

Table S2. The Gene Ontology (GO) enrichment terms for AMed and AAdv dilation-related DEGs.

AMed GO BP								
ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:004211	T cell activation	27/144	451/18493	1.22E-16	3.3E-13	2.49E-13	399/11314/	27
GO:007061	leukocyte proliferation	21/144	283/18493	5.99E-15	8.09E-12	6.12E-12	11314/202/	21
GO:004662	lymphocyte proliferation	20/144	264/18493	1.88E-14	1.46E-11	1.11E-11	11314/202/	20
GO:003292	mononuclear cell proliferation	20/144	266/18493	2.17E-14	1.46E-11	1.11E-11	11314/202/	20
GO:004571	positive regulation of cell proliferation	23/144	397/18493	5.59E-14	3.02E-11	2.29E-11	54518/355/	23
GO:002241	positive regulation of cell growth	19/144	251/18493	8.98E-14	4.04E-11	3.06E-11	3553/3606/	19
GO:000181	positive regulation of cell cycle	23/144	422/18493	2.02E-13	7.79E-11	5.9E-11	64135/513/	23
GO:004205	T cell proliferation	16/144	178/18493	6.49E-13	2.19E-10	1.66E-10	3553/3606/	16
GO:190302	positive regulation of cell cycle	17/144	214/18493	8.98E-13	2.56E-10	1.94E-10	3553/3606/	17
GO:000714	leukocyte chemotaxis	20/144	327/18493	1.04E-12	2.56E-10	1.94E-10	11314/355/	20
GO:007061	regulation of cell proliferation	17/144	216/18493	1.04E-12	2.56E-10	1.94E-10	11314/355/	17
GO:190302	regulation of cell cycle	19/144	293/18493	1.43E-12	3.22E-10	2.44E-10	11314/355/	19
GO:005067	positive regulation of cell growth	14/144	132/18493	1.98E-12	4.12E-10	3.12E-10	3553/3606/	14
GO:003292	positive regulation of cell cycle	14/144	133/18493	2.2E-12	4.19E-10	3.17E-10	3553/3606/	14
GO:005081	positive regulation of cell cycle	21/144	384/18493	2.32E-12	4.19E-10	3.17E-10	3553/3606/	21
GO:002241	regulation of cell growth	21/144	388/18493	2.83E-12	4.78E-10	3.62E-10	11314/355/	21
GO:007061	positive regulation of cell cycle	14/144	139/18493	4.05E-12	6.43E-10	4.87E-10	3553/3606/	14
GO:005081	positive regulation of cell cycle	16/144	202/18493	4.56E-12	6.85E-10	5.18E-10	3553/3606/	16
GO:005067	regulation of cell growth	16/144	205/18493	5.72E-12	7.92E-10	5.99E-10	11314/355/	16
GO:004211	neutrophil chemotaxis	23/144	498/18493	6.15E-12	7.92E-10	5.99E-10	4973/1131/	23
GO:003292	regulation of cell cycle	16/144	206/18493	6.16E-12	7.92E-10	5.99E-10	11314/355/	16
GO:000265	positive regulation of cell cycle	20/144	372/18493	1.1E-11	1.36E-09	1.03E-09	3553/3606/	20
GO:004211	positive regulation of cell cycle	12/144	97/18493	1.26E-11	1.49E-09	1.12E-09	3553/3606/	12
GO:000691	phagocytosis	19/144	342/18493	2.14E-11	2.41E-09	1.83E-09	54209/113/	19
GO:004331	neutrophil chemotaxis	22/144	485/18493	2.63E-11	2.85E-09	2.15E-09	4973/1131/	22
GO:005081	regulation of cell cycle	18/144	305/18493	2.78E-11	2.89E-09	2.18E-09	11314/355/	18
GO:000221	neutrophil chemotaxis	22/144	488/18493	2.97E-11	2.97E-09	2.25E-09	4973/1131/	22
GO:000242	neutrophil chemotaxis	22/144	499/18493	4.56E-11	4.4E-09	3.33E-09	4973/1131/	22
GO:003272	positive regulation of cell cycle	10/144	63/18493	5.37E-11	5E-09	3.79E-09	51311/355/	10
GO:003262	regulation of cell cycle	11/144	95/18493	1.94E-10	1.74E-08	1.32E-08	51311/355/	11
GO:004212	regulation of cell cycle	13/144	153/18493	2.11E-10	1.84E-08	1.39E-08	3553/3606/	13
GO:004205	cytokine biosynthesis	11/144	105/18493	5.79E-10	4.88E-08	3.7E-08	51311/355/	11
GO:003261	interferon-gamma production	11/144	106/18493	6.41E-10	5.09E-08	3.86E-08	51311/355/	11
GO:004211	cytokine biosynthesis	11/144	106/18493	6.41E-10	5.09E-08	3.86E-08	51311/355/	11
GO:005121	positive regulation of cell cycle	17/144	333/18493	9.58E-10	7.4E-08	5.6E-08	3553/3606/	17
GO:004202	regulation of cell cycle	10/144	94/18493	3.1E-09	2.32E-07	1.76E-07	51311/355/	10
GO:005122	regulation of cell cycle	19/144	472/18493	4.81E-09	3.51E-07	2.66E-07	11314/355/	19
GO:000265	positive regulation of cell cycle	13/144	209/18493	9.69E-09	6.89E-07	5.21E-07	80328/113/	13
GO:004801	antigen presentation	11/144	139/18493	1.16E-08	8.02E-07	6.07E-07	54209/972/	11
GO:004211	positive regulation of cell cycle	8/144	57/18493	1.33E-08	8.99E-07	6.8E-07	51311/355/	8
GO:004501	positive thymocyte proliferation	5/144	13/18493	3.27E-08	2.15E-06	1.63E-06	917/916/17	5
GO:005091	leukocyte chemotaxis	18/144	478/18493	3.51E-08	2.26E-06	1.71E-06	4973/1131/	18
GO:000271	regulation of cell cycle	12/144	196/18493	4.38E-08	2.75E-06	2.08E-06	80328/113/	12
GO:000271	immune response	17/144	445/18493	7.05E-08	4.33E-06	3.27E-06	11314/108/	17
GO:003262	interleukin-10 production	10/144	132/18493	8.31E-08	4.99E-06	3.77E-06	64135/513/	10
GO:003211	positive regulation of cell cycle	14/144	297/18493	8.49E-08	4.99E-06	3.77E-06	9450/3553/	14
GO:000242	antigen presentation	9/144	101/18493	9.31E-08	5.35E-06	4.05E-06	54209/972/	9
GO:000251	antigen presentation	9/144	102/18493	1.01E-07	5.71E-06	4.32E-06	54209/972/	9
GO:005102	positive regulation of cell cycle	16/144	404/18493	1.08E-07	5.93E-06	4.49E-06	64135/513/	16
GO:000221	lymphocyte chemotaxis	11/144	174/18493	1.18E-07	6.38E-06	4.83E-06	54518/202/	11
GO:001981	antigen presentation	11/144	175/18493	1.25E-07	6.63E-06	5.02E-06	54209/972/	11
GO:000242	immune response	16/144	414/18493	1.5E-07	7.79E-06	5.9E-06	11314/917/	16
GO:004211	macrophage chemotaxis	8/144	80/18493	2.01E-07	1E-05	7.6E-06	51311/229/	8

GO:005076	regulation of	8/144	80/18493	2.01E-07	1E-05	7.6E-06	11314/3553	8
GO:000691	phagocytosis	9/144	112/18493	2.28E-07	1.1E-05	8.32E-06	54209/1131	9
