BP	GO:007162 vocalization	8/1638	18/18670	6.77E-05	0.001206	0.000925	NRXN3/NF	8
BP	GO:009017 chondrocyte	8/1638	18/18670	6.77E-05	0.001206	0.000925	COL6A1/C	8
BP	GO:005127 regulation	19/1638	82/18670	6.84E-05	0.001215	0.000932	APLN/AN	19
BP	GO:008600 membrane	14/1638	50/18670	6.90E-05	0.001222	0.000937	ANK2/ATP	14
BP	GO:004269 ovulation cycle	17/1638	69/18670	7.19E-05	0.001267	0.000972	AFP/AXL/E	17
BP	GO:006007 regulation	27/1638	140/18670	7.56E-05	0.001329	0.001019	ADCYAP1/	27
BP	GO:000749 endoderm	18/1638	76/18670	7.77E-05	0.001344	0.001031	COL4A2/C	18
BP	GO:199026 neutrophil	24/1638	118/18670	7.79E-05	0.001344	0.001031	CCR7/IL1R	24
BP	GO:003437 triglyceride	7/1638	14/18670	7.79E-05	0.001344	0.001031	APOA1/AF	7
BP	GO:003637 sodium ion	7/1638	14/18670	7.79E-05	0.001344	0.001031	ATP1A2/A	7
BP	GO:002289 regulation	43/1638	268/18670	7.82E-05	0.001344	0.001031	ACTN2/AN	43
BP	GO:004273 fibrinolysis	10/1638	28/18670	7.89E-05	0.001344	0.001031	APOH/SER	10
BP	GO:006051 prostate gland	10/1638	28/18670	7.89E-05	0.001344	0.001031	AR/ESR1/F	10
BP	GO:008502 extracellular matrix	10/1638	28/18670	7.89E-05	0.001344	0.001031	COL1A2/H	10
BP	GO:000320 cardiac chamber	31/1638	171/18670	7.90E-05	0.001344	0.001031	ANK2/COL	31

BP	GO:008601	membrane	9/1638	23/18670	7.90E-05	0.001344	0.001031	ANK2/ATP	9
BP	GO:003241	regulation	42/1638	260/18670	8.06E-05	0.001362	0.001045	ACTN2/AN	42
BP	GO:190303	regulation	32/1638	179/18670	8.06E-05	0.001362	0.001045	APOH/SER	32
BP	GO:004816	regulation	33/1638	187/18670	8.16E-05	0.001375	0.001055	ADGRB1/C	33
BP	GO:003059	neutrophil	22/1638	104/18670	8.28E-05	0.001391	0.001067	CCR7/ITGA	22
BP	GO:001071	regulation	20/1638	90/18670	8.35E-05	0.001397	0.001072	COL1A1/E	20
BP	GO:004326	regulation	22/1638	105/18670	9.62E-05	0.001604	0.00123	ACTN2/AC	22
BP	GO:004657	positive re	16/1638	64/18670	9.64E-05	0.001604	0.00123	APOA1/CC	16
BP	GO:005081	regulation	19/1638	84/18670	9.68E-05	0.001606	0.001232	APOH/SER	19
BP	GO:014011	export acro	11/1638	34/18670	9.81E-05	0.001622	0.001244	ATP1A2/A	11
BP	GO:004301	camera-ty	48/1638	314/18670	0.000106	0.001748	0.001341	ALDH1A3/	48
BP	GO:000342	growth pla	8/1638	19/18670	0.000108	0.001773	0.00136	COL6A1/C	8
BP	GO:004405	regulation	12/1638	40/18670	0.000109	0.001778	0.001364	APOA1/AF	12
BP	GO:005128	positive re	12/1638	40/18670	0.000109	0.001778	0.001364	APLN/CA	12
BP	GO:005127	negative re	56/1638	384/18670	0.00011	0.001782	0.001367	AGTR2/AP	56
BP	GO:003233	regulation	14/1638	52/18670	0.00011	0.001783	0.001368	NKX3-2/C	14
BP	GO:005088	neuromusc	14/1638	52/18670	0.00011	0.001783	0.001368	ADCY5/AL	14
BP	GO:003502	positive re	10/1638	29/18670	0.000111	0.001789	0.001372	APOA1/CC	10
BP	GO:005067	positive re	35/1638	206/18670	0.000111	0.001789	0.001372	AGTR1/AP	35
BP	GO:000762	locomotor	34/1638	198/18670	0.000112	0.001794	0.001376	ADCY5/AL	34
BP	GO:000715	heterophili	13/1638	46/18670	0.000112	0.001795	0.001377	CBLN1/ITC	13
BP	GO:000193	endothelia	33/1638	191/18670	0.000124	0.00198	0.001519	AGTR1/AP	33
BP	GO:000320	cardiac ch	25/1638	129/18670	0.000127	0.00201	0.001541	COL11A1/	25
BP	GO:005080	negative re	17/1638	72/18670	0.000127	0.00201	0.001541	BCHE/CBL	17
BP	GO:000269	regulation	64/1638	458/18670	0.000131	0.002067	0.001585	A2M/APO	64
BP	GO:000751	skeletal m	29/1638	160/18670	0.000133	0.00209	0.001603	CASQ1/CA	29
BP	GO:007037	ERK1 and	148/1638	317/18670	0.000134	0.002103	0.001613	ADCYAP1/	48
BP	GO:007037	regulation	46/1638	300/18670	0.000136	0.002125	0.00163	ADCYAP1/	46
BP	GO:004001	negative re	57/1638	396/18670	0.000136	0.002125	0.00163	AGTR2/AP	57
BP	GO:003240	regulation	44/1638	283/18670	0.000137	0.002125	0.00163	ACTN2/AN	44
BP	GO:000193	regulation	31/1638	176/18670	0.000137	0.002125	0.00163	AGTR1/AP	31
BP	GO:000260	regulation	6/1638	11/18670	0.000142	0.002192	0.001681	CCR7/FCG	6
BP	GO:000695	acute-pha	13/1638	47/18670	0.000143	0.002197	0.001685	AHSG/CNF	13
BP	GO:006035	cartilage d	13/1638	47/18670	0.000143	0.002197	0.001685	ANXA6/CC	13
BP	GO:004866	regulation	30/1638	169/18670	0.000151	0.002316	0.001776	APOD/CNI	30
BP	GO:006184	antimicrob	17/1638	73/18670	0.000152	0.002324	0.001783	DEFB1/DEI	17
BP	GO:000736	gastrulatio	32/1638	185/18670	0.000153	0.002329	0.001786	APLN/CA	32
BP	GO:004583	positive re	27/1638	146/18670	0.000158	0.0024	0.001841	AGTR1/AB	27
BP	GO:001000	glial cell di	36/1638	218/18670	0.000161	0.002438	0.00187	DLX1/DLX	36
BP	GO:005080	regulation	36/1638	218/18670	0.000161	0.002438	0.00187	ADGRB1/A	36
BP	GO:003017	negative re	35/1638	210/18670	0.000164	0.002476	0.001899	CAV1/NKX	35
BP	GO:006057	morphoge	9/1638	25/18670	0.000168	0.002525	0.001936	AR/FGF10	9
BP	GO:002176	limbic syst	22/1638	109/18670	0.000171	0.002552	0.001957	ALDH1A3/	22
BP	GO:190004	negative re	14/1638	54/18670	0.000171	0.002552	0.001957	APOH/SER	14
BP	GO:000672	isoprenoid	26/1638	139/18670	0.000171	0.002552	0.001957	ADH1B/AL	26
BP	GO:005170	multi-orga	16/1638	67/18670	0.000172	0.002561	0.001965	AVP/CX3C	16
BP	GO:005080	regulation	37/1638	227/18670	0.000173	0.002562	0.001965	ADGRB1/A	37
BP	GO:000341	growth pla	11/1638	36/18670	0.000175	0.002584	0.001982	ANXA6/CC	11
BP	GO:000182	mesoneph	21/1638	102/18670	0.000178	0.002624	0.002013	AGTR2/FG	21
BP	GO:000206	chondrocy	13/1638	48/18670	0.00018	0.002643	0.002027	COL6A1/C	13
BP	GO:003085	prostate gl	13/1638	48/18670	0.00018	0.002643	0.002027	AR/ESR1/F	13
BP	GO:000761	memory	23/1638	117/18670	0.000186	0.002717	0.002084	CNR1/CX3	23
BP	GO:004865	smooth m	30/1638	171/18670	0.000187	0.002729	0.002093	APOD/CNI	30
BP	GO:004864	animal org	15/1638	61/18670	0.000193	0.00279	0.00214	AR/NKX3-	15
BP	GO:000183	epithelial t	26/1638	140/18670	0.000193	0.00279	0.00214	COL1A1/E	26
BP	GO:007207	kidney epit	26/1638	140/18670	0.000193	0.00279	0.00214	AGTR2/EPI	26
BP	GO:004521	cell-cell ju	28/1638	156/18670	0.000204	0.002934	0.002251	ANK2/CAV	28
BP	GO:004856	embryonic	44/1638	288/18670	0.000204	0.002934	0.002251	ALDH1A3/	44
BP	GO:003362	cell adhesi	16/1638	68/18670	0.000207	0.002968	0.002277	COL16A1/	16
BP	GO:000995	proximal/c	10/1638	31/18670	0.000209	0.002968	0.002277	DLX1/DLX	10
BP	GO:005148	positive re	10/1638	31/18670	0.000209	0.002968	0.002277	AGTR1/CA	10
BP	GO:009917	regulation	10/1638	31/18670	0.000209	0.002968	0.002277	CBLN1/NT	10

BP	GO:009890 regulation	14/1638	55/18670	0.000211	0.002996	0.002298	ANK2/CAC	14
BP	GO:006041 muscle tiss	18/1638	82/18670	0.000219	0.003094	0.002373	ACTC1/CC	18
BP	GO:004854 digestive ti	13/1638	49/18670	0.000226	0.003187	0.002444	FGF10/FO	13
BP	GO:001652 negative re	30/1638	173/18670	0.000231	0.003251	0.002493	APOH/AD	30
BP	GO:000758 respiratory	15/1638	62/18670	0.000234	0.00328	0.002516	PHOX2A/A	15
BP	GO:006007 synapse m	9/1638	26/18670	0.000237	0.003316	0.002544	CX3CR1/N	9
BP	GO:007200 nephron d	26/1638	142/18670	0.000244	0.003408	0.002614	ACTA2/AC	26
BP	GO:000704 cell-substr	20/1638	97/18670	0.000246	0.003428	0.002629	ACTN2/AP	20
BP	GO:004571 positive re	19/1638	90/18670	0.000253	0.003517	0.002698	GLI3/HGF/	19
BP	GO:004231 vasoconstr	17/1638	76/18670	0.000256	0.003537	0.002713	ACTA2/AC	17
BP	GO:000193 positive re	22/1638	112/18670	0.000257	0.003541	0.002716	AGTR1/AP	22
BP	GO:006041 heart grow	22/1638	112/18670	0.000257	0.003541	0.002716	AGTR2/NK	22
BP	GO:007037 positive re	35/1638	215/18670	0.000262	0.003594	0.002757	ADCYAP1/	35
BP	GO:000246 dendritic c	6/1638	12/18670	0.000262	0.003594	0.002757	CCR7/FCG	6
BP	GO:005501 cardiac m	21/1638	105/18670	0.000272	0.003712	0.002847	AGTR2/NK	21
BP	GO:005086 negative re	33/1638	199/18670	0.000274	0.003732	0.002863	AXL/BPI/C	33
BP	GO:000166 ameboidal	63/1638	461/18670	0.000275	0.003732	0.002863	AGTR2/AN	63
BP	GO:001017 body morp	13/1638	50/18670	0.000281	0.003812	0.002924	COL1A1/M	13
BP	GO:200018 negative re	30/1638	175/18670	0.000284	0.003839	0.002945	APOH/AD	30
BP	GO:003011 regulation	52/1638	363/18670	0.000295	0.003961	0.003038	CAV1/COL	52
BP	GO:001046 mesenchyr	12/1638	44/18670	0.000296	0.003961	0.003038	FGF7/FGFF	12
BP	GO:006171 leukocyte	12/1638	44/18670	0.000296	0.003961	0.003038	ADD2/CX3	12
BP	GO:005196 regulation	16/1638	70/18670	0.000296	0.003961	0.003038	ADCYAP1/	16
BP	GO:190351 positive re	56/1638	399/18670	0.0003	0.003992	0.003062	ADCYAP1/	56
BP	GO:005086 endocrine	18/1638	84/18670	0.000301	0.003992	0.003062	AGTR1/AG	18
BP	GO:009771 negative re	18/1638	84/18670	0.000301	0.003992	0.003062	ACTA2/AC	18
BP	GO:005086 regulation	31/1638	184/18670	0.000311	0.004122	0.003162	CD19/CD2	31
BP	GO:002151 telenceph	39/1638	251/18670	0.000323	0.004269	0.003275	ALDH1A3/	39
BP	GO:006034 bone morp	22/1638	114/18670	0.000334	0.004402	0.003377	ANXA6/CC	22
BP	GO:004566 positive re	15/1638	64/18670	0.000339	0.004462	0.003422	GLI3/HGF/	15
BP	GO:000659 thyroid ho	7/1638	17/18670	0.000349	0.004563	0.0035	CGA/DIO2	7
BP	GO:009711 postsynapt	7/1638	17/18670	0.000349	0.004563	0.0035	CBLN1/NT	7
BP	GO:006051 skeletal m	29/1638	169/18670	0.00035	0.004563	0.0035	CASQ1/CA	29
BP	GO:190441 positive re	16/1638	71/18670	0.000351	0.004576	0.00351	APLNR/AN	16
BP	GO:003592 steroid hor	8/1638	22/18670	0.000359	0.004669	0.003581	AGTR1/AG	8
BP	GO:006056 epithelial t	47/1638	322/18670	0.000369	0.004777	0.003664	AGTR2/AR	47
BP	GO:001993 cGMP-me	10/1638	33/18670	0.00037	0.004777	0.003664	CD36/GUC	10
BP	GO:009908 postsynapt	10/1638	33/18670	0.00037	0.004777	0.003664	CBLN1/GA	10
BP	GO:004358 ear develo	35/1638	219/18670	0.000374	0.004815	0.003693	ALDH1A3/	35
BP	GO:200002 regulation	39/1638	253/18670	0.00038	0.004877	0.003741	AGTR2/AR	39
BP	GO:003196 response t	28/1638	162/18670	0.000388	0.004971	0.003813	ADCYAP1/	28
BP	GO:000307 regulation	19/1638	93/18670	0.000394	0.005029	0.003858	ADRB3/AC	19
BP	GO:000315 outflow tra	17/1638	79/18670	0.000415	0.00528	0.00405	NKX2-5/EI	17
BP	GO:001922 transmissi	16/1638	72/18670	0.000415	0.00528	0.00405	AVP/DRDE	16
BP	GO:004877 tissue rem	30/1638	179/18670	0.000422	0.005355	0.004108	AGTR2/AX	30
BP	GO:003517 social beh	13/1638	52/18670	0.000426	0.005367	0.004117	AVP/CX3C	13
BP	GO:005170 intraspecie	13/1638	52/18670	0.000426	0.005367	0.004117	AVP/CX3C	13
BP	GO:007211 mesenchyr	13/1638	52/18670	0.000426	0.005367	0.004117	ACTA2/AC	13
BP	GO:009011 tissue migr	51/1638	360/18670	0.000438	0.005498	0.004217	ACTA2/AC	51
BP	GO:000804 motor neu	9/1638	28/18670	0.000446	0.005572	0.004274	ERBB2/NTI	9
BP	GO:003010 regulation	42/1638	281/18670	0.00045	0.005572	0.004274	AHSG/APC	42
BP	GO:000208 regulation	6/1638	13/18670	0.000451	0.005572	0.004274	ATP1A2/PI	6
BP	GO:000286 regulation	6/1638	13/18670	0.000451	0.005572	0.004274	ADCYAP1/	6
BP	GO:003000 cellular po	6/1638	13/18670	0.000451	0.005572	0.004274	ATP1A2/A	6
BP	GO:003806 collagen-a	6/1638	13/18670	0.000451	0.005572	0.004274	COL1A1/C	6
BP	GO:007020 protein he	6/1638	13/18670	0.000451	0.005572	0.004274	COL1A1/C	6
BP	GO:006044 mammary	12/1638	46/18670	0.000463	0.005679	0.004356	AR/CAV1/	12
BP	GO:001051 positive re	14/1638	59/18670	0.000463	0.005679	0.004356	ADCYAP1F	14
BP	GO:003110 neuron pr	14/1638	59/18670	0.000463	0.005679	0.004356	APOA1/AF	14
BP	GO:003297 regulation	54/1638	388/18670	0.000468	0.005725	0.004391	ACTN2/AC	54
BP	GO:009059 sensory or	39/1638	256/18670	0.000483	0.005892	0.004519	ALDH1A3/	39
BP	GO:004856 embryonic	10/1638	34/18670	0.000484	0.005893	0.00452	FGF10/FO	10