GO:003134	positive regulation of	16/144	427/18493	2.28E-07	1.1E-05	8.32E-06	80328/6413	16
GO:005076	positive regulation of	7/144	57/18493	2.86E-07	1.36E-05	1.03E-05	3553/3684	7
GO:003021	T cell differentiation	12/144	234/18493	3.02E-07	1.41E-05	1.07E-05	399/3606/9	12
GO:000265	regulation of	16/144	439/18493	3.31E-07	1.51E-05	1.15E-05	80328/1131	16
GO:000257	myeloid leucocyte	11/144	197/18493	4.13E-07	1.86E-05	1.41E-05	54209/2981	11
GO:009902	plasma membrane	9/144	121/18493	4.41E-07	1.95E-05	1.48E-05	54209/1131	9
GO:004506	thymic T cell	5/144	21/18493	4.91E-07	2.08E-05	1.57E-05	917/916/17	5
GO:005076	regulation of	12/144	245/18493	4.94E-07	2.08E-05	1.57E-05	54209/1131	12
GO:003267	regulation of	9/144	123/18493	5.07E-07	2.08E-05	1.57E-05	64135/5131	9
GO:005076	positive regulation of	9/144	123/18493	5.07E-07	2.08E-05	1.57E-05	64135/5131	9
GO:003005	lymphocyte	14/144	344/18493	5.08E-07	2.08E-05	1.57E-05	399/55619/	14
GO:003267	interleukin	7/144	62/18493	5.16E-07	2.08E-05	1.57E-05	3553/3606/	7
GO:000247	antigen presentation	9/144	126/18493	6.23E-07	2.47E-05	1.87E-05	972/2209/3	9
GO:004205	interleukin	5/144	22/18493	6.32E-07	2.47E-05	1.87E-05	3553/3606/	5
GO:003268	regulation of	9/144	127/18493	6.66E-07	2.57E-05	1.94E-05	64135/1081	9
GO:001032	membrane	9/144	129/18493	7.6E-07	2.85E-05	2.16E-05	54209/1131	9
GO:003268	tumor necrosis	9/144	129/18493	7.6E-07	2.85E-05	2.16E-05	64135/1081	9
GO:003267	regulation of	7/144	66/18493	7.96E-07	2.94E-05	2.23E-05	51311/3553	7
GO:000276	positive regulation of	9/144	131/18493	8.65E-07	3.11E-05	2.36E-05	80328/3553	9
GO:190355	regulation of	9/144	131/18493	8.65E-07	3.11E-05	2.36E-05	64135/1081	9
GO:003016	regulation of	12/144	260/18493	9.28E-07	3.3E-05	2.5E-05	11314/3553	12
GO:001988	antigen presentation	9/144	134/18493	1.05E-06	3.67E-05	2.78E-05	972/2209/3	9
GO:007176	tumor necrosis	9/144	135/18493	1.11E-06	3.81E-05	2.89E-05	64135/1081	9
GO:004506	negative thymocyte	4/144	11/18493	1.12E-06	3.81E-05	2.89E-05	916/1794/9	4
GO:000228	T cell activation	8/144	101/18493	1.22E-06	4.12E-05	3.12E-05	54518/3606	8
GO:190355	positive regulation of	14/144	373/18493	1.33E-06	4.43E-05	3.35E-05	64135/5131	14
GO:003274	positive regulation of	6/144	46/18493	1.46E-06	4.79E-05	3.63E-05	51311/3553	6
GO:003267	interleukin	7/144	73/18493	1.59E-06	5.09E-05	3.85E-05	51311/3553	7
GO:003276	positive regulation of	7/144	73/18493	1.59E-06	5.09E-05	3.85E-05	64135/8480	7
GO:004588	positive regulation of	9/144	141/18493	1.6E-06	5.09E-05	3.85E-05	3553/3684/	9
GO:015007	neuroinflammation	6/144	47/18493	1.66E-06	5.16E-05	3.91E-05	51311/3553	6
GO:004333	negative T cell	4/144	12/18493	1.66E-06	5.16E-05	3.91E-05	916/1794/9	4
GO:005076	regulation of	10/144	184/18493	1.81E-06	5.54E-05	4.2E-05	64135/5131	10
GO:004506	T cell selection	6/144	48/18493	1.88E-06	5.71E-05	4.32E-05	917/916/92	6
GO:000282	regulation of	9/144	144/18493	1.91E-06	5.73E-05	4.34E-05	3553/3606/	9
GO:005076	positive regulation of	10/144	186/18493	1.99E-06	5.91E-05	4.47E-05	54209/3606	10
GO:190355	positive regulation of	7/144	76/18493	2.09E-06	6.15E-05	4.65E-05	64135/8480	7
GO:000276	regulation of	9/144	146/18493	2.14E-06	6.22E-05	4.71E-05	80328/3553	9
GO:004506	positive regulation of	4/144	13/18493	2.39E-06	6.73E-05	5.1E-05	3553/916/9	4
GO:006005	regulation of	4/144	13/18493	2.39E-06	6.73E-05	5.1E-05	11314/3684	4
GO:000222	response to	13/144	337/18493	2.39E-06	6.73E-05	5.1E-05	54209/9450	13
GO:005084	T cell receptor	9/144	150/18493	2.68E-06	7.46E-05	5.64E-05	11314/917/	9
GO:003274	positive regulation of	7/144	81/18493	3.22E-06	8.88E-05	6.72E-05	64135/5131	7
GO:190511	regulation of	4/144	14/18493	3.32E-06	9.06E-05	6.86E-05	11314/3684	4
GO:009752	myeloid leucocyte	10/144	199/18493	3.65E-06	9.86E-05	7.46E-05	11314/3553	10
GO:000281	regulation of	9/144	157/18493	3.9E-06	0.000104	7.89E-05	3553/3606/	9
GO:000246	adaptive immunity	13/144	354/18493	4.1E-06	0.000109	8.22E-05	80328/5131	13
GO:007121	cellular response	10/144	206/18493	4.97E-06	0.00013	9.86E-05	54209/9450	10
GO:000177	leukocyte	7/144	88/18493	5.62E-06	0.000146	0.000111	202309/550	7
GO:005066	cytokine secretion	10/144	210/18493	5.89E-06	0.000151	0.000115	64135/5131	10
GO:004333	positive T cell	5/144	35/18493	7.18E-06	0.000183	0.000138	917/916/17	5
GO:004205	interferon-gamma	4/144	17/18493	7.76E-06	0.000196	0.000148	51311/3606	4
GO:003055	leukocyte chemotaxis	10/144	217/18493	7.86E-06	0.000197	0.000149	3553/5294/	10
GO:000274	MyD88-dependent	5/144	36/18493	8.29E-06	0.000205	0.000155	51311/1131	5
GO:003245	response to	12/144	324/18493	8.97E-06	0.00022	0.000167	54209/9450	12
GO:003031	osteoclast chemotaxis	7/144	95/18493	9.36E-06	0.000228	0.000172	54209/2981	7

GO:005072	positive reg	8/144	133/18493	9.6E-06	0.000232	0.000175	3553/3606	8
GO:004662	alpha-beta	8/144	134/18493	1.01E-05	0.00024	0.000182	11314/3606	8
GO:009752	granulocyte	8/144	134/18493	1.01E-05	0.00024	0.000182	11314/3553	8
GO:000222	pattern rec	9/144	179/18493	1.13E-05	0.000266	0.000201	64135/5131	9
GO:001982	antigen pro	7/144	98/18493	1.15E-05	0.000267	0.000202	972/3113/3	7
GO:000262	regulation	9/144	180/18493	1.18E-05	0.000273	0.000207	11314/3670	9
GO:004507	regulation	4/144	19/18493	1.25E-05	0.000286	0.000216	3553/916/9	4
GO:007122	cellular res	10/144	229/18493	1.26E-05	0.000286	0.000216	54209/9450	10
GO:000282	positive reg	7/144	100/18493	1.31E-05	0.000295	0.000224	3553/3606	7
GO:003052	neutrophil	7/144	101/18493	1.4E-05	0.000313	0.000237	3553/5294	7
GO:000272	innate imm	10/144	233/18493	1.46E-05	0.000324	0.000245	64135/5131	10
GO:004252	tumor necr	4/144	20/18493	1.55E-05	0.000338	0.000256	10859/1524	4
GO:004252	regulation	4/144	20/18493	1.55E-05	0.000338	0.000256	10859/1524	4
GO:005122	positive reg	13/144	402/18493	1.6E-05	0.000346	0.000262	64135/5131	13
GO:000242	lymphocyte	12/144	344/18493	1.63E-05	0.00035	0.000265	80328/5131	12
GO:000272	regulation	14/144	465/18493	1.66E-05	0.000353	0.000267	64135/5131	14
GO:003002	myeloid ce	13/144	405/18493	1.73E-05	0.000365	0.000276	54209/2988	13
GO:000272	positive reg	7/144	105/18493	1.81E-05	0.000375	0.000284	80328/3553	7
GO:000282	positive reg	7/144	105/18493	1.81E-05	0.000375	0.000284	3553/3606	7
GO:006032	cell chemo	11/144	295/18493	2.02E-05	0.000416	0.000315	3553/5294	11
GO:005072	positive reg	10/144	246/18493	2.33E-05	0.000478	0.000361	64135/5131	10
GO:004302	regulation	14/144	481/18493	2.42E-05	0.000491	0.000371	399/9938/8	14
GO:199022	neutrophil	7/144	112/18493	2.75E-05	0.000554	0.000419	3553/5294	7
GO:000222	activation	10/144	252/18493	2.87E-05	0.000574	0.000434	64135/5131	10
GO:004502	regulation	12/144	365/18493	2.92E-05	0.000581	0.000439	80328/6413	12
GO:004502	positive reg	11/144	309/18493	3.09E-05	0.000609	0.000461	80328/6413	11
GO:000722	I-kappaB k	10/144	258/18493	3.5E-05	0.000685	0.000519	399/51311/	10
GO:005082	antigen rec	10/144	259/18493	3.62E-05	0.000703	0.000532	11314/917/	10
GO:190492	positive reg	13/144	437/18493	3.82E-05	0.000736	0.000557	64135/5131	13
GO:005072	regulation	13/144	438/18493	3.91E-05	0.000747	0.000565	64135/5131	13
GO:015007	regulation	4/144	25/18493	3.93E-05	0.000747	0.000565	3553/3606	4
GO:001992	second-me	13/144	439/18493	4E-05	0.000756	0.000572	54209/297	13
GO:007162	granulocyte	7/144	120/18493	4.28E-05	0.000804	0.000608	3553/5294	7
GO:003262	chemokine	6/144	82/18493	4.32E-05	0.000805	0.000609	3553/3606	6
GO:000272	positive reg	10/144	265/18493	4.39E-05	0.000807	0.000611	64135/5131	10
GO:190212	regulation	10/144	265/18493	4.39E-05	0.000807	0.000611	3606/10859	10
GO:000262	positive reg	7/144	121/18493	4.52E-05	0.000825	0.000624	3676/81704	7
GO:003632	dendritic c	4/144	26/18493	4.61E-05	0.000832	0.00063	5294/81704	4
GO:003212	activation	11/144	323/18493	4.62E-05	0.000832	0.00063	11314/3553	11
GO:000282	regulation	5/144	51/18493	4.7E-05	0.000841	0.000637	11314/3684	5
GO:001812	peptidyl-ty	12/144	387/18493	5.16E-05	0.000916	0.000693	54209/1131	12
GO:007142	cellular res	11/144	328/18493	5.31E-05	0.000937	0.00071	51311/3553	11
GO:001822	peptidyl-ty	12/144	390/18493	5.55E-05	0.000974	0.000737	54209/1131	12
GO:003262	regulation	5/144	53/18493	5.67E-05	0.000982	0.000743	3553/916/8	5
GO:003272	positive reg	5/144	53/18493	5.67E-05	0.000982	0.000743	3553/51284	5
GO:001972	calcium-m	9/144	220/18493	5.75E-05	0.000989	0.000748	54209/916/	9
GO:000712	negative re	10/144	276/18493	6.18E-05	0.001047	0.000793	11314/704/	10
GO:000262	positive reg	4/144	28/18493	6.24E-05	0.001047	0.000793	3553/5294	4
GO:000282	positive reg	4/144	28/18493	6.24E-05	0.001047	0.000793	3684/8673/	4
GO:003262	regulation	4/144	28/18493	6.24E-05	0.001047	0.000793	64135/5131	4
GO:004342	regulation	11/144	335/18493	6.42E-05	0.00107	0.00081	11314/3553	11
GO:000252	platelet de	7/144	128/18493	6.47E-05	0.001071	0.000811	3699/5157/	7
GO:003262	interferon-	4/144	29/18493	7.2E-05	0.001179	0.000892	64135/5131	4
GO:006012	positive reg	3/144	11/18493	7.29E-05	0.001179	0.000892	3684/3071/	3
GO:007062	response to	3/144	11/18493	7.29E-05	0.001179	0.000892	3606/240/9	3
GO:190512	positive reg	3/144	11/18493	7.29E-05	0.001179	0.000892	3684/3071/	3
GO:000222	toll-like rec	7/144	131/18493	7.49E-05	0.001202	0.00091	51311/1131	7
GO:007032	ERK1 and	11/144	341/18493	7.52E-05	0.001202	0.00091	54209/3553	11

GO:00421(B cell proli	6/144	91/18493	7.77E-05	0.001223	0.000925	11314/202	6
GO:00466(regulation	(6/144	91/18493	7.77E-05	0.001223	0.000925	11314/360	6
GO:00713(cellular res	8/144	178/18493	7.79E-05	0.001223	0.000925	834/2209/3	8
GO:00455(mast cell ac	5/144	57/18493	8.07E-05	0.00126	0.000954	399/11314/	5
GO:00017(B cell hom	4/144	30/18493	8.26E-05	0.001267	0.000959	202309/55	4
GO:00327(positive re	4/144	30/18493	8.26E-05	0.001267	0.000959	3553/916/9	4
GO:00425(antigen pro	4/144	30/18493	8.26E-05	0.001267	0.000959	2209/8673/	4
GO:00308(regulation	(5/144	59/18493	9.53E-05	0.001455	0.001101	11314/972/	5
GO:00704(thrombin-a	3/144	12/18493	9.66E-05	0.001466	0.00111	2149/1078	3
GO:19908(response to	6/144	95/18493	9.88E-05	0.001482	0.001122	54209/658	6
GO:19908(cellular res	6/144	95/18493	9.88E-05	0.001482	0.001122	54209/658	6
GO:00380(Fc-gamma	7/144	138/18493	0.000104	0.00155	0.001173	917/2214/3	7
GO:00466(alpha-beta	4/144	32/18493	0.000107	0.001588	0.001202	3606/916/1	4
GO:00024(Fc receptor	7/144	140/18493	0.000114	0.001678	0.00127	917/2214/3	7
GO:00017(microglial	(4/144	33/18493	0.000121	0.001767	0.001338	51311/512	4
GO:00022(leukocyte a	4/144	33/18493	0.000121	0.001767	0.001338	51311/512	4
GO:19021(positive re	7/144	142/18493	0.000124	0.0018	0.001362	3606/920/9	7
GO:00017(immunolog	3/144	13/18493	0.000125	0.0018	0.001362	84868/817	3
GO:00507(regulation	(12/144	425/18493	0.000125	0.0018	0.001362	3553/3606/	12