BP	GO:007050	calcium ion	17/1638	80/18670	0.000485	0.005893	0.00452	ATP2B4/CA	17
BP	GO:006035	endothelial	16/1638	73/18670	0.000489	0.005934	0.004552	ANXA6/CC	16
BP	GO:003233	negative regulation	8/1638	23/18670	0.000509	0.006142	0.004711	NKX3-2/EL	8
BP	GO:004357	regulation	8/1638	23/18670	0.000509	0.006142	0.004711	PHOX2A/FA	8
BP	GO:003015	negative regulation	13/1638	53/18670	0.00052	0.006239	0.004786	APOH/SER	13
BP	GO:004521	sarcomere	13/1638	53/18670	0.00052	0.006239	0.004786	ACTN2/CA	13
BP	GO:001046	regulation	29/1638	173/18670	0.000521	0.006239	0.004786	ACTN2/AC	29
BP	GO:009875	import across	21/1638	110/18670	0.000525	0.006273	0.004811	ATP1A2/AT	21
BP	GO:000176	neuron migration	27/1638	157/18670	0.00053	0.006327	0.004853	AXL/CCR4	27
BP	GO:001810	peptidyl-tyrosine	51/1638	363/18670	0.000532	0.006336	0.004859	ALK/AXL/E	51
BP	GO:003109	regeneration	32/1638	198/18670	0.000535	0.006356	0.004875	APOA1/AF	32
BP	GO:004864	muscle organ	18/1638	88/18670	0.000546	0.006469	0.004962	ACTC1/CC	18
BP	GO:002170	development	42/1638	284/18670	0.000562	0.006644	0.005096	AXL/ADGR	42
BP	GO:002176	hippocampus	17/1638	81/18670	0.000564	0.00666	0.005108	ALK/ATP2B	17
BP	GO:003057	collagen cross	12/1638	47/18670	0.000572	0.006737	0.005167	COL15A1/	12
BP	GO:009960	regulation	16/1638	74/18670	0.000574	0.006747	0.005175	ACTN2/CR	16
BP	GO:005104	positive regulation	58/1638	428/18670	0.000582	0.006821	0.005232	ADCYAP1/	58
BP	GO:003435	adherens junction	25/1638	142/18670	0.000587	0.006862	0.005263	ACTN2/AP	25
BP	GO:003134	positive regulation	53/1638	383/18670	0.000602	0.007025	0.005388	ADCYAP1/	53
BP	GO:004835	mesoderm	10/1638	35/18670	0.000625	0.007258	0.005567	FGFR1/FO	10
BP	GO:009880	regulation	10/1638	35/18670	0.000625	0.007258	0.005567	AGTR1/AC	10
BP	GO:000721	neuropeptide	20/1638	104/18670	0.000639	0.007395	0.005672	ADCYAP1/	20
BP	GO:003241	positive regulation	20/1638	104/18670	0.000639	0.007395	0.005672	ACTN2/AN	20
BP	GO:001821	peptidyl-tyrosine	51/1638	366/18670	0.000644	0.007435	0.005703	ALK/AXL/E	51
BP	GO:004885	inner ear development	31/1638	192/18670	0.000659	0.00758	0.005814	ALDH1A3/	31
BP	GO:005076	negative regulation	43/1638	295/18670	0.00066	0.00758	0.005814	ADCYAP1/	43
BP	GO:000165	ureteric bud	19/1638	97/18670	0.000683	0.007812	0.005992	AGTR2/FG	19
BP	GO:003225	regulation	19/1638	97/18670	0.000683	0.007812	0.005992	APOA1/CC	19
BP	GO:000803	neuron reconnection	12/1638	48/18670	0.000703	0.008006	0.006141	CNR1/EPH	12
BP	GO:190372	positive regulation	12/1638	48/18670	0.000703	0.008006	0.006141	CD19/CCR	12
BP	GO:000345	chondrocyte	8/1638	24/18670	0.000705	0.008015	0.006147	COL6A1/C	8
BP	GO:003020	glycosaminoglycan	27/1638	160/18670	0.000717	0.008135	0.00624	BGN/VCAI	27
BP	GO:190137	regulation	18/1638	90/18670	0.000723	0.008165	0.006263	ACTN2/AN	18
BP	GO:190305	negative regulation	18/1638	90/18670	0.000723	0.008165	0.006263	APOH/SER	18
BP	GO:005095	induction	6/1638	14/18670	0.000731	0.008215	0.006301	FGF10/VE	6
BP	GO:005191	regulation	6/1638	14/18670	0.000731	0.008215	0.006301	APOH/CPE	6
BP	GO:000755	hemostasis	48/1638	341/18670	0.000732	0.008215	0.006301	A2M/APOI	48
BP	GO:001047	regulation	11/1638	42/18670	0.000763	0.008545	0.006554	APOA1/CC	11
BP	GO:005196	negative regulation	45/1638	315/18670	0.000773	0.008634	0.006623	ADCYAP1/	45
BP	GO:007216	mesonephros	19/1638	98/18670	0.000779	0.008665	0.006646	AGTR2/FG	19
BP	GO:007216	mesonephros	19/1638	98/18670	0.000779	0.008665	0.006646	AGTR2/FG	19
BP	GO:005081	coagulation	48/1638	342/18670	0.000781	0.008666	0.006647	A2M/APOI	48
BP	GO:006104	negative regulation	16/1638	76/18670	0.000783	0.008666	0.006647	APOH/SER	16
BP	GO:004826	response to	9/1638	30/18670	0.000787	0.008666	0.006647	CRH/NTRK	9
BP	GO:005145	positive regulation	9/1638	30/18670	0.000787	0.008666	0.006647	CCR7/DPY	9
BP	GO:190560	regulation	9/1638	30/18670	0.000787	0.008666	0.006647	CBLN1/NT	9
BP	GO:003285	glomerular	14/1638	62/18670	0.00079	0.008675	0.006654	ACTA2/AG	14
BP	GO:005500	cardiac muscle	15/1638	69/18670	0.000795	0.008717	0.006686	ACTC1/CC	15
BP	GO:003094	regulation	10/1638	36/18670	0.000798	0.008729	0.006696	FGF10/ITG	10
BP	GO:003164	regulation	24/1638	137/18670	0.000804	0.008784	0.006737	AVP/CBLN	24
BP	GO:000110	response to	48/1638	343/18670	0.000833	0.009055	0.006945	APOB/ATP	48
BP	GO:000225	response to	48/1638	343/18670	0.000833	0.009055	0.006945	APOB/ATP	48
BP	GO:009005	negative regulation	29/1638	178/18670	0.000835	0.00906	0.006949	CAV1/NKX	29
BP	GO:000155	regulation	56/1638	416/18670	0.000842	0.009114	0.00699	AGTR1/AC	56
BP	GO:000602	aminoglycoside	28/1638	170/18670	0.000855	0.00924	0.007087	BGN/VCAI	28
BP	GO:000275	regulation	65/1638	500/18670	0.000861	0.009285	0.007122	ADCY5/AC	65
BP	GO:005070	regulation	62/1638	472/18670	0.000863	0.009285	0.007122	ADCY5/AC	62
BP	GO:005506	monovalent	26/1638	154/18670	0.000885	0.009408	0.007216	AGTR1/AC	26
BP	GO:006007	canonical	47/1638	335/18670	0.000888	0.009408	0.007216	CAV1/COL	47
BP	GO:001995	cAMP-mediated	30/1638	187/18670	0.000888	0.009408	0.007216	ADCY2/AC	30
BP	GO:190134	negative regulation	30/1638	187/18670	0.000888	0.009408	0.007216	APOH/AD	30
BP	GO:005138	response to	25/1638	146/18670	0.000892	0.009408	0.007216	ADCYAP1/	25

BP	GO:003437	chylomicron 5/1638	10/18670	0.000894	0.009408	0.007216	APOA1/AF	5
BP	GO:003806	collagen- α 5/1638	10/18670	0.000894	0.009408	0.007216	COL1A1/C	5
BP	GO:005191	negative regulation 5/1638	10/18670	0.000894	0.009408	0.007216	APOH/CPE	5
BP	GO:006051	prostatic blood vessel 5/1638	10/18670	0.000894	0.009408	0.007216	AR/FGF10/	5
BP	GO:009704	dendritic cell 5/1638	10/18670	0.000894	0.009408	0.007216	AXL/CCR7,	5
BP	GO:200066	regulation 5/1638	10/18670	0.000894	0.009408	0.007216	AXL/CCR7,	5
BP	GO:005090	neuromuscular junction 20/1638	107/18670	0.00093	0.009766	0.007491	ADCY5/AL	20
BP	GO:000759	blood coagulation 47/1638	336/18670	0.000946	0.009923	0.007611	A2M/APOI	47
BP	GO:000821	glucocorticoid 8/1638	25/18670	0.000958	0.009975	0.007651	APOA1/SE	8
BP	GO:002195	central nervous system 8/1638	25/18670	0.000958	0.009975	0.007651	CDH11/GL	8
BP	GO:003163	plasminogen 8/1638	25/18670	0.000958	0.009975	0.007651	APOH/CPE	8
BP	GO:003121	biomineralization 27/1638	163/18670	0.000959	0.009975	0.007651	AHSG/COI	27
BP	GO:004666	female sex 21/1638	115/18670	0.000961	0.009975	0.007651	ADCYAP1/	21
BP	GO:190188	regulation 26/1638	155/18670	0.000976	0.010114	0.007757	NKX2-5/Fc	26
BP	GO:001604	cell growth 63/1638	484/18670	0.000993	0.010269	0.007876	AGTR1/AC	63
BP	GO:004211	B cell activation 44/1638	310/18670	0.001004	0.010357	0.007944	CXCR5/CD	44
BP	GO:003444	substrate enzyme 19/1638	100/18670	0.001005	0.010357	0.007944	APOA1/AX	19
BP	GO:000830	associative learning 16/1638	78/18670	0.001052	0.010814	0.008295	ATP1A2/C	16
BP	GO:003327	response to 18/1638	93/18670	0.00108	0.011062	0.008485	BCHE/COL	18
BP	GO:003524	synaptic transmission 18/1638	93/18670	0.00108	0.011062	0.008485	ADCYAP1/	18
BP	GO:005081	negative regulation 13/1638	57/18670	0.001088	0.011125	0.008533	APOH/SER	13
BP	GO:000257	regulation 7/1638	20/18670	0.001099	0.011143	0.008547	CCR7/FCG	7
BP	GO:008601	atrial cardiomyocyte 7/1638	20/18670	0.001099	0.011143	0.008547	ANK2/CAC	7
BP	GO:008602	atrial cardiomyocyte 7/1638	20/18670	0.001099	0.011143	0.008547	ANK2/CAC	7
BP	GO:008606	atrial cardiomyocyte 7/1638	20/18670	0.001099	0.011143	0.008547	ANK2/CAC	7
BP	GO:003572	sodium ion 24/1638	140/18670	0.001101	0.011143	0.008547	ATP1A2/A	24
BP	GO:004247	odontogenesis 23/1638	132/18670	0.001103	0.011143	0.008547	COL1A1/C	23
BP	GO:001815	protein oxidation 6/1638	15/18670	0.001128	0.011356	0.008711	APOA1/AF	6
BP	GO:004685	negative regulation 6/1638	15/18670	0.001128	0.011356	0.008711	CALCA/IL6	6
BP	GO:004406	regulation 11/1638	44/18670	0.001162	0.011616	0.00891	AGTR1/AC	11
BP	GO:005148	regulation 11/1638	44/18670	0.001162	0.011616	0.00891	CCR7/DPY	11
BP	GO:200040	regulation 11/1638	44/18670	0.001162	0.011616	0.00891	APOD/CD	11
BP	GO:004860	reproduction 57/1638	431/18670	0.001163	0.011616	0.00891	ADCYAP1/	57
BP	GO:004854	response to 52/1638	385/18670	0.001173	0.011699	0.008974	ADCYAP1/	52
BP	GO:006082	regulation 41/1638	286/18670	0.001206	0.012005	0.009208	CAV1/COL	41
BP	GO:002167	nerve development 16/1638	79/18670	0.001214	0.012053	0.009245	PHOX2A/C	16
BP	GO:004566	negative regulation 12/1638	51/18670	0.001253	0.012394	0.009506	GDF10/IGF	12
BP	GO:004826	positive regulation 12/1638	51/18670	0.001253	0.012394	0.009506	C3/SERPIN	12
BP	GO:000715	activation 10/1638	38/18670	0.001262	0.012467	0.009562	ADCY2/AC	10
BP	GO:000254	monocyte 14/1638	65/18670	0.001292	0.012736	0.009769	CALCA/IL6	14
BP	GO:001088	regulation 9/1638	32/18670	0.001315	0.012922	0.009911	ANK2/ATP	9
BP	GO:000269	positive regulation 17/1638	87/18670	0.001316	0.012922	0.009911	CCR7/F7/V	17
BP	GO:005087	positive regulation 24/1638	142/18670	0.001347	0.013208	0.010131	IGHD/IGHC	24
BP	GO:004247	ear morphology 21/1638	118/18670	0.00135	0.013211	0.010133	ALDH1A3/	21
BP	GO:004873	gland development 57/1638	434/18670	0.001369	0.013342	0.010234	ADCYAP1/	57
BP	GO:006145	reproduction 57/1638	434/18670	0.001369	0.013342	0.010234	ADCYAP1/	57
BP	GO:007058	calcium ion 44/1638	315/18670	0.00139	0.013527	0.010376	APLN/AN	44
BP	GO:000268	negative regulation 60/1638	463/18670	0.001438	0.013971	0.010716	A2M/ADC	60
BP	GO:001895	phenol-co 19/1638	103/18670	0.00145	0.01406	0.010784	AGTR2/CG	19
BP	GO:190316	regulation 25/1638	151/18670	0.001462	0.014144	0.010848	APLN/AN	25
BP	GO:005070	regulation 32/1638	210/18670	0.001474	0.014234	0.010918	AGTR2/AP	32
BP	GO:000716	negative regulation 41/1638	289/18670	0.001476	0.014234	0.010918	APOA1/AF	41
BP	GO:000237	immunoglobulin 30/1638	193/18670	0.001486	0.014285	0.010957	CD22/FCG	30
BP	GO:007267	lymphocyte 20/1638	111/18670	0.001487	0.014285	0.010957	APOD/CCF	20
BP	GO:001017	embryonic 5/1638	11/18670	0.00152	0.014452	0.011085	MAB21L2/	5
BP	GO:006136	positive regulation 5/1638	11/18670	0.00152	0.014452	0.011085	APOA4/AF	5
BP	GO:000243	acute inflammation 7/1638	21/18670	0.001525	0.014452	0.011085	ADCYAP1/	7
BP	GO:003581	regulation 7/1638	21/18670	0.001525	0.014452	0.011085	AGTR1/AC	7
BP	GO:004240	thyroid hormone 7/1638	21/18670	0.001525	0.014452	0.011085	CGA/DIO2	7
BP	GO:190305	positive regulation 7/1638	21/18670	0.001525	0.014452	0.011085	CPB2/IL6/I	7
BP	GO:000165	branching 13/1638	59/18670	0.001526	0.014452	0.011085	AGTR2/FG	13
BP	GO:002188	forebrain cell 13/1638	59/18670	0.001526	0.014452	0.011085	AXL/GLI3/I	13