GO:00508(regulation	(13/144	493/18493	0.000129	0.001842	0.001394	54843/529	13
GO:00703(positive re	9/144	245/18493	0.000131	0.001859	0.001407	54209/214	9
GO:00302(monocyte c	4/144	34/18493	0.000136	0.001918	0.001452	920/972/14	4
GO:19031(mononucle	4/144	34/18493	0.000136	0.001918	0.001452	920/972/14	4
GO:00022(lymphocyte	5/144	64/18493	0.000141	0.001969	0.00149	202309/55	5
GO:00606(regulation	(13/144	498/18493	0.000142	0.001983	0.001501	11314/355	13
GO:00488(homeostasi	9/144	248/18493	0.000143	0.001985	0.001502	202309/55	9
GO:00024(T cell medi	6/144	102/18493	0.000146	0.002017	0.001527	80328/355	6
GO:01500(positive re	3/144	14/18493	0.000158	0.002167	0.00164	3553/3606/	3
GO:00343(response to	8/144	198/18493	0.000163	0.002211	0.001673	834/2209/3	8
GO:00027(regulation	(5/144	66/18493	0.000163	0.002211	0.001673	3553/3606/	5
GO:00712(cellular res	8/144	199/18493	0.000169	0.002277	0.001723	9450/3553/	8
GO:00019(leukocyte r	6/144	105/18493	0.000172	0.002306	0.001745	80328/360	6
GO:00508(negative re	6/144	106/18493	0.000181	0.002417	0.001829	11314/108	6
GO:00096(response to	10/144	315/18493	0.000183	0.002434	0.001842	64135/513	10
GO:00301(platelet act	7/144	152/18493	0.000189	0.002507	0.001898	5294/2149/	7
GO:00718(leukocyte a	6/144	107/18493	0.00019	0.002507	0.001898	10859/917/	6
GO:00434(positive re	9/144	258/18493	0.000193	0.002526	0.001912	3553/5294/	9
GO:00019(negative re	3/144	15/18493	0.000196	0.002539	0.001921	10859/848	3
GO:00466(gamma-del	3/144	15/18493	0.000196	0.002539	0.001921	10859/307	3
GO:20004(positive re	3/144	15/18493	0.000196	0.002539	0.001921	2149/7096/	3
GO:00330(T cell diffe	5/144	69/18493	0.000201	0.002586	0.001957	917/916/17	5
GO:19012(positive re	5/144	70/18493	0.000215	0.002754	0.002085	3553/3606/	5
GO:00719(positive re	10/144	323/18493	0.000224	0.002851	0.002158	3553/5294/	10
GO:00703(regulation	(10/144	324/18493	0.000229	0.002909	0.002202	54209/355	10
GO:00019(cell killing	7/144	158/18493	0.00024	0.00302	0.002286	80328/360	7
GO:00450(regulation	(3/144	16/18493	0.00024	0.00302	0.002286	51311/512	3
GO:00324(regulation	(6/144	113/18493	0.000256	0.003202	0.002424	64135/513	6
GO:00308(positive re	4/144	40/18493	0.000259	0.003211	0.00243	972/3071/5	4
GO:00619(glial cell ac	4/144	40/18493	0.000259	0.003211	0.00243	51311/512	4
GO:00550(calcium ior	12/144	461/18493	0.000265	0.003271	0.002475	160335/84	12
GO:00326(type I inter	6/144	114/18493	0.000269	0.003298	0.002496	64135/513	6
GO:00026(regulation	(3/144	17/18493	0.00029	0.003547	0.002685	916/84868/	3
GO:00326(regulation	(5/144	75/18493	0.000297	0.003603	0.002727	3553/5128	5
GO:00706(negative re	5/144	75/18493	0.000297	0.003603	0.002727	11314/108	5
GO:00026(negative re	7/144	164/18493	0.000302	0.003636	0.002752	11314/108	7
GO:00433(regulation	(4/144	42/18493	0.000314	0.003765	0.002849	11314/368	4
GO:00019(regulation	(5/144	76/18493	0.000316	0.003782	0.002862	80328/515	5
GO:00488(multicellul	12/144	471/18493	0.000322	0.003833	0.002901	3553/6588/	12

GO:004354	positive reg	11/144	405/18493	0.000336	0.003949	0.002989	9938/8477/	11
GO:000271	regulation	5/144	77/18493	0.000336	0.003949	0.002989	3553/3606/	5
GO:003264	regulation	5/144	77/18493	0.000336	0.003949	0.002989	51311/834/	5
GO:003134	negative re	3/144	18/18493	0.000346	0.004049	0.003065	10859/8480/	3
GO:005104	negative re	8/144	222/18493	0.000353	0.004115	0.003114	51311/1131/	8
GO:007124	cellular res	5/144	78/18493	0.000357	0.00414	0.003133	51311/3553/	5
GO:004671	viral entry	6/144	121/18493	0.00037	0.004274	0.003235	920/23601/	6
GO:003364	regulation	4/144	44/18493	0.000376	0.004283	0.003241	5294/916/3	4
GO:004333	mast cell d	4/144	44/18493	0.000376	0.004283	0.003241	11314/5294/	4
GO:005084	positive reg	4/144	44/18493	0.000376	0.004283	0.003241	54209/916/	4
GO:000685	receptor-m	10/144	346/18493	0.000386	0.004373	0.00331	10859/3670/	10
GO:190307	negative re	6/144	122/18493	0.000387	0.004373	0.00331	11314/1085/	6
GO:004664	positive reg	3/144	19/18493	0.000409	0.004576	0.003463	3606/916/5	3
GO:000227	mast cell a	4/144	45/18493	0.00041	0.004576	0.003463	11314/5294/	4
GO:000270	negative re	4/144	45/18493	0.00041	0.004576	0.003463	11314/1085/	4
GO:005160	defense res	8/144	228/18493	0.000422	0.004693	0.003552	64135/5131/	8
GO:000244	mast cell r	4/144	46/18493	0.000446	0.004901	0.003709	11314/5294/	4
GO:000247	antigen pro	4/144	46/18493	0.000446	0.004901	0.003709	2209/8673/	4
GO:000271	positive reg	4/144	46/18493	0.000446	0.004901	0.003709	3553/3606/	4
GO:004553	positive reg	5/144	83/18493	0.000476	0.005188	0.003927	3606/972/3	5
GO:003364	positive reg	3/144	20/18493	0.000478	0.005188	0.003927	916/3071/6	3
GO:009724	amyloid-be	3/144	20/18493	0.000478	0.005188	0.003927	3684/4481/	3
GO:000272	positive reg	4/144	47/18493	0.000485	0.005239	0.003965	3553/3606/	4
GO:007190	regulation	12/144	496/18493	0.000511	0.005504	0.004166	11314/3553/	12
GO:004644	regulation	6/144	129/18493	0.000521	0.005583	0.004225	11314/3606/	6
GO:004644	positive reg	5/144	85/18493	0.000531	0.005671	0.004292	11314/3606/	5
GO:003414	toll-like rec	3/144	21/18493	0.000555	0.005877	0.004448	51311/5128/	3
GO:004333	positive reg	3/144	21/18493	0.000555	0.005877	0.004448	3684/8673/	3
GO:003264	regulation	4/144	49/18493	0.000569	0.006005	0.004545	64135/5131/	4
GO:190370	positive reg	7/144	183/18493	0.000583	0.006125	0.004635	3606/920/9	7
GO:003261	interleukin	5/144	87/18493	0.000591	0.00614	0.004647	51311/834/	5
GO:007005	chemokine	5/144	87/18493	0.000591	0.00614	0.004647	54209/6580/	5
GO:200010	regulation	5/144	87/18493	0.000591	0.00614	0.004647	10859/917/	5
GO:005084	negative re	7/144	184/18493	0.000602	0.006193	0.004687	11314/1085/	7
GO:000271	regulation	6/144	133/18493	0.000612	0.006193	0.004687	3553/3606/	6
GO:003024	entry into l	6/144	133/18493	0.000612	0.006193	0.004687	920/23601/	6
GO:004444	entry into l	6/144	133/18493	0.000612	0.006193	0.004687	920/23601/	6
GO:005184	entry into c	6/144	133/18493	0.000612	0.006193	0.004687	920/23601/	6
GO:005184	entry into c	6/144	133/18493	0.000612	0.006193	0.004687	920/23601/	6
GO:190485	regulation	6/144	133/18493	0.000612	0.006193	0.004687	11314/3606/	6
GO:000191	T cell medi	4/144	50/18493	0.000615	0.006197	0.00469	80328/5157/	4
GO:003134	regulation	5/144	88/18493	0.000623	0.00623	0.004715	80328/5157/	5
GO:190485	positive reg	5/144	88/18493	0.000623	0.00623	0.004715	11314/3606/	5
GO:000268	negative re	11/144	437/18493	0.000634	0.006316	0.00478	11314/1085/	11
GO:003272	positive reg	3/144	22/18493	0.000639	0.006344	0.004801	64135/5131/	3
GO:000244	immune re	6/144	135/18493	0.000662	0.006444	0.004877	917/2214/3	6
GO:000275	negative re	6/144	135/18493	0.000662	0.006444	0.004877	51311/3553/	6
GO:003805	Fc-gamma	6/144	135/18493	0.000662	0.006444	0.004877	917/2214/3	6
GO:003805	Fc receptor	7/144	187/18493	0.000662	0.006444	0.004877	917/2214/3	7
GO:003260	interferon-l	4/144	51/18493	0.000663	0.006444	0.004877	64135/5131/	4
GO:200010	negative re	4/144	51/18493	0.000663	0.006444	0.004877	10859/8170/	4
GO:006033	interferon-g	5/144	90/18493	0.00069	0.00668	0.005056	2209/3113/	5
GO:004307	regulation	4/144	52/18493	0.000714	0.006827	0.005167	3684/8486/	4
GO:006074	positive reg	4/144	52/18493	0.000714	0.006827	0.005167	64135/5420/	4
GO:005124	negative re	6/144	137/18493	0.000715	0.006827	0.005167	11314/1085/	6
GO:000720	positive reg	9/144	309/18493	0.000717	0.006827	0.005167	8477/5294/	9
GO:000271	positive reg	5/144	91/18493	0.000726	0.006827	0.005167	3553/3606/	5
GO:004801	vascular en	5/144	91/18493	0.000726	0.006827	0.005167	3553/3071/	5

GO:00024 dendritic c	3/144	23/18493	0.00073	0.006827	0.005167	5294/1880/	3
GO:00327 positive re	3/144	23/18493	0.00073	0.006827	0.005167	916/84868/	3
GO:00900 positive re	3/144	23/18493	0.00073	0.006827	0.005167	972/3071/7	3
GO:20007 positive re	3/144	23/18493	0.00073	0.006827	0.005167	64135/513/	3
GO:20004 regulation	3/144	24/18493	0.00083	0.007731	0.005851	2149/7096/	3
GO:00456 positive re	5/144	94/18493	0.000841	0.007803	0.005905	3606/972/3	5
GO:19035 negative re	7/144	196/18493	0.000873	0.008079	0.006115	51311/113/	7
GO:00023 cytokine pr	5/144	95/18493	0.000882	0.00813	0.006153	3553/3606/	5
GO:00025 tolerance in	3/144	25/18493	0.000938	0.008587	0.006499	916/84868/	3
GO:00716 positive re	3/144	25/18493	0.000938	0.008587	0.006499	972/3071/7	3
GO:00316 lipopolysac	4/144	56/18493	0.000946	0.008632	0.006533	9450/3553/	4
GO:00072 phospholip	5/144	97/18493	0.000969	0.008811	0.006668	8477/2149/	5
GO:00457 positive re	7/144	200/18493	0.000983	0.008908	0.006742	3553/1524/	7
GO:00072 JAK-STAT	6/144	147/18493	0.001033	0.009328	0.00706	11314/360/	6
GO:19026 positive re	3/144	26/18493	0.001054	0.009492	0.007184	972/3071/7	3
GO:00072 integrin-me	5/144	99/18493	0.001062	0.009529	0.007212	3684/3676/	5
GO:00422 natural kill	4/144	58/18493	0.00108	0.009656	0.007308	80328/360/	4
GO:00508 regulation	5/144	100/18493	0.001111	0.009903	0.007495	54209/916/	5
GO:00726 T cell migr	4/144	59/18493	0.001151	0.010229	0.007741	5294/3676/	4
GO:00028 regulation	3/144	27/18493	0.001179	0.010342	0.007827	3553/3606/	3
GO:00105 positive re	3/144	27/18493	0.001179	0.010342	0.007827	3553/719/7	3
GO:00326 regulation	3/144	27/18493	0.001179	0.010342	0.007827	916/84868/	3
GO:00421 positive re	3/144	27/18493	0.001179	0.010342	0.007827	3606/3479/	3
GO:00976 STAT casc	6/144	151/18493	0.001186	0.010368	0.007847	11314/360/	6
GO:19012 regulation	5/144	102/18493	0.001214	0.010577	0.008005	3553/3606/	5
GO:00301 proteoglyc	4/144	60/18493	0.001226	0.010648	0.008059	176/658/34	4
GO:00075 blood coag	9/144	334/18493	0.001237	0.010707	0.008103	5294/2149/	9
GO:00069 cellular def	4/144	61/18493	0.001304	0.01119	0.008469	10219/152/	4
GO:00466 positive re	4/144	61/18493	0.001304	0.01119	0.008469	3606/916/3	4
GO:00433 regulation	3/144	28/18493	0.001313	0.01119	0.008469	11314/867/	3
GO:00726 interleukin	3/144	28/18493	0.001313	0.01119	0.008469	2149/7096/	3
GO:00900 regulation	3/144	28/18493	0.001313	0.01119	0.008469	972/3071/7	3
GO:00075 hemostasis	9/144	339/18493	0.001371	0.011641	0.00881	5294/2149/	9
GO:00726 lymphocyte	5/144	105/18493	0.001381	0.011696	0.008852	5294/3676/	5
GO:00022 natural kill	4/144	62/18493	0.001386	0.011698	0.008853	80328/360/	4
GO:00508 coagulation	9/144	340/18493	0.001399	0.011758	0.008899	5294/2149/	9
GO:20012 regulation	6/144	156/18493	0.001402	0.011758	0.008899	3553/658/3	6
GO:00330 regulation	3/144	29/18493	0.001457	0.012142	0.00919	11314/867/	3
GO:00466 regulation	3/144	29/18493	0.001457	0.012142	0.00919	3606/916/5	3
GO:00075 response to	7/144	216/18493	0.001532	0.012733	0.009637	3553/916/1	7
GO:00326 regulation	4/144	64/18493	0.00156	0.012922	0.00978	51311/834/	4
GO:19037 regulation	10/144	418/18493	0.001632	0.013478	0.0102	3606/1085/	10