BP	GO:006030	regulation	10/1638	39/18670	0.001566	0.0148	0.011352	ANK2/CAC	10
BP	GO:003410	homotypic	16/1638	81/18670	0.0016	0.015099	0.011581	COMP/CSI	16
BP	GO:001620	regulation	25/1638	152/18670	0.001607	0.015133	0.011607	NKX2-5/FO	25
BP	GO:001490	myotube c	20/1638	112/18670	0.001664	0.015526	0.011909	ADGRB1/A	20
BP	GO:003241	positive re	20/1638	112/18670	0.001664	0.015526	0.011909	ACTN2/AN	20
BP	GO:009860	regulation	20/1638	112/18670	0.001664	0.015526	0.011909	CACNB2/C	20
BP	GO:001000	specificatio	9/1638	33/18670	0.001669	0.015526	0.011909	AR/FGF10/	9
BP	GO:001080	regulation	9/1638	33/18670	0.001669	0.015526	0.011909	KLF9/FGF7	9
BP	GO:006060	mammary	9/1638	33/18670	0.001669	0.015526	0.011909	AR/CSF1R/	9
BP	GO:004350	endothelia	39/1638	273/18670	0.00167	0.015526	0.011909	AGTR2/AP	39
BP	GO:004400	regulation	6/1638	16/18670	0.001672	0.015526	0.011909	ATP1A2/PI	6
BP	GO:005190	negative re	8/1638	27/18670	0.001678	0.015556	0.011932	AGTR2/CN	8
BP	GO:006000	roof of mo	17/1638	89/18670	0.001706	0.015782	0.012105	FOXF2/FO	17
BP	GO:004320	apoptotic c	11/1638	46/18670	0.001717	0.015863	0.012168	AXL/ADGR	11
BP	GO:004860	negative re	14/1638	67/18670	0.001757	0.016182	0.012412	APOD/CNI	14
BP	GO:003010	platelet ac	25/1638	153/18670	0.001764	0.016182	0.012412	AXL/COL1	25
BP	GO:004580	positive re	25/1638	153/18670	0.001764	0.016182	0.012412	AHSG/APC	25
BP	GO:005100	actin filam	25/1638	153/18670	0.001764	0.016182	0.012412	ADD2/APC	25
BP	GO:000690	regulation	18/1638	97/18670	0.001782	0.016257	0.012469	ANK2/ATP	18
BP	GO:004870	oligodendri	18/1638	97/18670	0.001782	0.016257	0.012469	DLX1/DLX	18
BP	GO:005150	response t	18/1638	97/18670	0.001782	0.016257	0.012469	ALDH3A1/	18
BP	GO:007250	reactive ox	40/1638	284/18670	0.001916	0.017451	0.013385	AGTR1/AG	40
BP	GO:000190	postsynapti	10/1638	40/18670	0.001926	0.017515	0.013434	CEL/GLRB/	10
BP	GO:003240	response t	45/1638	330/18670	0.002006	0.018211	0.013968	APOB/ATP	45
BP	GO:005090	positive ch	14/1638	68/18670	0.002038	0.018464	0.014162	CCR4/DEF	14
BP	GO:002150	spinal corc	19/1638	106/18670	0.002052	0.018563	0.014238	PHOX2A/E	19
BP	GO:006090	endocrine	11/1638	47/18670	0.002067	0.018593	0.014261	AGTR1/AG	11
BP	GO:006130	trabecula r	11/1638	47/18670	0.002067	0.018593	0.014261	COL1A1/N	11
BP	GO:003360	integrin ac	7/1638	22/18670	0.002069	0.018593	0.014261	COL16A1/	7
BP	GO:000260	regulation	20/1638	114/18670	0.002073	0.018593	0.014261	CCR7/F7/V	20
BP	GO:190380	regulation	21/1638	122/18670	0.002073	0.018593	0.014261	CAV1/CIDI	21
BP	GO:009860	inorganic c	16/1638	83/18670	0.002086	0.018643	0.0143	ATP1A2/A	16
BP	GO:009950	inorganic i	16/1638	83/18670	0.002086	0.018643	0.0143	ATP1A2/A	16
BP	GO:003220	positive re	13/1638	61/18670	0.002101	0.018749	0.014381	APOA1/CC	13
BP	GO:002150	pallium de	27/1638	172/18670	0.002158	0.019222	0.014744	ALK/ATP2B	27
BP	GO:003430	protein-lip	8/1638	28/18670	0.002171	0.019245	0.014761	AGTR1/AP	8
BP	GO:003430	plasma lip	8/1638	28/18670	0.002171	0.019245	0.014761	AGTR1/AP	8
BP	GO:004560	negative re	8/1638	28/18670	0.002171	0.019245	0.014761	DLX1/DLX	8
BP	GO:004850	rhythmic p	41/1638	295/18670	0.002178	0.019274	0.014783	AFP/AXL/k	41
BP	GO:005180	membrane	17/1638	91/18670	0.002189	0.019334	0.014829	ANK2/ATP	17
BP	GO:004880	artery mor	15/1638	76/18670	0.002228	0.019654	0.015075	APOB/COL	15
BP	GO:004860	regulation	25/1638	156/18670	0.002318	0.020411	0.015655	NKX2-5/FO	25
BP	GO:000750	myoblast f	10/1638	41/18670	0.00235	0.020544	0.015757	ADGRB1/A	10
BP	GO:003510	forelimb m	10/1638	41/18670	0.00235	0.020544	0.015757	CACNA1C	10
BP	GO:004400	membrane	10/1638	41/18670	0.00235	0.020544	0.015757	CAV1/CEL	10
BP	GO:190300	regulation	10/1638	41/18670	0.00235	0.020544	0.015757	AEBP1/CPI	10
BP	GO:006040	regulation	16/1638	84/18670	0.002371	0.020544	0.015757	NKX2-5/FO	16
BP	GO:003440	steroid est	6/1638	17/18670	0.002394	0.020544	0.015757	AGTR1/AP	6
BP	GO:003440	sterol ester	6/1638	17/18670	0.002394	0.020544	0.015757	AGTR1/AP	6
BP	GO:003440	cholesterol	6/1638	17/18670	0.002394	0.020544	0.015757	AGTR1/AP	6
BP	GO:003590	corticoster	6/1638	17/18670	0.002394	0.020544	0.015757	AGTR1/AG	6
BP	GO:004600	cGMP met	6/1638	17/18670	0.002394	0.020544	0.015757	GUCY1A1/	6
BP	GO:006000	inhibitory p	6/1638	17/18670	0.002394	0.020544	0.015757	NTSR1/RIN	6
BP	GO:006080	regulation	6/1638	17/18670	0.002394	0.020544	0.015757	DLX1/DLX	6
BP	GO:003020	dermatan	5/1638	12/18670	0.002419	0.020544	0.015757	BGN/VCAI	5
BP	GO:003370	phospholip	5/1638	12/18670	0.002419	0.020544	0.015757	APOA1/AF	5
BP	GO:003430	very-low-c	5/1638	12/18670	0.002419	0.020544	0.015757	APOA1/AF	5
BP	GO:004230	keratan sul	5/1638	12/18670	0.002419	0.020544	0.015757	LUM/OMC	5
BP	GO:004260	regulation	5/1638	12/18670	0.002419	0.020544	0.015757	AR/FGF2/F	5
BP	GO:005140	negative re	5/1638	12/18670	0.002419	0.020544	0.015757	ATP1A2/K	5
BP	GO:009700	presynapti	5/1638	12/18670	0.002419	0.020544	0.015757	CEL/CNTN	5
BP	GO:009910	regulation	5/1638	12/18670	0.002419	0.020544	0.015757	CBLN1/GA	5

BP	GO:009951 trans-synaptic transmission	5/1638	12/18670	0.002419	0.020544	0.015757	CNR1/F2RLN	5
BP	GO:015001 regulation of gene expression	5/1638	12/18670	0.002419	0.020544	0.015757	CBLN1/GABRA1	5
BP	GO:005042 regulation of synaptic transmission	13/1638	62/18670	0.002449	0.020764	0.015927	AGTR2/CNR1	13
BP	GO:005501 ventricular heart muscle tissue	11/1638	48/18670	0.002473	0.020936	0.016058	COL11A1/ACTN2	11
BP	GO:005502 regulation of gene expression	18/1638	100/18670	0.002531	0.02134	0.016368	NKX2-5/FOXP2	18
BP	GO:004321 negative regulation of gene expression	25/1638	157/18670	0.002533	0.02134	0.016368	ACTN2/ACTN1	25
BP	GO:006151 actin filament-based process	25/1638	157/18670	0.002533	0.02134	0.016368	ADD2/APC	25
BP	GO:004861 response to hypoxia	15/1638	77/18670	0.002548	0.02143	0.016437	APOA1/AFM1	15
BP	GO:000321 cardiac atrium muscle tissue	9/1638	35/18670	0.002604	0.021766	0.016695	ANK2/NKX2-5	9
BP	GO:001941 triglyceride metabolic process	9/1638	35/18670	0.002604	0.021766	0.016695	APOA1/AFM1	9
BP	GO:002191 central nervous system development	9/1638	35/18670	0.002604	0.021766	0.016695	CDH11/GLI3	9
BP	GO:005191 positive regulation of gene expression	9/1638	35/18670	0.002604	0.021766	0.016695	AVP/KCNE1	9
BP	GO:004851 embryonic development	55/1638	428/18670	0.002663	0.022223	0.017046	ALDH1A3/ALDH1A1	55
BP	GO:004881 multicellular organismal development	61/1638	485/18670	0.002677	0.022306	0.017109	ADCY2/ACTN2	61
BP	GO:001051 regulation of gene expression	14/1638	70/18670	0.00271	0.022539	0.017288	ADCYAP1F/ADCY1	14
BP	GO:005071 positive regulation of gene expression	29/1638	192/18670	0.002733	0.022696	0.017408	CD36/CNTN1	29
BP	GO:000741 axonal fasciculation	7/1638	23/18670	0.002752	0.022713	0.017421	CNR1/EPH2	7
BP	GO:003581 renal sodium ion transport	7/1638	23/18670	0.002752	0.022713	0.017421	AGTR1/AGTR2	7
BP	GO:007131 cellular response to hypoxia	7/1638	23/18670	0.002752	0.022713	0.017421	TNC/PENK	7
BP	GO:010601 neuron projection development	7/1638	23/18670	0.002752	0.022713	0.017421	CNR1/EPH2	7
BP	GO:000691 substrate-specific enzyme activity	8/1638	29/18670	0.002771	0.022727	0.017432	FN1/SNAI2	8
BP	GO:001061 cell communication	8/1638	29/18670	0.002771	0.022727	0.017432	ATP1A2/ATP1B1	8
BP	GO:003431 protein complex	8/1638	29/18670	0.002771	0.022727	0.017432	AGTR1/AP2	8
BP	GO:000261 negative regulation of gene expression	27/1638	175/18670	0.002772	0.022727	0.017432	AXL/BPI/CXCR4	27
BP	GO:009011 epithelium	47/1638	354/18670	0.002775	0.022727	0.017432	AGTR2/AP2	47
BP	GO:003031 embryonic development	21/1638	125/18670	0.00281	0.022937	0.017593	CACNA1C/CACNA1D	21
BP	GO:003511 embryonic development	21/1638	125/18670	0.00281	0.022937	0.017593	CACNA1C/CACNA1D	21
BP	GO:004651 developmental process	18/1638	101/18670	0.002833	0.023094	0.017714	ADCYAP1/ADCY1	18
BP	GO:200041 regulation of gene expression	13/1638	63/18670	0.002843	0.023131	0.017742	APOD/CD36	13
BP	GO:002191 pituitary gland development	10/1638	42/18670	0.002846	0.023131	0.017742	ADCYAP1/ADCY1	10
BP	GO:007201 nephron epithelial cell development	19/1638	109/18670	0.002852	0.023137	0.017747	AGTR2/FGF1	19
BP	GO:003501 cardiocyte	26/1638	167/18670	0.002894	0.023449	0.017986	ACTC1/ACTN2	26
BP	GO:005502 regulation of gene expression	15/1638	78/18670	0.002904	0.023453	0.017989	NKX2-5/FOXP2	15
BP	GO:007201 nephron epithelial cell development	15/1638	78/18670	0.002904	0.023453	0.017989	AGTR2/FGF1	15
BP	GO:002201 telencephalon development	12/1638	56/18670	0.002928	0.023614	0.018113	GLI3/POU3F1	12
BP	GO:000301 regulation of gene expression	11/1638	49/18670	0.002941	0.023642	0.018134	ADRB3/AC1	11
BP	GO:001071 regulation of gene expression	11/1638	49/18670	0.002941	0.023642	0.018134	CCN2/F2RLN	11
BP	GO:005181 positive regulation of gene expression	27/1638	176/18670	0.003008	0.024146	0.018521	AXL/CD191	27
BP	GO:004661 response to hypoxia	22/1638	134/18670	0.003034	0.024316	0.018651	ALDH3A1/ALDH1A3	22
BP	GO:003211 negative regulation of gene expression	48/1638	365/18670	0.00305	0.02441	0.018723	ADCYAP1/ADCY1	48
BP	GO:005101 negative regulation of gene expression	34/1638	238/18670	0.003188	0.025474	0.019539	AGTR2/AP2	34
BP	GO:001481 release of neurotransmitter	9/1638	36/18670	0.003206	0.025482	0.019545	ANK2/ATP1A2	9
BP	GO:007171 membrane transport	9/1638	36/18670	0.003206	0.025482	0.019545	CAV1/CEL	9
BP	GO:200031 regulation of gene expression	9/1638	36/18670	0.003206	0.025482	0.019545	ACTN2/CR	9
BP	GO:005081 positive regulation of gene expression	51/1638	394/18670	0.003208	0.025482	0.019545	AXL/CAV1	51
BP	GO:005041 catecholamine metabolic process	13/1638	64/18670	0.003287	0.026065	0.019993	AGTR2/CNR1	13
BP	GO:000671 glucocorticoid metabolic process	6/1638	18/18670	0.003327	0.026307	0.020178	CRH/CYP11B1	6
BP	GO:004851 embryonic development	6/1638	18/18670	0.003327	0.026307	0.020178	FGF10/FOXP2	6
BP	GO:001081 positive regulation of gene expression	10/1638	43/18670	0.003423	0.026821	0.020572	ADCYAP1F/ADCY1	10
BP	GO:003121 regulation of gene expression	10/1638	43/18670	0.003423	0.026821	0.020572	CACNA1C/CACNA1D	10
BP	GO:004641 neutral lipid metabolic process	10/1638	43/18670	0.003423	0.026821	0.020572	APOA1/AFM1	10
BP	GO:004641 acylglycerol metabolic process	10/1638	43/18670	0.003423	0.026821	0.020572	APOA1/AFM1	10
BP	GO:007021 sarcoplasmic reticulum calcium ion transport	10/1638	43/18670	0.003423	0.026821	0.020572	ANK2/ATP1A2	10
BP	GO:199051 potassium ion transport	10/1638	43/18670	0.003423	0.026821	0.020572	ATP1A2/ATP1B1	10
BP	GO:006041 lung morphogenesis	11/1638	50/18670	0.003477	0.027207	0.020868	FGF7/FGF1	11
BP	GO:000321 cardiac atrium muscle tissue	8/1638	30/18670	0.003492	0.027286	0.020929	NKX2-5/CACNA1C	8
BP	GO:004821 regulation of gene expression	18/1638	103/18670	0.003528	0.027522	0.02111	APOC3/C3	18
BP	GO:003051 adult behavior	23/1638	144/18670	0.003538	0.027563	0.021141	ALK/ATP1A2	23
BP	GO:000281 regulation of gene expression	7/1638	24/18670	0.003595	0.027758	0.021291	ADCYAP1/ADCY1	7
BP	GO:001081 regulation of gene expression	7/1638	24/18670	0.003595	0.027758	0.021291	ANK2/ATP1A2	7
BP	GO:002151 spinal cord development	7/1638	24/18670	0.003595	0.027758	0.021291	EVX1/GLI2	7
BP	GO:002151 subpallium development	7/1638	24/18670	0.003595	0.027758	0.021291	ALDH1A3/ALDH1A1	7

BP	GO:004406 regulation	7/1638	24/18670	0.003595	0.027758	0.021291	AGTR1/AC	7
BP	GO:006034 trabecula	f 7/1638	24/18670	0.003595	0.027758	0.021291	COL1A1/N	7
BP	GO:005068 cytokine	secretion 34/1638	240/18670	0.003649	0.02785	0.021361	AGTR2/AP	34
BP	GO:001045 negative	regulation 5/1638	13/18670	0.003649	0.02785	0.021361	SFRP2/SO	5
BP	GO:001085 positive	regulation 5/1638	13/18670	0.003649	0.02785	0.021361	FGF7/FGF1	5
BP	GO:001087 regulation	5/1638	13/18670	0.003649	0.02785	0.021361	AGTR1/AP	5
BP	GO:003020 dermatan	proteoglycan 5/1638	13/18670	0.003649	0.02785	0.021361	BGN/VCA	5
BP	GO:005096 detection	of 5/1638	13/18670	0.003649	0.02785	0.021361	HTR2A/KC	5
BP	GO:005100 negative	regulation 5/1638	13/18670	0.003649	0.02785	0.021361	ATP2B4/C	5
BP	GO:006060 lateral	sprouting 5/1638	13/18670	0.003649	0.02785	0.021361	AR/FGF10	5
BP	GO:004866 neuron	fat 13/1638	65/18670	0.003785	0.028766	0.022064	DLX1/DLX	13
BP	GO:006067 ureteric	bud 13/1638	65/18670	0.003785	0.028766	0.022064	AGTR2/FG	13
BP	GO:190101 regulation	13/1638	65/18670	0.003785	0.028766	0.022064	ACTN2/AN	13
BP	GO:004875 appendage	development 27/1638	179/18670	0.003819	0.028937	0.022195	CACNA1C	27
BP	GO:006017 limb	development 27/1638	179/18670	0.003819	0.028937	0.022195	CACNA1C	27
BP	GO:001701 regulation	20/1638	120/18670	0.003837	0.028999	0.022243	CAV1/CIDI	20
BP	GO:000242 production	of 39/1638	286/18670	0.003838	0.028999	0.022243	APOA1/AF	39
BP	GO:007154 dopamine	receptor 9/1638	37/18670	0.003913	0.029405	0.022555	PHOX2A/\	9
BP	GO:190351 release	of 9/1638	37/18670	0.003913	0.029405	0.022555	ANK2/ATP	9
BP	GO:200040 positive	regulation 9/1638	37/18670	0.003913	0.029405	0.022555	S100A7/C	9
BP	GO:000858 female	gonadotropin 17/1638	96/18670	0.003914	0.029405	0.022555	ADCYAP1/	17
BP	GO:001063 epithelial	cell 46/1638	351/18670	0.003921	0.029415	0.022562	AGTR2/AP	46
BP	GO:001922 regulation	12/1638	58/18670	0.003974	0.029727	0.022801	AGTR1/AT	12
BP	GO:003590 aorta	development 12/1638	58/18670	0.003974	0.029727	0.022801	COL3A1/L	12
BP	GO:003110 animal	organ 14/1638	73/18670	0.00405	0.030209	0.023171	APOA1/AF	14
BP	GO:003355 multicellul	ar 14/1638	73/18670	0.00405	0.030209	0.023171	ADCYAP1/	14
BP	GO:000721 dopamine	10/1638	44/18670	0.004087	0.030286	0.02323	ADCY5/AL	10
BP	GO:003808 vascular	endothelial 10/1638	44/18670	0.004087	0.030286	0.02323	DCN/VEGF	10
BP	GO:007162 regulation	10/1638	44/18670	0.004087	0.030286	0.02323	CCR7/RAR	10
BP	GO:003110 axon	regeneration 11/1638	51/18670	0.004089	0.030286	0.02323	APOA1/AF	11
BP	GO:004510 intermedia	l 11/1638	51/18670	0.004089	0.030286	0.02323	DES/GFAP	11
BP	GO:190535 regulation	27/1638	180/18670	0.004127	0.030526	0.023414	AGTR2/AR	27
BP	GO:009917 postsynap	tic 25/1638	163/18670	0.004209	0.031068	0.02383	CBLN1/CE	25
BP	GO:003295 regulation	45/1638	343/18670	0.004212	0.031068	0.02383	ACTN2/AC	45
BP	GO:000704 cell-	substrate 15/1638	81/18670	0.004226	0.031082	0.023841	ACTN2/AP	15
BP	GO:004804 focal	adhesion 15/1638	81/18670	0.004226	0.031082	0.023841	ACTN2/AP	15
BP	GO:005501 cardiac	muscle 16/1638	89/18670	0.004327	0.031782	0.024377	ACTC1/AC	16
BP	GO:002187 forebrain	cell 13/1638	66/18670	0.004343	0.031782	0.024377	CSF1R/DL	13
BP	GO:007217 mesoneph	ros 13/1638	66/18670	0.004343	0.031782	0.024377	AGTR2/FG	13
BP	GO:003469 response	to 8/1638	31/18670	0.004351	0.031782	0.024377	APOB/CCF	8
BP	GO:009710 postsynap	tic 8/1638	31/18670	0.004351	0.031782	0.024377	CBLN1/NT	8
BP	GO:000754 sex	differentiation 37/1638	270/18670	0.004398	0.032079	0.024605	ADCYAP1/	37
BP	GO:003228 myelin	associated 6/1638	19/18670	0.004506	0.032733	0.025107	ANK2/PMF	6
BP	GO:006097 cell	migration 6/1638	19/18670	0.004506	0.032733	0.025107	PDGFRB/S	6
BP	GO:200088 regulation	6/1638	19/18670	0.004506	0.032733	0.025107	AGTR1/AC	6
BP	GO:007052 platelet	aggregation 12/1638	59/18670	0.004599	0.033329	0.025564	COMP/CSI	12
BP	GO:007207 nephron	tubule 14/1638	74/18670	0.004601	0.033329	0.025564	AGTR2/FG	14
BP	GO:000717 transformati	on 29/1638	199/18670	0.004619	0.033379	0.025602	CAV1/CIDI	29
BP	GO:190486 excitatory	in 7/1638	25/18670	0.00462	0.033379	0.025602	CBLN1/NT	7
BP	GO:008600 ventricular	septum 9/1638	38/18670	0.004735	0.034117	0.026169	ANK2/CAC	9
BP	GO:190274 apoptotic	program 9/1638	38/18670	0.004735	0.034117	0.026169	CRYAB/NK	9
BP	GO:000718 adenylate	kinase 22/1638	139/18670	0.004778	0.034379	0.02637	ADCY2/AC	22
BP	GO:004684 bone	remodeling 16/1638	90/18670	0.004844	0.034608	0.026545	CALCA/CS	16
BP	GO:007167 mononucle	ar 16/1638	90/18670	0.004844	0.034608	0.026545	CALCA/IL6	16
BP	GO:004848 autonomic	regulation 10/1638	45/18670	0.00485	0.034608	0.026545	PHOX2A/E	10
BP	GO:005193 synaptic	transmission 10/1638	45/18670	0.00485	0.034608	0.026545	CNR1/CNF	10
BP	GO:190027 regulation	10/1638	45/18670	0.00485	0.034608	0.026545	ADCYAP1F	10
BP	GO:004667 response	to 43/1638	327/18670	0.00486	0.034608	0.026545	ACTC1/AD	43
BP	GO:003003 contractile	protein 17/1638	98/18670	0.004862	0.034608	0.026545	APOA1/CC	17
BP	GO:004314 stress	fiber 17/1638	98/18670	0.004862	0.034608	0.026545	APOA1/CC	17
BP	GO:001097 positive	regulation 38/1638	281/18670	0.00492	0.034967	0.02682	ADCYAP1/	38
BP	GO:003510 appendage	development 23/1638	148/18670	0.005	0.035395	0.027149	CACNA1C	23

BP	GO:003510	limb morphogenesis	23/1638	148/18670	0.005	0.035395	0.027149	CACNA1C	23
BP	GO:005159	response to stress	23/1638	148/18670	0.005	0.035395	0.027149	APOBEC1	23
BP	GO:007122	cellular response to stress	30/1638	209/18670	0.005011	0.035424	0.027171	APOB/AKR	30
BP	GO:000681	sodium ion transport	31/1638	218/18670	0.005043	0.035604	0.027309	ATP1A2/A	31
BP	GO:000328	ventricular septum development	14/1638	75/18670	0.00521	0.036689	0.028141	NKX2-5/C	14
BP	GO:002155	diencephalon development	14/1638	75/18670	0.00521	0.036689	0.028141	ADCYAP1	14
BP	GO:001024	establishment of planar polarity	5/1638	14/18670	0.00527	0.036813	0.028236	ATP1A2/A	5
BP	GO:003433	cell junction organization	5/1638	14/18670	0.00527	0.036813	0.028236	CSF1R/F2F	5
BP	GO:003535	regulation of cell cycle	5/1638	14/18670	0.00527	0.036813	0.028236	FABP5/LEF	5
BP	GO:004826	behavioral response	5/1638	14/18670	0.00527	0.036813	0.028236	NTRK1/TH	5
BP	GO:008606	bundle of myofibrils development	15/1638	14/18670	0.00527	0.036813	0.028236	CACNA2D	5
BP	GO:009715	GABAergic neuron development	5/1638	14/18670	0.00527	0.036813	0.028236	DLX1/DLX	5
BP	GO:003222	regulation of cell cycle	8/1638	32/18670	0.005363	0.037265	0.028583	CNR1/CNF	8
BP	GO:004590	positive regulation of cell cycle	8/1638	32/18670	0.005363	0.037265	0.028583	AVP/AVPR	8
BP	GO:006032	face morphogenesis	18/1638	32/18670	0.005363	0.037265	0.028583	COL1A1/M	8
BP	GO:006500	protein-lipid transport	8/1638	32/18670	0.005363	0.037265	0.028583	APOA1/AF	8
BP	GO:000995	anterior/posterior axis specification	31/1638	219/18670	0.005395	0.037435	0.028714	FOXF1/FO	31
BP	GO:000170	cell fate specification	17/1638	99/18670	0.005403	0.037443	0.028719	AR/EVX1/F	17
BP	GO:001407	response to stress	23/1638	149/18670	0.005435	0.037615	0.028852	ALDH3A1	23
BP	GO:000941	response to stress	39/1638	292/18670	0.005463	0.037758	0.028961	AGTR2/AL	39
BP	GO:003296	collagen biosynthesis	11/1638	53/18670	0.005568	0.038385	0.029442	COL1A1/C	11
BP	GO:004566	regulation of cell cycle	11/1638	53/18670	0.005568	0.038385	0.029442	MYF6/RIPC	11
BP	GO:004801	inositol lipid transport	27/1638	184/18670	0.005577	0.038397	0.029451	CSF1R/DC	27
BP	GO:000704	cell-cell junction organization	20/1638	124/18670	0.0056	0.038456	0.029496	ANK2/CAV	20
BP	GO:001401	regulation of cell cycle	20/1638	124/18670	0.0056	0.038456	0.029496	ADCYAP1	20
BP	GO:001081	negative regulation of cell cycle	13/1638	68/18670	0.005658	0.038755	0.029726	APOD/COI	13
BP	GO:003592	cellular response to stress	13/1638	68/18670	0.005658	0.038755	0.029726	DCN/VEGF	13
BP	GO:003004	muscle fiber development	9/1638	39/18670	0.005686	0.038845	0.029795	ACTC1/AC	9
BP	GO:003327	actin-myosin contractility	9/1638	39/18670	0.005686	0.038845	0.029795	ACTC1/AC	9
BP	GO:005073	regulation of cell cycle	35/1638	256/18670	0.005696	0.038865	0.02981	CAV1/CD3	35
BP	GO:005091	negative regulation of cell cycle	10/1638	46/18670	0.005721	0.03893	0.02986	APOA1/EP	10
BP	GO:005133	regulation of cell cycle	10/1638	46/18670	0.005721	0.03893	0.02986	CACNA1C	10
BP	GO:190355	negative regulation of cell cycle	30/1638	211/18670	0.005748	0.039065	0.029963	AGTR2/AP	30
BP	GO:001059	regulation of cell cycle	32/1638	229/18670	0.005769	0.039127	0.030011	AGTR2/AP	32
BP	GO:000242	immune response	58/1638	473/18670	0.005772	0.039127	0.030011	BLK/CD19	58
BP	GO:190101	positive regulation of cell cycle	7/1638	26/18670	0.005851	0.039615	0.030385	ACTN2/AN	7
BP	GO:003050	regulation of cell cycle	14/1638	76/18670	0.005884	0.039733	0.030476	AHSG/COI	14
BP	GO:007208	nephron epithelial cell development	14/1638	76/18670	0.005884	0.039733	0.030476	AGTR2/FG	14
BP	GO:009956	chemical synapse development	18/1638	108/18670	0.005898	0.039777	0.03051	CBLN1/CH	18
BP	GO:000762	copulation	6/1638	20/18670	0.005966	0.040082	0.030743	AVP/CNR1	6
BP	GO:003410	negative regulation of cell cycle	6/1638	20/18670	0.005966	0.040082	0.030743	CALCA/IL6	6
BP	GO:004874	smooth muscle cell development	6/1638	20/18670	0.005966	0.040082	0.030743	COL3A1/M	6
BP	GO:005149	regulation of cell cycle	15/1638	84/18670	0.006001	0.040264	0.030883	APOA1/CC	15
BP	GO:007170	tumor necrosis factor production	25/1638	168/18670	0.006237	0.041799	0.032061	AXL/BPI/C	25
BP	GO:005115	regulation of cell cycle	19/1638	117/18670	0.006331	0.042371	0.0325	ADGRB1/N	19
BP	GO:003016	proteoglycan synthesis	13/1638	69/18670	0.006425	0.042899	0.032905	BGN/VCAI	13
BP	GO:003235	response to stress	21/1638	134/18670	0.006446	0.042899	0.032905	ADCYAP1F	21
BP	GO:005099	regulation of cell cycle	11/1638	54/18670	0.00645	0.042899	0.032905	ABCD2/AP	11
BP	GO:006100	cell differentiation	11/1638	54/18670	0.00645	0.042899	0.032905	ACTA2/FO	11
BP	GO:007020	protein tripartite complex assembly	11/1638	54/18670	0.00645	0.042899	0.032905	COL1A1/C	11
BP	GO:001648	peptide hormone secretion	8/1638	33/18670	0.006545	0.043366	0.033262	CGA/CMA	8
BP	GO:003511	embryonic development	8/1638	33/18670	0.006545	0.043366	0.033262	CACNA1C	8
BP	GO:005195	regulation of cell cycle	8/1638	33/18670	0.006545	0.043366	0.033262	ATP1A2/A	8
BP	GO:004470	multi-organ system development	31/1638	222/18670	0.006575	0.043495	0.033361	ADCYAP1	31
BP	GO:003268	regulation of cell cycle	24/1638	160/18670	0.006581	0.043495	0.033361	AXL/BPI/C	24
BP	GO:005083	defense response	17/1638	101/18670	0.00663	0.043762	0.033567	TNFSF8/CI	17
BP	GO:004870	embryonic development	20/1638	126/18670	0.006704	0.044019	0.033764	NKX3-2/C	20
BP	GO:007208	nephron epithelial cell development	16/1638	93/18670	0.006705	0.044019	0.033764	AGTR2/FG	16
BP	GO:004880	genitalia development	10/1638	47/18670	0.006708	0.044019	0.033764	AR/AXL/ES	10
BP	GO:190311	regulation of cell cycle	10/1638	47/18670	0.006708	0.044019	0.033764	ANK2/ATP	10
BP	GO:003430	primary alcohol metabolism	15/1638	85/18670	0.006711	0.044019	0.033764	ADH1B/AI	15
BP	GO:000199	regulation of cell cycle	9/1638	40/18670	0.006778	0.04424	0.033933	AGTR1/AC	9

BP	GO:000761 mating	9/1638	40/18670	0.006778	0.04424	0.033933	AVP/CNR1	9
BP	GO:000918 cyclic nucleotide	9/1638	40/18670	0.006778	0.04424	0.033933	ADCY2/AC	9
BP	GO:005082 defense response	9/1638	40/18670	0.006778	0.04424	0.033933	CTSG/ELAI	9
BP	GO:000181 negative regulation of	39/1638	296/18670	0.006841	0.044601	0.03421	ABCD2/AP	39
BP	GO:001082 regulation of	12/1638	62/18670	0.006955	0.045174	0.03465	ADGRB1/N	12
BP	GO:003164 killing of cell	12/1638	62/18670	0.006955	0.045174	0.03465	CTSG/DEFI	12
BP	GO:004436 disruption of	12/1638	62/18670	0.006955	0.045174	0.03465	CTSG/DEFI	12
BP	GO:001921 regulation of	51/1638	410/18670	0.007036	0.04564	0.035007	AGTR1/AB	51
BP	GO:005125 positive regulation of	43/1638	334/18670	0.00705	0.04568	0.035038	AXL/CAV1	43
BP	GO:000602 glycosaminoglycan	18/1638	110/18670	0.007152	0.046283	0.0355	BGN/VCAI	18
BP	GO:006038 innervation of	7/1638	27/18670	0.007312	0.047041	0.036082	GABRA5/IS	7
BP	GO:001701 protein nitric oxide	5/1638	15/18670	0.007341	0.047041	0.036082	ATP2B4/DI	5
BP	GO:001811 peptidyl-cleavage	5/1638	15/18670	0.007341	0.047041	0.036082	ATP2B4/DI	5
BP	GO:003360 negative regulation of	5/1638	15/18670	0.007341	0.047041	0.036082	AGTR2/CN	5
BP	GO:005065 dermatan sulfate	5/1638	15/18670	0.007341	0.047041	0.036082	BGN/VCAI	5
BP	GO:006051 ventral spiracle	5/1638	15/18670	0.007341	0.047041	0.036082	EVX1/GLI2	5
BP	GO:006058 cell fate commitment	5/1638	15/18670	0.007341	0.047041	0.036082	EVX1/GLI2	5
BP	GO:190184 regulation of	5/1638	15/18670	0.007341	0.047041	0.036082	CACNA2D	5
BP	GO:000322 ventricular	11/1638	55/18670	0.007439	0.047334	0.036306	COL11A1/	11
BP	GO:004355 regulation of	11/1638	55/18670	0.007439	0.047334	0.036306	CD19/CCR	11
BP	GO:006133 renal tubule	14/1638	78/18670	0.007439	0.047334	0.036306	AGTR2/FG	14
BP	GO:000602 proteoglycan	16/1638	94/18670	0.00744	0.047334	0.036306	BGN/COL1	16
BP	GO:006095 kidney morphogenesis	16/1638	94/18670	0.00744	0.047334	0.036306	AGTR2/FG	16
BP	GO:007016 regulation of	16/1638	94/18670	0.00744	0.047334	0.036306	AHSG/COI	16
BP	GO:004592 positive regulation of	36/1638	270/18670	0.007577	0.048148	0.03693	AVP/ERBB	36
BP	GO:000195 regulation of	19/1638	119/18670	0.0076	0.048235	0.036997	APOD/CD	19
BP	GO:001097 regulation of	60/1638	499/18670	0.007642	0.048441	0.037155	ADCYAP1/	60
BP	GO:011005 regulation of	35/1638	261/18670	0.007678	0.048611	0.037286	ACTN2/AC	35
BP	GO:003072 ovulation	6/1638	21/18670	0.007742	0.048901	0.037508	AFP/INH	6
BP	GO:004848 sympathetic	6/1638	21/18670	0.007742	0.048901	0.037508	PHOX2A/N	6
BP	GO:001010 potassium	10/1638	48/18670	0.007822	0.049114	0.037671	ATP1A2/A	10
BP	GO:001633 calcium-dependent	10/1638	48/18670	0.007822	0.049114	0.037671	CDH9/CD	10
BP	GO:004326 positive regulation of	10/1638	48/18670	0.007822	0.049114	0.037671	ACTN2/AN	10
BP	GO:004685 regulation of	10/1638	48/18670	0.007822	0.049114	0.037671	CALCA/CS	10
BP	GO:006032 face development	10/1638	48/18670	0.007822	0.049114	0.037671	ALDH1A3/	10
BP	GO:004804 embryonic	8/1638	34/18670	0.007914	0.049368	0.037866	ALDH1A3/	8
BP	GO:003164 positive regulation of	12/1638	63/18670	0.007923	0.049368	0.037866	HGF/NTSR	12
BP	GO:002240 regulation of	50/1638	403/18670	0.007931	0.049368	0.037866	APOA1/CA	50
BP	GO:004566 negative regulation of	31/1638	225/18670	0.007963	0.049368	0.037866	DLX1/DLX	31
BP	GO:004251 retinol metabolism	9/1638	41/18670	0.008023	0.049368	0.037866	ADH1B/AC	9
BP	GO:004326 negative regulation of	9/1638	41/18670	0.008023	0.049368	0.037866	ACTN2/AC	9
BP	GO:004828 lung alveolus	9/1638	41/18670	0.008023	0.049368	0.037866	FGF10/FO	9
BP	GO:009027 regulation of	9/1638	41/18670	0.008023	0.049368	0.037866	CRH/GCG/	9
BP	GO:190138 positive regulation of	9/1638	41/18670	0.008023	0.049368	0.037866	ACTN2/AN	9
BP	GO:000176 establishment of	4/1638	10/18670	0.00805	0.049368	0.037866	CCR7/CCL	4
BP	GO:003537 sterol import	4/1638	10/18670	0.00805	0.049368	0.037866	APOA1/AF	4
BP	GO:004455 relaxation of	4/1638	10/18670	0.00805	0.049368	0.037866	GUCY1A1/	4
BP	GO:005100 positive regulation of	4/1638	10/18670	0.00805	0.049368	0.037866	APOA4/AF	4
BP	GO:006034 bone trabeculae	4/1638	10/18670	0.00805	0.049368	0.037866	COL1A1/N	4
BP	GO:007005 glucagon secretion	4/1638	10/18670	0.00805	0.049368	0.037866	CRH/IL6/LI	4
BP	GO:007050 cholesterol	4/1638	10/18670	0.00805	0.049368	0.037866	APOA1/AF	4
BP	GO:009710 presynaptic	4/1638	10/18670	0.00805	0.049368	0.037866	CEL/NLGN	4
BP	GO:009891 retrograde	4/1638	10/18670	0.00805	0.049368	0.037866	CNR1/FAB	4
BP	GO:200042 regulation of	4/1638	10/18670	0.00805	0.049368	0.037866	C3/C4A/C	4
BP	GO:200083 positive regulation of	4/1638	10/18670	0.00805	0.049368	0.037866	CRH/GALR	4
BP	GO:000715 leukocyte	43/1638	337/18670	0.008216	0.050287	0.038571	ADD2/APC	43
BP	GO:005500 cardiac cell	16/1638	95/18670	0.008238	0.050287	0.038571	ACTC1/AC	16
BP	GO:006133 renal tubule	16/1638	95/18670	0.008238	0.050287	0.038571	AGTR2/FG	16
BP	GO:011002 regulation of	16/1638	95/18670	0.008238	0.050287	0.038571	APOA1/CC	16
BP	GO:003264 tumor necrosis	24/1638	163/18670	0.008268	0.050355	0.038623	AXL/BPI/C	24
BP	GO:190355 regulation of	24/1638	163/18670	0.008268	0.050355	0.038623	AXL/BPI/C	24
BP	GO:000301 renal system	19/1638	120/18670	0.008308	0.050508	0.03874	ADCY2/AC	19