GO:00301 extracellular	9/144	348/18493	0.001641	0.013481	0.010203	7045/176/3	9
GO:00324 lysosome	4/144	65/18493	0.001652	0.013481	0.010203	11314/529/	4
GO:00324 positive re	4/144	65/18493	0.001652	0.013481	0.010203	64135/513/	4
GO:00336 cell adhesion	4/144	65/18493	0.001652	0.013481	0.010203	5294/916/3	4
GO:00069 humoral ir	9/144	349/18493	0.001673	0.013612	0.010302	54209/945/	9
GO:00514 regulation	9/144	350/18493	0.001706	0.013839	0.010474	8477/5294/	9
GO:00510 negative re	11/144	495/18493	0.001729	0.013982	0.010582	51311/113/	11
GO:00018 tissue home	7/144	221/18493	0.001746	0.014073	0.010651	29887/214/	7
GO:00026 negative re	5/144	111/18493	0.001767	0.014073	0.010651	11314/108/	5
GO:00327 positive re	3/144	31/18493	0.001772	0.014073	0.010651	64135/513/	3
GO:00425 superoxide	3/144	31/18493	0.001772	0.014073	0.010651	3684/1536/	3
GO:00514 positive re	3/144	31/18493	0.001772	0.014073	0.010651	8477/2149/	3
GO:19026 regulation	3/144	31/18493	0.001772	0.014073	0.010651	972/3071/7	3
GO:00607 regulation	6/144	165/18493	0.001864	0.014766	0.011175	64135/542/	6
GO:00105 regulation	3/144	32/18493	0.001944	0.015351	0.011618	3553/719/7	3
GO:00431 regulation	7/144	226/18493	0.001981	0.015597	0.011804	399/3553/8	7

GO:000276	regulation of	5/144	114/18493	0.001986	0.015597	0.011804	10859/920	5
GO:190401	positive regulation of	7/144	228/18493	0.002082	0.016303	0.012339	3553/1524	7
GO:000191	regulation of	3/144	33/18493	0.002126	0.016501	0.012488	51571/108	3
GO:003262	interleukin	3/144	33/18493	0.002126	0.016501	0.012488	916/84868	3
GO:004572	respiratory	3/144	33/18493	0.002126	0.016501	0.012488	5294/1536	3
GO:002242	negative regulation of	6/144	170/18493	0.002166	0.016708	0.012645	11314/108	6
GO:003292	negative regulation of	4/144	70/18493	0.002171	0.016708	0.012645	11314/108	4
GO:005067	negative regulation of	4/144	70/18493	0.002171	0.016708	0.012645	11314/108	4
GO:000202	chondrocyte	5/144	117/18493	0.002225	0.017076	0.012924	7045/1766	5
GO:001057	vascular endothelial cell	3/144	34/18493	0.002319	0.01769	0.013388	3553/7197	3
GO:001092	positive regulation of	3/144	34/18493	0.002319	0.01769	0.013388	11314/578	3
GO:000231	B cell activation	4/144	72/18493	0.002407	0.018213	0.013784	202309/55	4
GO:000998	cell-cell contact	4/144	72/18493	0.002407	0.018213	0.013784	84868/235	4
GO:007022	lymphocyte	4/144	72/18493	0.002407	0.018213	0.013784	917/81704	4
GO:003802	NIK/NF- κ B	5/144	120/18493	0.002485	0.018747	0.014189	3553/3606	5
GO:000276	negative regulation of	3/144	35/18493	0.002522	0.018874	0.014284	10859/848	3
GO:007262	interleukin	3/144	35/18493	0.002522	0.018874	0.014284	64135/513	3
GO:003261	interleukin	4/144	73/18493	0.002532	0.018874	0.014284	51311/834	4
GO:000172	establishment of	2/144	10/18493	0.002601	0.018874	0.014284	81704/179	2
GO:000182	serotonin signaling	2/144	10/18493	0.002601	0.018874	0.014284	10859/220	2
GO:000262	regulation of	2/144	10/18493	0.002601	0.018874	0.014284	916/3559	2
GO:000282	positive regulation of	2/144	10/18493	0.002601	0.018874	0.014284	718/2207	2
GO:001072	regulation of	2/144	10/18493	0.002601	0.018874	0.014284	2977/7422	2
GO:005112	regulation of	2/144	10/18493	0.002601	0.018874	0.014284	11314/360	2
GO:007035	response to	2/144	10/18493	0.002601	0.018874	0.014284	54209/929	2
GO:007122	cellular response to	2/144	10/18493	0.002601	0.018874	0.014284	54209/929	2
GO:007264	type I interferon	2/144	10/18493	0.002601	0.018874	0.014284	64135/108	2
GO:200002	regulation of	2/144	10/18493	0.002601	0.018874	0.014284	2124/6423	2
GO:200112	regulation of	2/144	10/18493	0.002601	0.018874	0.014284	10859/553	2
GO:004211	B cell activation	8/144	303/18493	0.002606	0.018874	0.014284	11314/202	8
GO:000687	cellular calcium ion	10/144	448/18493	0.002701	0.019504	0.014761	8477/5294	10
GO:003411	homotypic cell-cell	4/144	76/18493	0.002931	0.021111	0.015978	288/5294/5	4
GO:000282	negative regulation of	3/144	37/18493	0.00296	0.02113	0.015992	10859/848	3
GO:200062	positive regulation of	3/144	37/18493	0.00296	0.02113	0.015992	1524/5788	3
GO:004312	positive regulation of	6/144	181/18493	0.002961	0.02113	0.015992	3553/834/2	6
GO:003018	B cell differentiation	5/144	125/18493	0.002965	0.02113	0.015992	55619/367	5
GO:000172	establishment of	2/144	11/18493	0.003163	0.022073	0.016706	81704/179	2
GO:003245	detection of	2/144	11/18493	0.003163	0.022073	0.016706	54209/709	2
GO:004252	positive regulation of	2/144	11/18493	0.003163	0.022073	0.016706	7096/1536	2
GO:004521	cell-cell junction	2/144	11/18493	0.003163	0.022073	0.016706	2149/1436	2
GO:004534	type I interferon	2/144	11/18493	0.003163	0.022073	0.016706	51311/512	2
GO:004594	negative regulation of	2/144	11/18493	0.003163	0.022073	0.016706	10859/848	2
GO:007024	mucus secretion	2/144	11/18493	0.003163	0.022073	0.016706	54843/867	2
GO:190252	regulation of	2/144	11/18493	0.003163	0.022073	0.016706	11314/368	2
GO:000271	positive regulation of	3/144	38/18493	0.003195	0.022186	0.016791	5788/718/2	3
GO:000282	positive regulation of	3/144	38/18493	0.003195	0.022186	0.016791	5788/718/2	3
GO:003302	regulation of	3/144	39/18493	0.003442	0.023838	0.018041	11314/867	3
GO:005072	negative regulation of	5/144	131/18493	0.003626	0.025045	0.018955	11314/108	5
GO:000282	negative regulation of	3/144	40/18493	0.0037	0.025365	0.019197	10859/848	3
GO:004602	regulation of	3/144	40/18493	0.0037	0.025365	0.019197	3606/3479	3