BP	GO:001406	positive re	15/1638	87/18670	0.008332	0.050508	0.03874	DCN/F2/F	15
BP	GO:004584	positive re	15/1638	87/18670	0.008332	0.050508	0.03874	FGF2/FGFF	15
BP	GO:004863	positive re	15/1638	87/18670	0.008332	0.050508	0.03874	FGF2/FGFF	15
BP	GO:006056	developm	32/1638	235/18670	0.008412	0.050938	0.03907	S1PR1/EP	32
BP	GO:004801	phosphatic	26/1638	181/18670	0.008476	0.051207	0.039276	CSF1R/DC	26
BP	GO:005114	regulation	26/1638	181/18670	0.008476	0.051207	0.039276	ADGRB1/N	26
BP	GO:000076	syncytium	11/1638	56/18670	0.008541	0.051483	0.039488	ADGRB1/A	11
BP	GO:014025	cell-cell fu	11/1638	56/18670	0.008541	0.051483	0.039488	ADGRB1/A	11
BP	GO:190351	mucopolys	18/1638	112/18670	0.008614	0.05186	0.039777	BGN/VCA	18
BP	GO:001481	muscle cel	17/1638	104/18670	0.008884	0.053425	0.040978	IGF1/IGFB	17
BP	GO:004355	regulation	12/1638	64/18670	0.008993	0.053604	0.041116	CD19/CCR	12
BP	GO:004656	glycerolip	12/1638	64/18670	0.008993	0.053604	0.041116	APOA1/AF	12
BP	GO:004824	lymphocyt	12/1638	64/18670	0.008993	0.053604	0.041116	S100A7/C	12
BP	GO:190044	regulation	12/1638	64/18670	0.008993	0.053604	0.041116	ACTN2/CR	12
BP	GO:190367	positive re	12/1638	64/18670	0.008993	0.053604	0.041116	AGTR1/AP	12
BP	GO:000265	regulation	7/1638	28/18670	0.009026	0.053604	0.041116	ELANE/IL1	7
BP	GO:000318	aortic valv	7/1638	28/18670	0.009026	0.053604	0.041116	ELN/SLIT3	7
BP	GO:003368	regulation	7/1638	28/18670	0.009026	0.053604	0.041116	CCN1/NPF	7
BP	GO:003437	plasma lip	7/1638	28/18670	0.009026	0.053604	0.041116	APOA1/AF	7
BP	GO:004576	regulation	7/1638	28/18670	0.009026	0.053604	0.041116	CACNA1C	7
BP	GO:200046	positive re	7/1638	28/18670	0.009026	0.053604	0.041116	RELN/RGS	7
BP	GO:007182	protein-lip	10/1638	49/18670	0.009074	0.053832	0.04129	AGTR1/AP	10
BP	GO:004801	vascular er	16/1638	96/18670	0.009103	0.053943	0.041375	AXL/FGF1C	16
BP	GO:005115	positive re	13/1638	72/18670	0.009231	0.054639	0.041909	ADGRB1/K	13
BP	GO:190186	positive re	15/1638	88/18670	0.009251	0.054639	0.041909	FGF2/FGFF	15
BP	GO:190188	regulation	15/1638	88/18670	0.009251	0.054639	0.041909	APOD/CA	15
BP	GO:009962	cardiac m	9/1638	42/18670	0.009435	0.055658	0.042691	ANK2/CAC	9
BP	GO:011011	negative r	8/1638	35/18670	0.009488	0.055909	0.042884	CPB2/FOX	8
BP	GO:000758	response t	30/1638	219/18670	0.009662	0.056874	0.043623	ALDH3A1/	30
BP	GO:000204	sprouting	26/1638	183/18670	0.009735	0.057238	0.043903	AGTR1/AP	26
BP	GO:000664	triglyceride	17/1638	105/18670	0.009758	0.057252	0.043914	APOA1/AF	17
BP	GO:190115	carbohydr	27/1638	192/18670	0.009759	0.057252	0.043914	APOBEC1/	27
BP	GO:000919	cyclic nucl	6/1638	22/18670	0.009869	0.057351	0.043989	ADCY2/AC	6
BP	GO:002151	spinal corc	6/1638	22/18670	0.009869	0.057351	0.043989	EVX1/GLI2	6
BP	GO:003128	positive re	6/1638	22/18670	0.009869	0.057351	0.043989	CACNA1C	6
BP	GO:004566	positive re	6/1638	22/18670	0.009869	0.057351	0.043989	MYF6/RIPC	6
BP	GO:005265	cyclic purin	6/1638	22/18670	0.009869	0.057351	0.043989	ADCY2/AC	6
BP	GO:000178	neutrophil	5/1638	16/18670	0.009917	0.057351	0.043989	AXL/IL6/IT	5
BP	GO:000695	compleme	5/1638	16/18670	0.009917	0.057351	0.043989	C3/C7/CR1	5
BP	GO:004303	negative re	5/1638	16/18670	0.009917	0.057351	0.043989	BPI/FCGR2	5
BP	GO:005065	dermatan	5/1638	16/18670	0.009917	0.057351	0.043989	BGN/VCA	5
BP	GO:005123	sequesterin	5/1638	16/18670	0.009917	0.057351	0.043989	LCN2/S100	5
BP	GO:007059	dendrite s	5/1638	16/18670	0.009917	0.057351	0.043989	CNTN2/PA	5
BP	GO:190515	regulation	5/1638	16/18670	0.009917	0.057351	0.043989	C3/CD36/F	5
BP	GO:200084	regulation	5/1638	16/18670	0.009917	0.057351	0.043989	AGTR1/AG	5
BP	GO:000694	regulation	12/1638	65/18670	0.010172	0.058693	0.045019	ATP1A2/C	12
BP	GO:007267	T cell migr	12/1638	65/18670	0.010172	0.058693	0.045019	APOD/S1P	12
BP	GO:000719	adenylate	15/1638	89/18670	0.01025	0.058837	0.045129	ADCY2/AC	15
BP	GO:003266	chemokine	15/1638	89/18670	0.01025	0.058837	0.045129	ADCYAP1/	15
BP	GO:004642	positive re	15/1638	89/18670	0.01025	0.058837	0.045129	CSF1R/CYF	15
BP	GO:190101	regulation	15/1638	89/18670	0.01025	0.058837	0.045129	ANK2/ATP	15
BP	GO:004688	positive re	20/1638	131/18670	0.010252	0.058837	0.045129	ADCYAP1/	20
BP	GO:000686	superoxide	13/1638	73/18670	0.010354	0.05922	0.045423	APOA4/CI	13
BP	GO:004362	response t	13/1638	73/18670	0.010354	0.05922	0.045423	APOA1/AF	13
BP	GO:190352	positive re	13/1638	73/18670	0.010354	0.05922	0.045423	AVP/AVPR	13
BP	GO:000269	positive re	47/1638	380/18670	0.010364	0.05922	0.045423	AXL/CAV1	47
BP	GO:001071	positive re	10/1638	50/18670	0.010473	0.059715	0.045803	COL1A1/IL	10
BP	GO:004516	intermedia	10/1638	50/18670	0.010473	0.059715	0.045803	DES/GFAP	10
BP	GO:003502	regulation	21/1638	140/18670	0.010546	0.060066	0.046072	APOA1/AF	21
BP	GO:190296	regulation	44/1638	352/18670	0.010744	0.061124	0.046883	ACTN2/AC	44
BP	GO:004859	eye morph	22/1638	149/18670	0.010772	0.061222	0.046958	ALDH1A3/	22
BP	GO:000301	respiratory	7/1638	29/18670	0.011016	0.061988	0.047546	ATP1A2/N	7

BP	GO:001088 regulation	7/1638	29/18670	0.011016	0.061988	0.047546	ANK2/ATP	7
BP	GO:003222 negative regulation	7/1638	29/18670	0.011016	0.061988	0.047546	S1PR1/MY	7
BP	GO:005088 regulation	7/1638	29/18670	0.011016	0.061988	0.047546	BLK/CD19	7
BP	GO:005507 potassium ion transport	7/1638	29/18670	0.011016	0.061988	0.047546	ATP1A2/ATP	7
BP	GO:006044 epithelial cell morphogenesis	7/1638	29/18670	0.011016	0.061988	0.047546	FGF10/FOXP	7
BP	GO:000198 negative regulation	9/1638	43/18670	0.011026	0.061988	0.047546	APOD1/MY	9
BP	GO:002175 cerebral cortex development	9/1638	43/18670	0.011026	0.061988	0.047546	GLI3/POU3	9
BP	GO:004361 keratinocyte differentiation	9/1638	43/18670	0.011026	0.061988	0.047546	KLF9/FGF7	9
BP	GO:008600 regulation	9/1638	43/18670	0.011026	0.061988	0.047546	ANK2/ATP	9
BP	GO:004247 inner ear development	16/1638	98/18670	0.011048	0.061988	0.047546	ALDH1A3/	16
BP	GO:005084 regulation	16/1638	98/18670	0.011048	0.061988	0.047546	ATP2B4/C	16
BP	GO:000726 Rho protein signaling	28/1638	203/18670	0.011088	0.062006	0.04756	AGTR1/AP	28
BP	GO:004255 myelination	20/1638	132/18670	0.011117	0.062006	0.04756	ABCD2/AN	20
BP	GO:004555 regulation	20/1638	132/18670	0.011117	0.062006	0.04756	RUNX1T1/	20
BP	GO:004595 regulation	20/1638	132/18670	0.011117	0.062006	0.04756	APOA1/AF	20
BP	GO:000694 syncytium formation	11/1638	58/18670	0.011122	0.062006	0.04756	ADGRB1/A	11
BP	GO:007138 cellular response	11/1638	58/18670	0.011122	0.062006	0.04756	ADCYAP1/	11
BP	GO:000602 aminoglycoside resistance	18/1638	115/18670	0.011246	0.062632	0.04804	BGN/VCA	18
BP	GO:001045 regulation	8/1638	36/18670	0.011283	0.06264	0.048046	AR/FGF2/F	8
BP	GO:190262 regulation	8/1638	36/18670	0.011283	0.06264	0.048046	CCR7/IL1R	8
BP	GO:000165 metanephros development	15/1638	90/18670	0.011331	0.06264	0.048046	AGTR2/FBI	15
BP	GO:000995 dorsal/ventral axis	15/1638	90/18670	0.011331	0.06264	0.048046	EVX1/GLI1	15
BP	GO:001403 neural crest development	15/1638	90/18670	0.011331	0.06264	0.048046	ANXA6/EC	15
BP	GO:003433 adherens junction	15/1638	90/18670	0.011331	0.06264	0.048046	ACTN2/AP	15
BP	GO:004247 odontogenesis	15/1638	90/18670	0.011331	0.06264	0.048046	DLX1/DLX	15
BP	GO:190488 cranial skeletal development	12/1638	66/18670	0.011467	0.063326	0.048572	DLX2/FOX	12
BP	GO:003027 negative regulation	14/1638	82/18670	0.01152	0.063485	0.048694	AHSG/GDF	14
BP	GO:005511 regulation	14/1638	82/18670	0.01152	0.063485	0.048694	ANK2/ATP	14
BP	GO:003167 cellular response	13/1638	74/18670	0.01158	0.063751	0.048899	COL1A1/F	13
BP	GO:000176 establishment of	4/1638	11/18670	0.011781	0.063794	0.048931	CCR7/CCL	4
BP	GO:000618 cGMP biosynthesis	4/1638	11/18670	0.011781	0.063794	0.048931	GUCY1A1/	4
BP	GO:002152 ventral spiracle	4/1638	11/18670	0.011781	0.063794	0.048931	EVX1/GLI2	4
BP	GO:002185 cerebral cortex	4/1638	11/18670	0.011781	0.063794	0.048931	DLX1/DLX	4
BP	GO:003227 regulation	4/1638	11/18670	0.011781	0.063794	0.048931	CRH/INHB	4
BP	GO:003362 negative regulation	4/1638	11/18670	0.011781	0.063794	0.048931	CYP1B1/SE	4
BP	GO:003593 glucocorticoid	4/1638	11/18670	0.011781	0.063794	0.048931	CRH/GALR	4
BP	GO:004521 cell-cell junction	4/1638	11/18670	0.011781	0.063794	0.048931	CSF1R/F2F	4
BP	GO:006037 cardiac muscle	4/1638	11/18670	0.011781	0.063794	0.048931	ISL1/GREN	4
BP	GO:006057 cell fate specification	4/1638	11/18670	0.011781	0.063794	0.048931	EVX1/GLI2	4
BP	GO:006085 establishment of	4/1638	11/18670	0.011781	0.063794	0.048931	TPPA/RECI	4
BP	GO:007253 fibroblast chemotaxis	4/1638	11/18670	0.011781	0.063794	0.048931	LEP/PDGF	4
BP	GO:009888 synapse pruning	4/1638	11/18670	0.011781	0.063794	0.048931	C3/CX3CR	4
BP	GO:009915 regulation	4/1638	11/18670	0.011781	0.063794	0.048931	CBLN1/NT	4
BP	GO:190256 regulation	4/1638	11/18670	0.011781	0.063794	0.048931	FCGR2B/IT	4
BP	GO:190590 regulation	4/1638	11/18670	0.011781	0.063794	0.048931	FGFR1/SFR	4
BP	GO:000150 regulation	44/1638	354/18670	0.011804	0.063849	0.048973	AGTR2/AT	44
BP	GO:000190 cell killing	24/1638	168/18670	0.011854	0.064054	0.04913	C3/CD1C/	24
BP	GO:005088 antigen receptor	40/1638	316/18670	0.011912	0.064303	0.049322	BLK/CD19	40
BP	GO:001003 response to	45/1638	364/18670	0.012021	0.064585	0.049538	APBB1/AP	45
BP	GO:002154 cranial nerve	10/1638	51/18670	0.012031	0.064585	0.049538	PHOX2A/C	10
BP	GO:005095 regulation	10/1638	51/18670	0.012031	0.064585	0.049538	AGTR2/AT	10
BP	GO:005145 positive regulation	10/1638	51/18670	0.012031	0.064585	0.049538	APOA1/CC	10
BP	GO:009736 response to	10/1638	51/18670	0.012031	0.064585	0.049538	CCR7/CNR	10
BP	GO:000722 smoothened	20/1638	133/18670	0.012038	0.064585	0.049538	EVC/FGF1	20
BP	GO:004513 development	30/1638	223/18670	0.012317	0.066018	0.050637	ADCYAP1/	30
BP	GO:000955 detection of	6/1638	23/18670	0.012382	0.066027	0.050644	C4B/TREM	6
BP	GO:003053 male genital	6/1638	23/18670	0.012382	0.066027	0.050644	AR/FGF10/	6
BP	GO:004510 intermediate	6/1638	23/18670	0.012382	0.066027	0.050644	DES/GFAP	6
BP	GO:005134 positive regulation	6/1638	23/18670	0.012382	0.066027	0.050644	CACNA1C	6
BP	GO:200005 regulation	6/1638	23/18670	0.012382	0.066027	0.050644	SFRP1/SFR	6
BP	GO:002306 signal release	55/1638	462/18670	0.012439	0.066266	0.050827	ADCY5/AC	55
BP	GO:001490 smooth muscle	15/1638	91/18670	0.012499	0.066519	0.051021	IGF1/IGFB	15

BP	GO:004684 filopodium	11/1638	59/18670	0.012617	0.067004	0.051393	CCR7/DPY	11
BP	GO:009775 positive re	11/1638	59/18670	0.012617	0.067004	0.051393	ADCYAP1/	11
BP	GO:190330 regulation	23/1638	160/18670	0.012628	0.067004	0.051393	CACNB2/C	23
BP	GO:190384 negative re	14/1638	83/18670	0.012771	0.067693	0.051922	CAV1/CIDI	14
BP	GO:190465 glucose tra	17/1638	108/18670	0.012798	0.067697	0.051925	C3/EDNRA	17
BP	GO:000315 endocardia	9/1638	44/18670	0.01281	0.067697	0.051925	FOXF1/ISL	9
BP	GO:003296 regulation	9/1638	44/18670	0.01281	0.067697	0.051925	CCN2/F2/F	9
BP	GO:006003 cardiac m	12/1638	67/18670	0.012885	0.068025	0.052177	NKX2-5/FO	12
BP	GO:000170 mesoderm	13/1638	75/18670	0.012916	0.06805	0.052195	FGFR1/FO	13
BP	GO:000742 peripheral	13/1638	75/18670	0.012916	0.06805	0.052195	ADGRB1/E	13
BP	GO:000727 ensheathm	20/1638	134/18670	0.013019	0.06829	0.05238	ABCD2/AM	20
BP	GO:000836 axon ensh	20/1638	134/18670	0.013019	0.06829	0.05238	ABCD2/AM	20
BP	GO:000265 positive re	5/1638	17/18670	0.013052	0.06829	0.05238	ELANE/IL1	5
BP	GO:002151 ventral spir	5/1638	17/18670	0.013052	0.06829	0.05238	EVX1/GLI2	5
BP	GO:003598 chondrocy	5/1638	17/18670	0.013052	0.06829	0.05238	COMP/CC	5
BP	GO:003614 phosphatic	5/1638	17/18670	0.013052	0.06829	0.05238	PLA2G1B/I	5
BP	GO:190494 midbrain c	5/1638	17/18670	0.013052	0.06829	0.05238	LMX1A/SF	5
BP	GO:009002 regulation	7/1638	30/18670	0.013305	0.069146	0.053037	CCR7/CCL	7
BP	GO:006007 excitatory	16/1638	100/18670	0.013307	0.069146	0.053037	CBLN1/CH	16
BP	GO:200102 regulation	16/1638	100/18670	0.013307	0.069146	0.053037	ATP1A2/C	16
BP	GO:000315 regulation	8/1638	37/18670	0.013316	0.069146	0.053037	AR/FGF10/	8
BP	GO:003107 embryonic	8/1638	37/18670	0.013316	0.069146	0.053037	ALDH1A3/	8
BP	GO:004592 positive re	8/1638	37/18670	0.013316	0.069146	0.053037	ABCD2/AP	8
BP	GO:006032 head morp	8/1638	37/18670	0.013316	0.069146	0.053037	COL1A1/N	8
BP	GO:004862 regulation	43/1638	347/18670	0.013321	0.069146	0.053037	AR/NKX2-	43
BP	GO:002260 regulation	57/1638	484/18670	0.013634	0.070703	0.054231	APOA1/AC	57
BP	GO:000962 response t	10/1638	52/18670	0.013756	0.071004	0.054462	CTSG/ELAI	10
BP	GO:006042 positive re	10/1638	52/18670	0.013756	0.071004	0.054462	FGF2/FGFF	10
BP	GO:190002 regulation	10/1638	52/18670	0.013756	0.071004	0.054462	APOA1/FB	10
BP	GO:200017 positive re	10/1638	52/18670	0.013756	0.071004	0.054462	CX3CR1/FI	10
BP	GO:190489 positive re	15/1638	92/18670	0.013759	0.071004	0.054462	CSF1R/CYF	15
BP	GO:005114 positive re	17/1638	109/18670	0.013962	0.071979	0.055209	ADGRB1/K	17
BP	GO:001491 regulation	14/1638	84/18670	0.014125	0.072679	0.055746	IGF1/IGFBF	14
BP	GO:004544 myoblast c	14/1638	84/18670	0.014125	0.072679	0.055746	IGF1/ISL1/	14
BP	GO:005189 regulation	11/1638	60/18670	0.01426	0.073229	0.056168	APOD/COI	11
BP	GO:009010 regulation	11/1638	60/18670	0.01426	0.073229	0.056168	APOD/COI	11
BP	GO:001401 negative re	9/1638	45/18670	0.0148	0.075857	0.058184	ADCYAP1/	9
BP	GO:007182 plasma lip	9/1638	45/18670	0.0148	0.075857	0.058184	AGTR1/AP	9
BP	GO:000840 gonad dev	29/1638	217/18670	0.01489	0.076244	0.058481	ADCYAP1/	29
BP	GO:004870 embryonic	15/1638	93/18670	0.015116	0.077323	0.059309	COL11A1/	15
BP	GO:001064 regulation	6/1638	24/18670	0.015311	0.078017	0.059841	APOD/F7/I	6
BP	GO:005099 positive re	6/1638	24/18670	0.015311	0.078017	0.059841	ABCD2/AP	6
BP	GO:008600 cell comm	6/1638	24/18670	0.015311	0.078017	0.059841	ATP1A2/A	6
BP	GO:200102 regulation	6/1638	24/18670	0.015311	0.078017	0.059841	FGF2/FGFF	6
BP	GO:002240 negative re	25/1638	181/18670	0.015487	0.078801	0.060442	APOA1/DI	25
BP	GO:001071 positive re	22/1638	154/18670	0.015494	0.078801	0.060442	APOA1/FG	22
BP	GO:001403 mesenchyr	14/1638	85/18670	0.015587	0.079113	0.060681	ANXA6/EC	14
BP	GO:005071 positive re	14/1638	85/18670	0.015587	0.079113	0.060681	FN1/MAP1	14
BP	GO:190102 positive re	8/1638	38/18670	0.015604	0.079113	0.060681	ANK2/CAC	8
BP	GO:001004 response t	10/1638	53/18670	0.015661	0.079113	0.060681	APOBEC1/	10
BP	GO:002187 forebrain r	10/1638	53/18670	0.015661	0.079113	0.060681	CSF1R/DL	10
BP	GO:003163 zymogen a	10/1638	53/18670	0.015661	0.079113	0.060681	APOH/C1F	10
BP	GO:190551 macrophag	10/1638	53/18670	0.015661	0.079113	0.060681	CX3CR1/C	10
BP	GO:000991 hormone t	40/1638	322/18670	0.015906	0.079456	0.060944	ADCY5/AC	40
BP	GO:200037 positive re	16/1638	102/18670	0.015911	0.079456	0.060944	AGTR1/AC	16
BP	GO:000267 positive re	7/1638	31/18670	0.015917	0.079456	0.060944	C3/CCR7/C	7
BP	GO:000340 axis elong	7/1638	31/18670	0.015917	0.079456	0.060944	ESR1/FGF1	7
BP	GO:001076 regulation	7/1638	31/18670	0.015917	0.079456	0.060944	FGF2/HAS	7
BP	GO:003368 osteoblast	7/1638	31/18670	0.015917	0.079456	0.060944	CCN1/NPF	7
BP	GO:004431 wound hea	7/1638	31/18670	0.015917	0.079456	0.060944	COL5A1/FI	7
BP	GO:006029 long-term	7/1638	31/18670	0.015917	0.079456	0.060944	CBLN1/DR	7
BP	GO:008601 membrane	7/1638	31/18670	0.015917	0.079456	0.060944	CACNA2D	7

BP	GO:009050	epiboly inv 7/1638	31/18670	0.015917	0.079456	0.060944	COL5A1/FI	7
BP	GO:009962	ventricular 7/1638	31/18670	0.015917	0.079456	0.060944	ANK2/CAC	7
BP	GO:200040	positive re 7/1638	31/18670	0.015917	0.079456	0.060944	S100A7/CO	7
BP	GO:004830	mesoderm 13/1638	77/18670	0.015939	0.079456	0.060944	FGFR1/FO	13
BP	GO:005190	catecholam 13/1638	77/18670	0.015939	0.079456	0.060944	AGTR2/CN	13
BP	GO:004270	embryonic 11/1638	61/18670	0.016059	0.079899	0.061284	GLI2/GLI3/	11
BP	GO:007130	cellular res 11/1638	61/18670	0.016059	0.079899	0.061284	ADCYAP1/	11
BP	GO:001050	positive re 19/1638	128/18670	0.01608	0.079931	0.061308	FGF2/FGFF	19
BP	GO:007130	cellular res 12/1638	69/18670	0.01612	0.080054	0.061403	COL1A1/E	12
BP	GO:000260	negative re 4/1638	12/18670	0.016463	0.081373	0.062414	ADCYAP1/	4
BP	GO:000280	negative re 4/1638	12/18670	0.016463	0.081373	0.062414	ADCYAP1/	4
BP	GO:000290	negative re 4/1638	12/18670	0.016463	0.081373	0.062414	A2M/SERP	4
BP	GO:008600	AV node c 4/1638	12/18670	0.016463	0.081373	0.062414	CACNA1C,	4
BP	GO:009950	regulation 4/1638	12/18670	0.016463	0.081373	0.062414	GRIA1/ITPI	4
BP	GO:000160	temperatu 24/1638	173/18670	0.016595	0.081947	0.062855	ADCYAP1/	24
BP	GO:005180	negative re 5/1638	18/18670	0.016792	0.08277	0.063486	APOD/TH	5
BP	GO:009700	craniofacia 5/1638	18/18670	0.016792	0.08277	0.063486	GLI3/MMP	5
BP	GO:004680	regulation 34/1638	266/18670	0.016845	0.08295	0.063624	ADCY5/AC	34
BP	GO:000960	response t 28/1638	210/18670	0.016975	0.083369	0.063945	ATP1A2/C	28
BP	GO:000240	inflammato 9/1638	46/18670	0.017009	0.083369	0.063945	ADCYAP1/	9
BP	GO:001970	antibacteri 9/1638	46/18670	0.017009	0.083369	0.063945	CTSG/DEF	9
BP	GO:003360	regulation 9/1638	46/18670	0.017009	0.083369	0.063945	CYP1B1/FC	9
BP	GO:004570	negative re 9/1638	46/18670	0.017009	0.083369	0.063945	ADRB3/AC	9
BP	GO:006020	long-term 14/1638	86/18670	0.017162	0.084042	0.064462	CRH/CX3C	14
BP	GO:190210	negative re 16/1638	103/18670	0.017353	0.084761	0.065014	DTX1/ERBI	16
BP	GO:000660	acylglycer 19/1638	129/18670	0.017357	0.084761	0.065014	APOA1/AF	19
BP	GO:003470	cellular ho 19/1638	129/18670	0.017357	0.084761	0.065014	ADH1B/AC	19
BP	GO:001080	regulation 13/1638	78/18670	0.017639	0.085979	0.065948	C3/EDNRA	13
BP	GO:002190	central ner 13/1638	78/18670	0.017639	0.085979	0.065948	CDH11/GL	13
BP	GO:007160	anatomica 23/1638	165/18670	0.017774	0.086558	0.066392	ADGRB3/C	23
BP	GO:003270	negative re 12/1638	70/18670	0.01795	0.086869	0.06663	AXL/BPI/C	12
BP	GO:005070	positive re 12/1638	70/18670	0.01795	0.086869	0.06663	AHSG/APC	12
BP	GO:006030	SMAD pro 12/1638	70/18670	0.01795	0.086869	0.06663	AFP/BMP3	12
BP	GO:000320	cardiac seq 17/1638	112/18670	0.017954	0.086869	0.06663	ANK2/NKX	17
BP	GO:000860	hexose tra 17/1638	112/18670	0.017954	0.086869	0.06663	C3/EDNRA	17
BP	GO:001710	regulation 17/1638	112/18670	0.017954	0.086869	0.06663	CACNB2/C	17
BP	GO:004850	camera-ty 17/1638	112/18670	0.017954	0.086869	0.06663	ALDH1A3/	17
BP	GO:005500	positive re 11/1638	62/18670	0.018022	0.087121	0.066823	FGF2/FGFF	11
BP	GO:001070	fibroblast 8/1638	39/18670	0.018163	0.087561	0.067161	FGF2/HAS	8
BP	GO:003810	neurotropl 8/1638	39/18670	0.018163	0.087561	0.067161	AGTR2/NC	8
BP	GO:005190	regulation 8/1638	39/18670	0.018163	0.087561	0.067161	F2R/FABP	8
BP	GO:000190	lymph vess 6/1638	25/18670	0.018686	0.089634	0.068751	FOXC2/PR	6
BP	GO:000200	positive re 6/1638	25/18670	0.018686	0.089634	0.068751	FGFR1/FO	6
BP	GO:003100	hair follicle 6/1638	25/18670	0.018686	0.089634	0.068751	FGF7/FGF1	6
BP	GO:007220	cell differe 6/1638	25/18670	0.018686	0.089634	0.068751	POU3F3/T	6
BP	GO:009000	regulation 6/1638	25/18670	0.018686	0.089634	0.068751	SERPINE1/	6
BP	GO:004860	positive re 25/1638	184/18670	0.018703	0.089634	0.068751	FGF2/FGFF	25
BP	GO:000660	neutral lipi 19/1638	130/18670	0.018712	0.089634	0.068751	APOA1/AF	19
BP	GO:000190	response t 7/1638	32/18670	0.018872	0.08977	0.068855	CNR2/DRE	7
BP	GO:000310	aortic valv 7/1638	32/18670	0.018872	0.08977	0.068855	ELN/SLIT3	7
BP	GO:000760	long-term 7/1638	32/18670	0.018872	0.08977	0.068855	GRIA1/NF	7
BP	GO:004250	retinoic aci 7/1638	32/18670	0.018872	0.08977	0.068855	ADH1B/AC	7
BP	GO:006130	heart trabe 7/1638	32/18670	0.018872	0.08977	0.068855	NKX2-5/S	7
BP	GO:009050	epiboly 7/1638	32/18670	0.018872	0.08977	0.068855	COL5A1/FI	7
BP	GO:009960	regulation 7/1638	32/18670	0.018872	0.08977	0.068855	ANK2/CAC	7
BP	GO:000240	immune re 20/1638	139/18670	0.018911	0.08977	0.068855	FCGR2B/IC	20
BP	GO:003800	Fc-gamma 20/1638	139/18670	0.018911	0.08977	0.068855	FCGR2B/IC	20
BP	GO:005150	regulation 20/1638	139/18670	0.018911	0.08977	0.068855	ATP1A2/C	20
BP	GO:000270	negative re 21/1638	148/18670	0.019012	0.090169	0.069161	APOA1/AF	21
BP	GO:190590	regulation 22/1638	157/18670	0.01903	0.090174	0.069166	AGTR1/AC	22
BP	GO:004660	regulation 17/1638	113/18670	0.019463	0.092107	0.070648	NKX2-5/FC	17
BP	GO:000150	vasculoger 13/1638	79/18670	0.019473	0.092107	0.070648	APLN/CA	13