GO:009702	dendritic cell	3/144	40/18493	0.0037	0.025365	0.019197	54209/108	3
GO:000251	T cell tolerance	2/144	12/18493	0.003776	0.025497	0.019297	916/3559	2
GO:000271	negative regulation of	2/144	12/18493	0.003776	0.025497	0.019297	10859/848	2
GO:000282	regulation of	2/144	12/18493	0.003776	0.025497	0.019297	718/2207	2
GO:003811	interleukin	2/144	12/18493	0.003776	0.025497	0.019297	3561/3559	2
GO:004507	positive regulation of	2/144	12/18493	0.003776	0.025497	0.019297	51311/512	2
GO:005112	NK T cell	2/144	12/18493	0.003776	0.025497	0.019297	11314/360	2
GO:014002	exocytic process	4/144	82/18493	0.003855	0.025967	0.019652	54843/534	4

GO:000701	actin filament	9/144	397/18493	0.003954	0.026523	0.020074	399/9938/8	9
GO:000181	negative regulation	7/144	256/18493	0.003957	0.026523	0.020074	64135/51311/1088	7
GO:003161	cellular response	7/144	258/18493	0.004129	0.027602	0.02089	1277/2350/7	7
GO:000261	positive regulation	4/144	84/18493	0.004202	0.028026	0.021211	972/3071/7	4
GO:000241	inflammatory response	3/144	42/18493	0.004251	0.028072	0.021246	3559/718/2	3
GO:004201	T-helper 1 cell activation	3/144	42/18493	0.004251	0.028072	0.021246	3553/3606/7	3
GO:004221	regulation of gene expression	3/144	42/18493	0.004251	0.028072	0.021246	80328/1088/3	3
GO:007161	regulation of cell growth	3/144	42/18493	0.004251	0.028072	0.021246	972/3071/7	3
GO:004301	extracellular matrix organization	9/144	402/18493	0.004288	0.028251	0.021381	7045/176/3	9
GO:003011	natural killer cell activation	4/144	85/18493	0.004384	0.028552	0.021609	80328/3606/7	4
GO:004551	regulation of cell cycle	5/144	137/18493	0.004386	0.028552	0.021609	3606/972/3	5
GO:000241	complement activation	2/144	13/18493	0.00444	0.028552	0.021609	2359/719	2
GO:003271	positive regulation of cell growth	2/144	13/18493	0.00444	0.028552	0.021609	3553/3606	2
GO:003301	positive regulation of cell cycle	2/144	13/18493	0.00444	0.028552	0.021609	8673/2207	2
GO:003571	interleukin-2 production	2/144	13/18493	0.00444	0.028552	0.021609	920/3561	2
GO:004331	positive regulation of cell cycle	2/144	13/18493	0.00444	0.028552	0.021609	8673/2207	2
GO:004541	regulation of cell cycle	2/144	13/18493	0.00444	0.028552	0.021609	51311/51281	2
GO:007131	cellular response	2/144	13/18493	0.00444	0.028552	0.021609	920/3561	2
GO:007131	cellular response	2/144	13/18493	0.00444	0.028552	0.021609	3561/3559	2
GO:000601	proteoglycan synthesis	4/144	86/18493	0.00457	0.02932	0.022191	176/658/34	4
GO:007251	cellular division	10/144	483/18493	0.004591	0.029384	0.022239	8477/5294/6	10
GO:000271	regulation of gene expression	3/144	44/18493	0.004849	0.030888	0.023377	80328/1088/3	3
GO:005071	activated T cell activation	3/144	44/18493	0.004849	0.030888	0.023377	3606/3479/7	3
GO:000241	production of complement	7/144	268/18493	0.00507	0.031929	0.024165	202309/3553/7	7
GO:000691	complement activation	2/144	14/18493	0.005153	0.031929	0.024165	11326/718	2
GO:003431	cell junction organization	2/144	14/18493	0.005153	0.031929	0.024165	2149/1436	2
GO:003551	G protein-coupled receptor signaling	2/144	14/18493	0.005153	0.031929	0.024165	53829/2857	2
GO:004221	interleukin-2 production	2/144	14/18493	0.005153	0.031929	0.024165	51311/51281	2
GO:007061	response to hypoxia	2/144	14/18493	0.005153	0.031929	0.024165	3561/3559	2
GO:007061	response to hypoxia	2/144	14/18493	0.005153	0.031929	0.024165	920/3561	2
GO:190391	regulation of gene expression	2/144	14/18493	0.005153	0.031929	0.024165	1524/1880	2
GO:190441	positive regulation of cell cycle	2/144	14/18493	0.005153	0.031929	0.024165	64135/8480	2
GO:000201	chondrocyte differentiation	3/144	45/18493	0.005166	0.031929	0.024165	176/658/64	3
GO:003241	negative regulation of cell growth	3/144	45/18493	0.005166	0.031929	0.024165	64135/1088/3	3
GO:003271	positive regulation of cell growth	3/144	45/18493	0.005166	0.031929	0.024165	51311/834/6	3
GO:004471	multi-organism development	3/144	45/18493	0.005166	0.031929	0.024165	64135/920/7	3
GO:000191	positive regulation of cell cycle	3/144	46/18493	0.005495	0.033887	0.025647	54209/834/6	3
GO:005121	cartilage development	6/144	206/18493	0.005555	0.034098	0.025807	7045/176/1	6
GO:007121	cellular response	6/144	206/18493	0.005555	0.034098	0.025807	1277/2350/7	6
GO:004561	positive regulation of cell growth	4/144	91/18493	0.005583	0.034194	0.025879	920/972/30	4
GO:006031	bone development	6/144	208/18493	0.005817	0.035546	0.026903	10859/1277/6	6
GO:000281	positive regulation of cell cycle	2/144	15/18493	0.005916	0.035747	0.027055	3606/972	2
GO:000681	serotonin transporter activity	2/144	15/18493	0.005916	0.035747	0.027055	10859/2207	2
GO:003261	regulation of cell growth	2/144	15/18493	0.005916	0.035747	0.027055	3553/3606	2
GO:003261	negative regulation of cell growth	2/144	15/18493	0.005916	0.035747	0.027055	51311/1088/3	2
GO:200111	regulation of cell cycle	2/144	15/18493	0.005916	0.035747	0.027055	10859/3071/7	2
GO:005171	interaction	6/144	209/18493	0.005951	0.035881	0.027156	920/2360/1	6
GO:005091	regulation of gene expression	6/144	210/18493	0.006088	0.036623	0.027718	972/3071/1	6
GO:000251	acute inflammation	6/144	211/18493	0.006227	0.037266	0.028204	3553/5294/6	6
GO:000261	regulation of cell cycle	5/144	149/18493	0.006236	0.037266	0.028204	3553/5294/6	5
GO:006101	membrane organization	5/144	149/18493	0.006236	0.037266	0.028204	219285/548/5	5