BP	GO:000275 positive regulation of	36/1638	288/18670	0.019536	0.092323	0.070813	ADCYAP1/	36
BP	GO:009956 synaptic vesicle	26/1638	194/18670	0.019639	0.092725	0.071122	AMPH/CA	26
BP	GO:003275 positive regulation of	15/1638	96/18670	0.019809	0.093445	0.071674	ADCYAP1/	15
BP	GO:004255 positive regulation of	12/1638	71/18670	0.019932	0.093944	0.072057	CSF1R/FLT	12
BP	GO:004311 receptor cell-cell	10/1638	55/18670	0.020046	0.094311	0.072339	FLNA/GLR	10
BP	GO:004427 sulfur compound	10/1638	55/18670	0.020046	0.094311	0.072339	BGN/CDO	10
BP	GO:003541 protein localization	11/1638	63/18670	0.020159	0.094756	0.07268	GRIN2A/M	11
BP	GO:190290 positive regulation of	27/1638	204/18670	0.020509	0.096319	0.073878	ACTN2/AP	27
BP	GO:000706 plasma membrane	16/1638	105/18670	0.020535	0.096354	0.073905	ABCD2/AN	16
BP	GO:005082 defense response	14/1638	88/18670	0.020673	0.096914	0.074335	ADGRB1/B	14
BP	GO:200037 regulation of	26/1638	195/18670	0.020833	0.097579	0.074845	AGTR1/AC	26
BP	GO:004544 fat cell differentiation	29/1638	223/18670	0.020901	0.097812	0.075024	RUNX1T1/	29
BP	GO:001983 cytolysis	8/1638	40/18670	0.021009	0.098143	0.075278	C7/F2/GZM	8
BP	GO:005193 regulation of	8/1638	40/18670	0.021009	0.098143	0.075278	F2R/FABP5	8
BP	GO:001574 monosaccharide	17/1638	114/18670	0.021068	0.09816	0.075291	C3/EDNRA	17
BP	GO:000171 mesoderm	5/1638	19/18670	0.021181	0.09816	0.075291	FGFR1/FO	5
BP	GO:000254 chronic inflammation	5/1638	19/18670	0.021181	0.09816	0.075291	S100A8/C	5
BP	GO:000292 positive regulation of	5/1638	19/18670	0.021181	0.09816	0.075291	C3/CCR7/F	5
BP	GO:003094 positive regulation of	5/1638	19/18670	0.021181	0.09816	0.075291	FGF10/ITG	5
BP	GO:004848 parasympathetic	5/1638	19/18670	0.021181	0.09816	0.075291	PHOX2A/V	5
BP	GO:009858 detection of	5/1638	19/18670	0.021181	0.09816	0.075291	C4B/TREM	5
BP	GO:009891 regulation of	5/1638	19/18670	0.021181	0.09816	0.075291	CACNA1C,	5
BP	GO:190174 positive regulation of	5/1638	19/18670	0.021181	0.09816	0.075291	ADGRB1/N	5
CC	GO:006202 collagen-collagen	158/1730	406/19717	3.36E-63	1.80E-60	1.34E-60	A2M/AEBF	158
CC	GO:004442 extracellular	27/1730	51/19717	6.91E-16	1.33E-13	9.88E-14	COL1A1/C	27
CC	GO:000578 endoplasmic	74/1730	309/19717	7.43E-16	1.33E-13	9.88E-14	AFP/AHSG	74
CC	GO:004444 contractile	58/1730	221/19717	1.45E-14	1.95E-12	1.45E-12	ACTA2/AC	58
CC	GO:004329 contractile	59/1730	234/19717	5.88E-14	6.30E-12	4.69E-12	ACTA2/AC	59
CC	GO:003001 sarcomere	54/1730	204/19717	8.03E-14	6.89E-12	5.13E-12	ACTC1/AC	54
CC	GO:000558 collagen triple	33/1730	87/19717	9.52E-14	6.89E-12	5.13E-12	COL1A1/C	33
CC	GO:003001 myofibril	57/1730	224/19717	1.03E-13	6.89E-12	5.13E-12	ACTC1/AC	57
CC	GO:001981 immunoglobulin	46/1730	159/19717	1.71E-13	1.02E-11	7.59E-12	CD79A/CD	46
CC	GO:000989 external stimulus	81/1730	393/19717	2.38E-13	1.28E-11	9.51E-12	CXCR5/CA	81
CC	GO:000560 basement	34/1730	95/19717	2.92E-13	1.42E-11	1.06E-11	COL4A2/C	34
CC	GO:009706 synaptic membrane	86/1730	432/19717	3.32E-13	1.48E-11	1.10E-11	ACTN2/AN	86
CC	GO:007256 blood microvillus	41/1730	147/19717	1.29E-11	5.30E-10	3.95E-10	A2M/ACTC	41
CC	GO:003167 I band	40/1730	143/19717	2.07E-11	7.91E-10	5.89E-10	ACTC1/AC	40
CC	GO:003001 Z disc	38/1730	132/19717	2.54E-11	9.08E-10	6.76E-10	ACTN2/AN	38
CC	GO:004238 sarcolemma	37/1730	136/19717	2.77E-10	9.29E-09	6.92E-09	ANK2/ATP	37
CC	GO:000153 cornified epithelial	24/1730	65/19717	4.27E-10	1.31E-08	9.73E-09	CSTA/DSC	24
CC	GO:004521 postsynaptic	64/1730	323/19717	4.39E-10	1.31E-08	9.73E-09	ACTN2/AN	64
CC	GO:003109 platelet alpha	28/1730	91/19717	1.97E-09	5.54E-08	4.13E-08	A2M/ACTC	28
CC	GO:009864 complex oligomer	12/1730	19/19717	5.64E-09	1.51E-07	1.12E-07	COL1A1/C	12
CC	GO:004302 neuronal cell-cell	83/1730	497/19717	7.54E-09	1.92E-07	1.43E-07	ADCYAP1/	83
CC	GO:009880 plasma membrane	56/1730	295/19717	2.60E-08	6.12E-07	4.56E-07	CD79A/CD	56
CC	GO:009897 glutamatergic	63/1730	349/19717	2.63E-08	6.12E-07	4.56E-07	ACTC1/AC	63
CC	GO:003109 platelet alpha	22/1730	67/19717	2.78E-08	6.21E-07	4.62E-07	A2M/ACTC	22
CC	GO:004210 T cell receptor	32/1730	127/19717	3.30E-08	7.07E-07	5.26E-07	TRAV6/TRI	32
CC	GO:009924 intrinsic coiled-coil	37/1730	164/19717	6.74E-08	1.39E-06	1.03E-06	ATP2B4/CI	37
CC	GO:004257 immunoglobulin	22/1730	72/19717	1.19E-07	2.37E-06	1.76E-06	IGHD/IGHC	22
CC	GO:190249 transmembrane	57/1730	324/19717	2.93E-07	5.60E-06	4.17E-06	ATP1A2/A	57
CC	GO:004320 perikaryon	31/1730	134/19717	4.24E-07	7.84E-06	5.84E-06	ADCYAP1/	31
CC	GO:003470 cation channel	43/1730	220/19717	4.60E-07	8.21E-06	6.11E-06	CACNA1C,	43
CC	GO:000588 intermediate	42/1730	214/19717	5.55E-07	9.59E-06	7.14E-06	DES/GFAP,	42
CC	GO:004512 membrane	55/1730	315/19717	6.03E-07	1.01E-05	7.52E-06	ADCY2/AC	55
CC	GO:199035 transporter	57/1730	332/19717	6.68E-07	1.05E-05	7.85E-06	ATP1A2/A	57
CC	GO:009885 membrane	55/1730	316/19717	6.69E-07	1.05E-05	7.85E-06	ADCY2/AC	55
CC	GO:000591 cell-cell junction	71/1730	459/19717	1.76E-06	2.67E-05	1.99E-05	ADCYAP1F	71
CC	GO:009893 intrinsic coiled-coil	28/1730	122/19717	1.79E-06	2.67E-05	1.99E-05	CDH9/CDH	28
CC	GO:004485 plasma membrane	26/1730	109/19717	1.92E-06	2.78E-05	2.07E-05	ADCYAP1F	26
CC	GO:009858 membrane	55/1730	328/19717	2.21E-06	3.12E-05	2.32E-05	ADCY2/AC	55
CC	GO:009969 integral coiled-coil	32/1730	152/19717	2.54E-06	3.49E-05	2.59E-05	ATP2B4/CI	32

CC	GO:004511intermedia	45/1730	251/19717	3.00E-06	4.02E-05	2.99E-05	ADCY5/DE	45
CC	GO:000579Golgi lumen	24/1730	102/19717	6.07E-06	7.94E-05	5.91E-05	BGN/CGA/	24
CC	GO:009898GABA-erg	19/1730	71/19717	7.68E-06	9.80E-05	7.30E-05	ATP2B3/CI	19
CC	GO:003470ion channel	50/1730	301/19717	8.23E-06	0.000103	7.64E-05	CACNA1C,	50
CC	GO:004271presynaptic	32/1730	161/19717	9.06E-06	0.000108	8.07E-05	APBB1/ATI	32
CC	GO:000558fibrillar collagen	7/1730	11/19717	9.51E-06	0.000108	8.07E-05	COL1A1/C	7
CC	GO:003228symmetric	7/1730	11/19717	9.51E-06	0.000108	8.07E-05	CHRM2/N	7
CC	GO:009864banded collagen	7/1730	11/19717	9.51E-06	0.000108	8.07E-05	COL1A1/C	7
CC	GO:003122anchored cell	33/1730	170/19717	1.11E-05	0.000124	9.24E-05	ART4/CA4,	33
CC	GO:003471secretory granule	52/1730	321/19717	1.14E-05	0.000124	9.24E-05	A2M/ACTN	52
CC	GO:001470intercalated disc	15/1730	50/19717	1.55E-05	0.000166	0.000124	ANK2/ATP	15
CC	GO:000561interstitial matrix	7/1730	12/19717	2.11E-05	0.000222	0.000165	ECM2/TNC	7
CC	GO:009905integral component	25/1730	117/19717	2.35E-05	0.000241	0.000179	CDH9/CDH	25
CC	GO:006020cytoplasmic	53/1730	338/19717	2.38E-05	0.000241	0.000179	A2M/ACTN	53
CC	GO:003198vesicle lumen	53/1730	339/19717	2.59E-05	0.000254	0.000189	A2M/ACTN	53
CC	GO:003031T-tubule	15/1730	52/19717	2.61E-05	0.000254	0.000189	ANK2/ATP	15
CC	GO:004264actomyosium	19/1730	79/19717	3.97E-05	0.00038	0.000283	ACTC1/LPI	19
CC	GO:004262chylomicron	7/1730	13/19717	4.22E-05	0.000397	0.000295	APOA1/AF	7
CC	GO:000590caveola	19/1730	80/19717	4.78E-05	0.000431	0.000321	ADCYAP1F	19
CC	GO:000172stress fiber	17/1730	67/19717	4.82E-05	0.000431	0.000321	LPP/MYLK	17
CC	GO:009751contractile	17/1730	67/19717	4.82E-05	0.000431	0.000321	LPP/MYLK	17
CC	GO:009951postsynaptic	53/1730	348/19717	5.33E-05	0.000468	0.000348	ACTN2/AC	53
CC	GO:009898neuron terminal	53/1730	350/19717	6.22E-05	0.000538	0.0004	ACTN2/AC	53
CC	GO:003241actin filament	18/1730	75/19717	6.48E-05	0.000551	0.00041	CRYAB/LPI	18
CC	GO:003005cell-substrate	60/1730	412/19717	6.67E-05	0.000559	0.000416	ACTC1/AC	60
CC	GO:009888intrinsic component	19/1730	82/19717	6.87E-05	0.000566	0.000421	ATP2B4/CI	19
CC	GO:003470potassium channel	21/1730	96/19717	7.18E-05	0.000583	0.000434	DPP6/GRIK	21
CC	GO:003470sodium channel	9/1730	23/19717	7.91E-05	0.000633	0.000471	GRIK3/GRI	9
CC	GO:003221asymmetric	50/1730	328/19717	8.36E-05	0.000659	0.00049	ACTN2/AC	50
CC	GO:000592cell-substrate	59/1730	408/19717	9.33E-05	0.000725	0.000539	ACTC1/AC	59
CC	GO:004429cell-cell contact	17/1730	71/19717	0.000106	0.00081	0.000603	ANK2/ATP	17
CC	GO:004303costamere	8/1730	19/19717	0.000108	0.000816	0.000607	ANK2/DMN	8
CC	GO:000592focal adhesion	58/1730	405/19717	0.000139	0.001035	0.00077	ACTC1/AC	58
CC	GO:001652sarcoplasmic	18/1730	80/19717	0.000158	0.001158	0.000862	CACNA2D	18
CC	GO:004511apical part	55/1730	384/19717	0.000204	0.001474	0.001097	ANK2/ATP	55
CC	GO:000830integrin component	10/1730	31/19717	0.000209	0.001476	0.001099	ITGA1/ITG	10
CC	GO:000571vacuolar lumen	30/1730	172/19717	0.000209	0.001476	0.001099	APOB/BGN	30
CC	GO:001406postsynaptic	48/1730	324/19717	0.000229	0.001592	0.001185	ACTN2/AC	48
CC	GO:001632apical plasma	47/1730	318/19717	0.000279	0.001919	0.001428	ANK2/ATP	47
CC	GO:003326axon part	54/1730	382/19717	0.000322	0.002184	0.001625	ADCYAP1/	54
CC	GO:004511basal part	13/1730	51/19717	0.000348	0.002303	0.001714	ERBB2/FAF	13
CC	GO:004319dendritic spine	29/1730	169/19717	0.000351	0.002303	0.001714	ACTN2/AP	29
CC	GO:001652sarcoplasmic	16/1730	71/19717	0.000352	0.002303	0.001714	CACNA2D	16
CC	GO:004430neuron spine	29/1730	171/19717	0.00043	0.002759	0.002054	ACTN2/AP	29
CC	GO:009961postsynaptic	20/1730	101/19717	0.000432	0.002759	0.002054	ACTN2/CE	20
CC	GO:004665anchored cell	14/1730	59/19717	0.000464	0.002926	0.002178	CA4/CNTN	14
CC	GO:000807voltage-gated	18/1730	87/19717	0.000474	0.002952	0.002197	DPP6/KCN	18
CC	GO:009861protein complex	10/1730	34/19717	0.000485	0.002986	0.002222	ITGA1/ITG	10
CC	GO:004509keratin filament	19/1730	95/19717	0.000523	0.003185	0.00237	KRT4/KRT5	19
CC	GO:004430main axon	15/1730	68/19717	0.000678	0.004081	0.003038	ANK2/APB	15
CC	GO:009894intrinsic component	7/1730	19/19717	0.000773	0.004606	0.003428	ATP2B4/CI	7
CC	GO:004878presynaptic	9/1730	30/19717	0.000788	0.004642	0.003455	ATP2B4/CI	9
CC	GO:004319dendritic spine	10/1730	36/19717	0.000799	0.004654	0.003464	FLNA/HTR	10
CC	GO:000152microfibril	5/1730	10/19717	0.000894	0.005154	0.003836	FBN1/LTBF	5
CC	GO:009894intrinsic component	16/1730	77/19717	0.000911	0.005194	0.003866	CDH10/EP	16
CC	GO:003125cell projection	48/1730	345/19717	0.000953	0.005374	0.004	CA4/CA9/	48
CC	GO:003436very-low-density	7/1730	20/19717	0.0011	0.00608	0.004526	APOA1/AF	7
CC	GO:003438triglyceride	7/1730	20/19717	0.0011	0.00608	0.004526	APOA1/AF	7
CC	GO:009051cation-transporter	6/1730	15/19717	0.001129	0.006176	0.004597	ATP1A2/A	6
CC	GO:004320lysosomal	18/1730	95/19717	0.001397	0.007566	0.005632	APOB/BGN	18
CC	GO:009905integral component	15/1730	73/19717	0.001466	0.007857	0.005848	ATP2B4/CI	15
CC	GO:004282platelet derived	7/1730	21/19717	0.001527	0.008101	0.00603	APOH/ITIH	7

CC	GO:003017	filopodium	19/1730	104/19717	0.001636	0.008596	0.006398	ACTA2/AC	19
CC	GO:009906	integral co	15/1730	74/19717	0.001692	0.008806	0.006555	CDH10/EP	15
CC	GO:003125	leading ed	27/1730	170/19717	0.001823	0.00936	0.006966	AMPH/CSF	27
CC	GO:009868	Schaffer cc	16/1730	82/19717	0.001834	0.00936	0.006966	CDH11/DC	16
CC	GO:015003	distal axon	40/1730	285/19717	0.002056	0.010398	0.007739	ADCYAP1/	40
CC	GO:004429	cell body r	8/1730	28/19717	0.002173	0.010887	0.008103	CD22/CX3	8
CC	GO:003109	platelet al	6/1730	17/19717	0.002396	0.01189	0.008849	CD36/ITGE	6
CC	GO:009914	anchored c	5/1730	12/19717	0.00242	0.011902	0.008859	CNTN1/CN	5
CC	GO:004878	presynapti	14/1730	71/19717	0.003114	0.015172	0.011293	ATP2B4/CI	14
CC	GO:003152	filopodium	6/1730	18/19717	0.003329	0.016077	0.011966	DMD/GAP	6
CC	GO:006007	excitatory	11/1730	50/19717	0.003482	0.016662	0.012402	CBLN1/DG	11
CC	GO:009879	presynapse	61/1730	491/19717	0.003569	0.016929	0.0126	ADCYAP1/	61
CC	GO:009883	postsynapt	14/1730	74/19717	0.004608	0.021667	0.016127	ACTN2/EP	14
CC	GO:000151	voltage-g	5/1730	14/19717	0.005273	0.024364	0.018134	SCN1B/SC	5
CC	GO:003108	platelet de	5/1730	14/19717	0.005273	0.024364	0.018134	APOH/ITIH	5
CC	GO:003301	sarcoplasr	9/1730	39/19717	0.005692	0.026076	0.019408	CASQ1/CA	9
CC	GO:003436	high-dens	7/1730	26/19717	0.005856	0.0266	0.019799	APOA1/AF	7
CC	GO:000591	cell-cell ac	19/1730	117/19717	0.006345	0.028578	0.021271	CDH9/CDH	19
CC	GO:003259	dendrite r	9/1730	40/19717	0.006785	0.030304	0.022556	GABRA4/C	9
CC	GO:003280	neuronal c	7/1730	27/19717	0.007318	0.032006	0.023822	CD22/CX3	7
CC	GO:003326	node of R	5/1730	15/19717	0.007345	0.032006	0.023822	MYOC/SCI	5
CC	GO:009905	integral co	5/1730	15/19717	0.007345	0.032006	0.023822	ATP2B4/CI	5
CC	GO:009853	ATPase de	6/1730	21/19717	0.007747	0.033488	0.024925	ATP1A2/A	6
CC	GO:009888	actin-base	29/1730	208/19717	0.008576	0.036774	0.027371	ACTA2/AC	29
CC	GO:004320	myelin she	10/1730	49/19717	0.009084	0.038643	0.028762	ERBB2/GN	10
CC	GO:003258	neuron prc	11/1730	57/19717	0.009778	0.041267	0.030716	GABRA4/C	11
CC	GO:003128	lamellipod	6/1730	22/19717	0.009876	0.041355	0.03078	CSPG4/FAI	6
CC	GO:001634	catenin coi	7/1730	29/19717	0.011024	0.045804	0.034092	CDH9/CDH	7
CC	GO:006007	inhibitory	5/1730	17/19717	0.013059	0.053842	0.040075	NLGN4Y/S	5
CC	GO:003042	growth coi	24/1730	171/19717	0.01458	0.059655	0.044402	APBB1/CN	24
CC	GO:009914	intrinsic co	10/1730	53/19717	0.015676	0.063655	0.047379	EPHA7/GR	10
CC	GO:000589	sodium:po	4/1730	12/19717	0.016469	0.065877	0.049032	ATP1A2/A	4
CC	GO:003327	paranode	14/1730	12/19717	0.016469	0.065877	0.049032	KCNA1/CN	4
CC	GO:004430	neuron prc	20/1730	138/19717	0.017626	0.069981	0.052087	ADCYAP1/	20
CC	GO:003558	specific gr	11/1730	62/19717	0.018041	0.071104	0.052923	BPI/ELANE	11
CC	GO:003005	desmosom	6/1730	25/19717	0.018697	0.073152	0.054447	DSC2/DSG	6
CC	GO:003042	site of pol	24/1730	176/19717	0.020134	0.078201	0.058206	APBB1/CN	24
CC	GO:001601	dystrophin	5/1730	19/19717	0.021191	0.080555	0.059957	DMD/PGM	5
CC	GO:003136	anchored c	5/1730	19/19717	0.021191	0.080555	0.059957	CA4/FOLR	5
CC	GO:009066	glycoprote	5/1730	19/19717	0.021191	0.080555	0.059957	DMD/PGM	5
CC	GO:003259	dendritic s	4/1730	13/19717	0.022166	0.08367	0.062276	GRIA1/PAL	4
CC	GO:000992	basal plasr	7/1730	34/19717	0.025909	0.097114	0.072282	ERBB2/ITG	7
MF	GO:000520	extracellul	84/1526	163/17697	3.98E-46	3.44E-43	2.82E-43	AEBP1/BGI	84
MF	GO:000553	glycosamir	78/1526	229/17697	1.43E-27	6.19E-25	5.08E-25	ANXA6/AF	78
MF	GO:000820	heparin bir	59/1526	169/17697	9.06E-22	2.61E-19	2.14E-19	APOB/APC	59
MF	GO:004801	receptor li	97/1526	482/17697	1.42E-15	3.06E-13	2.51E-13	ADCYAP1/	97
MF	GO:190168	sulfur com	63/1526	250/17697	3.53E-15	6.09E-13	5.00E-13	ANXA6/AF	63
MF	GO:003002	extracellul	23/1526	41/17697	1.25E-14	1.79E-12	1.47E-12	COL1A1/C	23
MF	GO:006113	peptidase	51/1526	219/17697	3.61E-11	4.45E-09	3.65E-09	A2M/AHSC	51
MF	GO:003041	peptidase	45/1526	182/17697	6.17E-11	6.18E-09	5.07E-09	A2M/AHSC	45
MF	GO:000517	integrin bir	37/1526	132/17697	6.44E-11	6.18E-09	5.07E-09	ACTN2/CC	37
MF	GO:000551	collagen b	25/1526	67/17697	9.67E-11	8.35E-09	6.85E-09	AEBP1/CO	25
MF	GO:000486	endopepti	43/1526	175/17697	2.03E-10	1.58E-08	1.30E-08	A2M/AHSC	43
MF	GO:006113	endopepti	44/1526	182/17697	2.20E-10	1.58E-08	1.30E-08	A2M/AHSC	44
MF	GO:001983	growth fac	36/1526	137/17697	8.34E-10	5.53E-08	4.54E-08	A2M/CD36	36
MF	GO:000852	G protein-	36/1526	146/17697	5.38E-09	3.32E-07	2.72E-07	ADCYAP1F	36
MF	GO:000486	serine-typ	27/1526	94/17697	1.35E-08	7.79E-07	6.39E-07	A2M/SERP	27
MF	GO:000165	peptide re	36/1526	152/17697	1.68E-08	9.08E-07	7.46E-07	ADCYAP1F	36
MF	GO:001995	cytokine bi	32/1526	128/17697	2.63E-08	1.34E-06	1.10E-06	A2M/CXCF	32
MF	GO:000512	cytokine ac	45/1526	220/17697	3.67E-08	1.76E-06	1.45E-06	BMP3/TNF	45
MF	GO:003002	extracellul	12/1526	22/17697	4.62E-08	2.10E-06	1.72E-06	BGN/HAPL	12
MF	GO:000471	transmem	20/1526	62/17697	1.23E-07	5.30E-06	4.35E-06	ALK/AXL/C	20

MF	GO:000382 antigen binding	35/1526	160/17697	2.17E-07	8.92E-06	7.32E-06	CD1C/CD1	35
MF	GO:000166 G protein-coupled	51/1526	280/17697	2.35E-07	9.22E-06	7.57E-06	ADCYAP1/	51
MF	GO:003498 immunoglobulin	22/1526	76/17697	2.52E-07	9.47E-06	7.77E-06	FLNA/IGHI	22
MF	GO:000526 cation channel	55/1526	319/17697	5.12E-07	1.83E-05	1.50E-05	ANXA6/CA	55
MF	GO:001915 transmembrane	22/1526	79/17697	5.30E-07	1.83E-05	1.50E-05	ALK/AXL/C	22
MF	GO:005084 extracellular	18/1526	57/17697	7.46E-07	2.48E-05	2.03E-05	BGN/COL1	18
MF	GO:000196 fibronectin	12/1526	27/17697	8.25E-07	2.64E-05	2.16E-05	CCN2/CTS	12
MF	GO:000521 ion channel	66/1526	416/17697	8.84E-07	2.72E-05	2.24E-05	ANXA6/CA	66
MF	GO:000485 enzyme inhibitor	61/1526	375/17697	9.76E-07	2.91E-05	2.39E-05	A2M/AHSC	61
MF	GO:001507 potassium	33/1526	159/17697	1.67E-06	4.81E-05	3.95E-05	ATP1A2/A	33
MF	GO:002283 ion gated	55/1526	334/17697	2.25E-06	6.26E-05	5.14E-05	ANXA6/CA	55
MF	GO:002283 substrate	66/1526	428/17697	2.43E-06	6.55E-05	5.37E-05	ANXA6/CA	66
MF	GO:004687 metal ion	67/1526	438/17697	2.71E-06	7.09E-05	5.82E-05	ANXA6/AT	67
MF	GO:000517 hormone	27/1526	122/17697	4.05E-06	0.000103	8.45E-05	ADCYAP1/	27
MF	GO:002283 gated	55/1526	343/17697	5.12E-06	0.000126	0.000104	ANXA6/CA	55
MF	GO:001526 channel	68/1526	456/17697	5.58E-06	0.000134	0.00011	ANXA6/CA	68
MF	GO:002283 passive	68/1526	457/17697	6.02E-06	0.00014	0.000115	ANXA6/CA	68
MF	GO:000524 voltage-gated	35/1526	197/17697	3.04E-05	0.000672	0.000552	CACNA1C	35
MF	GO:002283 voltage-gated	35/1526	197/17697	3.04E-05	0.000672	0.000552	CACNA1C	35
MF	GO:000526 potassium	25/1526	123/17697	4.23E-05	0.000913	0.00075	GRIK3/GRI	25
MF	GO:001995 chemokine	11/1526	32/17697	4.44E-05	0.000934	0.000767	A2M/CXCF	11
MF	GO:005083 cell adhesion	69/1526	499/17697	5.87E-05	0.001205	0.00099	ACTN2/CA	69
MF	GO:000552 insulin-like	10/1526	28/17697	6.80E-05	0.001365	0.001121	CCN2/IGF	10
MF	GO:000510 frizzled	12/1526	39/17697	6.99E-05	0.00137	0.001125	MYOC/RO	12
MF	GO:000823 serine-type	32/1526	182/17697	8.03E-05	0.001539	0.001263	C1R/C1S/C	32
MF	GO:000425 serine-type	29/1526	160/17697	9.78E-05	0.001834	0.001505	C1R/C1S/C	29
MF	GO:001527 outward	7/1526	15/17697	0.000121	0.002204	0.00181	KCNA3/KC	7
MF	GO:001717 serine	32/1526	186/17697	0.000123	0.002204	0.00181	C1R/C1S/C	32
MF	GO:000524 voltage-gated	19/1526	87/17697	0.000126	0.002219	0.001822	KCNA1/KC	19
MF	GO:004840 platelet-derived	6/1526	11/17697	0.000129	0.002219	0.001822	COL1A1/C	6
MF	GO:000808 growth factor	29/1526	163/17697	0.000137	0.002321	0.001906	BMP3/CCN	29
MF	GO:000549 steroid	20/1526	95/17697	0.000145	0.002404	0.001974	ANXA6/AF	20
MF	GO:004339 proteoglycan	11/1526	36/17697	0.00015	0.002438	0.002002	COL5A1/C	11
MF	GO:002284 voltage-gated	26/1526	142/17697	0.000185	0.002959	0.002429	CACNA1C	26
MF	GO:001714 Wnt-protein	11/1526	37/17697	0.000197	0.003085	0.002533	AXL/FRZB/	11
MF	GO:001507 monovalent	54/1526	382/17697	0.000206	0.003178	0.002609	ATP1A2/A	54
MF	GO:000818 neuropeptide	13/1526	50/17697	0.000237	0.003584	0.002942	GALR1/GR	13
MF	GO:000823 metalloprotein	30/1526	181/17697	0.000382	0.005565	0.004569	AEBP1/CP	30
MF	GO:009863 cell adhesion	14/1526	59/17697	0.000388	0.005565	0.004569	DSC2/ITGA	14
MF	GO:000518 neuropeptide	9/1526	28/17697	0.000392	0.005565	0.004569	ADCYAP1/	9
MF	GO:000526 structural	20/1526	102/17697	0.000393	0.005565	0.004569	ADD2/ANI	20
MF	GO:000817 adenylate	6/1526	13/17697	0.00041	0.005712	0.004689	ADCY2/AC	6
MF	GO:000422 metalloenzyme	20/1526	103/17697	0.000449	0.006155	0.005052	FAP/MEP1	20
MF	GO:000527 sodium	11/1526	41/17697	0.000527	0.007107	0.005834	GRIK3/GRI	11
MF	GO:001995 C-C	8/1526	24/17697	0.000628	0.008332	0.00684	CXCR5/CC	8
MF	GO:000495 prostaglandin	5/1526	10/17697	0.000825	0.010644	0.008737	PTGDR/PT	5
MF	GO:004317 alcohol	17/1526	85/17697	0.000826	0.010644	0.008737	ADH7/AN	17
MF	GO:000512 cytokine	41/1526	286/17697	0.000861	0.010922	0.008965	BMP3/TNF	41
MF	GO:001508 sodium	25/1526	149/17697	0.00094	0.011762	0.009656	ATP1A2/A	25
MF	GO:000495 icosanoid	6/1526	15/17697	0.001029	0.01251	0.010269	PTGDR/PT	6
MF	GO:007049 oligosaccharide	6/1526	15/17697	0.001029	0.01251	0.010269	REG3A/SEI	6
MF	GO:003024 carbohydrate	39/1526	271/17697	0.001054	0.012638	0.010374	C4B/CD22	39
MF	GO:000166 G protein-coupled	8/1526	26/17697	0.001141	0.013127	0.010776	CXCR5/CC	8
MF	GO:000495 chemokine	8/1526	26/17697	0.001141	0.013127	0.010776	CXCR5/CC	8
MF	GO:007032 lipoprotein	8/1526	26/17697	0.001141	0.013127	0.010776	APOA1/AF	8
MF	GO:004237 chemokine	14/1526	66/17697	0.001277	0.014506	0.011907	DEFB1/DEI	14
MF	GO:000184 complement	7/1526	21/17697	0.001377	0.014971	0.012289	C4A/C4B/C	7
MF	GO:000495 prostanoid	5/1526	11/17697	0.001405	0.014971	0.012289	PTGDR/PT	5
MF	GO:000539 sodium	5/1526	11/17697	0.001405	0.014971	0.012289	ATP1A2/A	5
MF	GO:000855 potassium	5/1526	11/17697	0.001405	0.014971	0.012289	ATP1A2/A	5
MF	GO:009749 structural	5/1526	11/17697	0.001405	0.014971	0.012289	ELN/FBLN	5
MF	GO:007181 lipoprotein	9/1526	33/17697	0.001477	0.015326	0.012581	APOA1/AF	9

MF	GO:007181 protein-lipid 9/1526	33/17697	0.001477	0.015326	0.012581	APOA1/AF	9
MF	GO:000830 structural c 11/1526	46/17697	0.001492	0.015326	0.012581	ACTN2/CS	11
MF	GO:000819 metalloion c 6/1526	16/17697	0.001527	0.015326	0.012581	COL4A3/N	6
MF	GO:003016 low-density lipoprotein receptor 6/1526	16/17697	0.001527	0.015326	0.012581	CD36/CRP	6
MF	GO:001527 ligand-gate 23/1526	138/17697	0.001615	0.015836	0.012999	ANXA6/CF	23
MF	GO:002282 ligand-gate 23/1526	138/17697	0.001615	0.015836	0.012999	ANXA6/CF	23
MF	GO:000417 endopeptidase 55/1526	427/17697	0.001726	0.016734	0.013737	C1R/C1S/C	55
MF	GO:004282 peptidoglycan 6/1526	17/17697	0.00219	0.020995	0.017234	REG3A/TR	6
MF	GO:000418 metallopeptidase 8/1526	29/17697	0.002483	0.02337	0.019184	AEBP1/CP	8
MF	GO:001649 C-C chemokine 7/1526	23/17697	0.002491	0.02337	0.019184	CXCR5/CC	7
MF	GO:001548 cholesterol 11/1526	49/17697	0.002566	0.02381	0.019545	ANXA6/AF	11
MF	GO:004802 CCR chemokine 10/1526	43/17697	0.003016	0.027686	0.022727	DEFB1/DE	10
MF	GO:000202 protease b 21/1526	128/17697	0.003059	0.027788	0.02281	A2M/COL1	21
MF	GO:000122 DNA-binding 55/1526	439/17697	0.003168	0.028479	0.023378	AR/NKX2-	55
MF	GO:000517 vascular endothelial cell 5/1526	13/17697	0.003381	0.029774	0.024441	VEGFD/ITC	5
MF	GO:004204 neurexin family 5/1526	13/17697	0.003381	0.029774	0.024441	CEL/CPE/N	5
MF	GO:000178 phosphatidylcholine 12/1526	58/17697	0.003448	0.030047	0.024665	ANXA6/AX	12
MF	GO:005139 alpha-actinin 9/1526	37/17697	0.003482	0.030047	0.024665	CACNA1C	9
MF	GO:000504 scavenger 11/1526	51/17697	0.003578	0.030568	0.025093	CD36/TMF	11
MF	GO:004280 actinin binding 10/1526	46/17697	0.005062	0.042826	0.035155	CACNA1C	10
MF	GO:000471 protein tyrosine kinase 21/1526	134/17697	0.005298	0.044391	0.03644	ALK/AXL/E	21
MF	GO:000524 voltage-gated 6/1526	20/17697	0.005478	0.045027	0.036962	PKD2/SCN	6
MF	GO:000832 signaling pathway 6/1526	20/17697	0.005478	0.045027	0.036962	CD36/FCN	6
MF	GO:009910 ion channel 19/1526	118/17697	0.005781	0.047066	0.038636	CAV1/DPP	19
MF	GO:001568 ATPase activity 8/1526	33/17697	0.005898	0.047574	0.039052	ATP1A2/A	8
MF	GO:001624 channel receptor 22/1526	144/17697	0.005965	0.047665	0.039127	ATP2B4/C	22
MF	GO:004256 hormone receptor 17/1526	102/17697	0.006179	0.048924	0.040161	ADCYAP1F	17
MF	GO:000184 opsonin binding 5/1526	15/17697	0.00682	0.053022	0.043525	C4A/CR1/C	5
MF	GO:000516 platelet-derived 5/1526	15/17697	0.00682	0.053022	0.043525	VEGFD/IL1	5
MF	GO:000554 hyaluronic acid 6/1526	21/17697	0.007119	0.054067	0.044383	HAPLN1/V	6
MF	GO:003818 pattern recognition 6/1526	21/17697	0.007119	0.054067	0.044383	CD36/FCN	6
MF	GO:000550 fatty acid receptor 8/1526	34/17697	0.007142	0.054067	0.044383	FABP4/FA	8
MF	GO:000551 calmodulin 28/1526	200/17697	0.007283	0.054653	0.044864	ADD2/AEB	28
MF	GO:003293 sterol binding 11/1526	56/17697	0.007526	0.055992	0.045963	ANXA6/AF	11
MF	GO:000489 cytokine receptor 16/1526	96/17697	0.007755	0.057198	0.046953	CXCR5/CC	16
MF	GO:000800 chemokine 10/1526	49/17697	0.008062	0.058517	0.048036	CCL7/CCL	10
MF	GO:001508 calcium ion 21/1526	139/17697	0.008069	0.058517	0.048036	ANXA6/AT	21
MF	GO:009909 ligand-gate 17/1526	105/17697	0.00827	0.059473	0.048821	CHRNA3/C	17
MF	GO:000371 actin binding 52/1526	431/17697	0.00843	0.060121	0.049353	ACTN2/AC	52
MF	GO:000550 retinoid binding 8/1526	35/17697	0.008574	0.060648	0.049785	ADH7/FAB	8
MF	GO:005044 transforming 6/1526	22/17697	0.009087	0.063187	0.051869	CD36/LRR	6
MF	GO:001664 oxidoreductase 5/1526	16/17697	0.009225	0.063187	0.051869	LOX/LOXL	5
MF	GO:003028 structural c 5/1526	16/17697	0.009225	0.063187	0.051869	PI3/PKP1/S	5
MF	GO:004749 calcium-dependent 5/1526	16/17697	0.009225	0.063187	0.051869	PLA2G1B/I	5
MF	GO:009863 cell-cell adhesion 10/1526	50/17697	0.009318	0.063322	0.05198	DSC2/JUP	10
MF	GO:000486 cysteine-type 11/1526	58/17697	0.009827	0.066257	0.05439	AHSG/AVF	11
MF	GO:001984 isoprenoid 8/1526	36/17697	0.010209	0.068299	0.056065	ADH7/FAB	8
MF	GO:007085 growth factor 20/1526	134/17697	0.010896	0.072332	0.059376	MS4A1/EF	20
MF	GO:003612 BMP binding 4/1526	11/17697	0.011089	0.073055	0.05997	COMP/SO	4
MF	GO:005137 muscle alpha 6/1526	23/17697	0.011415	0.07463	0.061262	PKD2/PDL	6
MF	GO:001502 coreceptor 9/1526	44/17697	0.011509	0.074681	0.061304	CCR8/ITGE	9
MF	GO:001986 immunoglobulin 6/1526	24/17697	0.014134	0.089836	0.073745	MS4A1/CE	6
MF	GO:012001 intermembrane 6/1526	24/17697	0.014134	0.089836	0.073745	APOA1/AF	6
MF	GO:004205 chemoattractant 8/1526	38/17697	0.014157	0.089836	0.073745	DEFB4A/FC	8
MF	GO:000411 3',5'-cyclic 4/1526	12/17697	0.015515	0.095179	0.07813	PDE2A/PD	4
MF	GO:001617 superoxide 4/1526	12/17697	0.015515	0.095179	0.07813	NOX1/NO	4
MF	GO:003199 insulin-like 4/1526	12/17697	0.015515	0.095179	0.07813	IGFBP4/IG	4
MF	GO:003369 sialic acid 14/1526	12/17697	0.015515	0.095179	0.07813	CD22/FCN	4
MF	GO:001712 cholesterol 5/1526	18/17697	0.015661	0.095179	0.07813	APOA1/AF	5
MF	GO:012002 intermembrane 5/1526	18/17697	0.015661	0.095179	0.07813	APOA1/AF	5