GO:001601	immunoglobulin production	6/144	212/18493	0.006368	0.037971	0.028738	51311/20281	6
GO:000011	activation of cell cycle	5/144	150/18493	0.006412	0.038146	0.02887	3553/3479/7	5
GO:001971	B cell mediated immunity	6/144	213/18493	0.006512	0.038656	0.029257	51311/20281	6
GO:005071	negative regulation of cell cycle	3/144	49/18493	0.006557	0.038841	0.029397	11314/5788/6	3
GO:003231	positive regulation of cell cycle	6/144	214/18493	0.006658	0.03935	0.029781	3553/288/3	6
GO:000291	positive regulation of cell cycle	2/144	16/18493	0.006727	0.039379	0.029804	5788/718	2
GO:003261	granulocyte activation	2/144	16/18493	0.006727	0.039379	0.029804	3553/3606	2

GO:00330: negative re 2/144	16/18493	0.006727	0.039379	0.029804	23601/2207	2
GO:00315: actin cytosol 4/144	96/18493	0.006736	0.039379	0.029804	8477/14367	4
GO:01201: positive re 4/144	96/18493	0.006736	0.039379	0.029804	6588/36067	4
GO:19033: positive re 3/144	50/18493	0.006937	0.040467	0.030627	3684/86737	3
GO:19021: negative re 4/144	98/18493	0.007238	0.042132	0.031887	10859/9727	4
GO:00019: regulation 5/144	155/18493	0.007342	0.042645	0.032275	54209/65807	5
GO:00025: regulation 2/144	17/18493	0.007585	0.043589	0.03299	54209/9727	2
GO:00027: negative re 2/144	17/18493	0.007585	0.043589	0.03299	10859/57887	2
GO:00107: positive re 2/144	17/18493	0.007585	0.043589	0.03299	3606/44817	2
GO:00610: positive re 2/144	17/18493	0.007585	0.043589	0.03299	972/22077	2
GO:19039: regulation 2/144	17/18493	0.007585	0.043589	0.03299	3684/57887	2
GO:00027: regulation 3/144	52/18493	0.007734	0.04407	0.033354	5788/71827	3
GO:00027: positive re 3/144	52/18493	0.007734	0.04407	0.033354	920/972/217	3
GO:00028: regulation 3/144	52/18493	0.007734	0.04407	0.033354	5788/71827	3
GO:00301: collagen fil 3/144	52/18493	0.007734	0.04407	0.033354	176/1277/67	3
GO:20012: negative re 6/144	222/18493	0.007912	0.044991	0.034051	3553/15247	6
GO:00315: ruffle organ 3/144	53/18493	0.008152	0.046159	0.034935	29887/14367	3
GO:00465: positive re 3/144	53/18493	0.008152	0.046159	0.034935	8477/21497	3
GO:00971: extrinsic at 6/144	224/18493	0.008251	0.046622	0.035285	3553/658/37	6
GO:00027: positive re 2/144	18/18493	0.00849	0.047378	0.035857	3553/36067	2
GO:00072: I-kappaB p 2/144	18/18493	0.00849	0.047378	0.035857	51284/15247	2
GO:00320: response to 2/144	18/18493	0.00849	0.047378	0.035857	288/9297	2
GO:00330: positive re 2/144	18/18493	0.00849	0.047378	0.035857	8673/22077	2
GO:00456: regulation 2/144	18/18493	0.00849	0.047378	0.035857	920/9727	2
GO:00985: detection o 2/144	18/18493	0.00849	0.047378	0.035857	54209/70907	2
GO:00451: cellular ext 3/144	54/18493	0.008583	0.047798	0.036175	5294/36767	3
GO:20012: negative re 4/144	104/18493	0.00889	0.04941	0.037395	3553/34797	4

AMed GO CC

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:00098: external sic 19/150	359/19659	3.65E-11	9.02E-09	6.65E-09	51311/36847	19		
GO:00708: tertiary gra 9/150	73/19659	4.41E-09	3.98E-07	2.94E-07	4973/113147	9		
GO:00708: tertiary gra 12/150	164/19659	4.84E-09	3.98E-07	2.94E-07	4973/113147	12		
GO:00306: secretory g 15/150	295/19659	8.15E-09	5.04E-07	3.71E-07	4973/113147	15		
GO:00432: receptor co 16/150	396/19659	6.38E-08	3.15E-06	2.32E-06	4973/54518/917/	16		
GO:00426: MHC class 5/150	16/19659	9.87E-08	4.06E-06	3E-06	972/3113/37	5		
GO:00301: endocytic v 13/150	293/19659	4.06E-07	1.24E-05	9.16E-06	51284/70907	13		
GO:00425: specific gra 10/150	160/19659	4.24E-07	1.24E-05	9.16E-06	4973/22918/	10		
GO:00355: specific gra 8/150	91/19659	4.74E-07	1.24E-05	9.16E-06	4973/22918/	8		
GO:00306: endocytic v 10/150	163/19659	5.03E-07	1.24E-05	9.16E-06	7096/972/27	10		
GO:00426: MHC prote 5/150	25/19659	1.14E-06	2.55E-05	1.88E-05	972/3113/37	5		
GO:00306: clathrin-co: 8/150	107/19659	1.64E-06	3.38E-05	2.49E-05	917/920/977	8		
GO:00421: T cell rece 4/150	17/19659	7.17E-06	0.000136	0.0001	54518/917/	4		
GO:00602: cytoplasmic 12/150	338/19659	1.13E-05	0.000187	0.000138	3699/60367	12		
GO:00319: vesicle lurr 12/150	339/19659	1.17E-05	0.000187	0.000138	3699/60367	12		
GO:00988: plasma me 9/150	184/19659	1.21E-05	0.000187	0.000138	54518/36847	9		
GO:00057: lysosomal 12/150	344/19659	1.35E-05	0.000191	0.000141	51311/53347	12		
GO:00988: lytic vacuo 12/150	345/19659	1.39E-05	0.000191	0.000141	51311/53347	12		
GO:00306: clathrin-co: 5/150	44/19659	2.07E-05	0.000269	0.000198	972/2209/37	5		
GO:00347: secretory g 11/150	321/19659	3.68E-05	0.000454	0.000335	3699/60367	11		
GO:00057: vacuolar m 12/150	397/19659	5.49E-05	0.000646	0.000476	51311/53347	12		
GO:00306: coated vesi 8/150	174/19659	5.8E-05	0.000651	0.00048	917/920/977	8		
GO:00715: integral co 4/150	29/19659	6.67E-05	0.000686	0.000506	972/3113/37	4		
GO:00985: luminal sic 4/150	29/19659	6.67E-05	0.000686	0.000506	972/3113/37	4		
GO:00301: clathrin-co: 8/150	180/19659	7.36E-05	0.000727	0.000536	917/920/977	8		
GO:00451: membrane 10/150	304/19659	0.000117	0.001063	0.000783	4973/36847	10		
GO:00453: clathrin-co: 5/150	63/19659	0.000119	0.001063	0.000783	972/2209/37	5		
GO:00988: membrane 10/150	305/19659	0.00012	0.001063	0.000783	4973/36847	10		

GO:000171:immunolog	4/150	34/19659	0.000126	0.001076	0.000793	399/916/84	4
GO:009851:membrane	10/150	316/19659	0.000161	0.001323	0.000976	4973/3684/	10
GO:010100:ficolin-1-ri	7/150	185/19659	0.000554	0.004413	0.003254	11314/229/	7
GO:003251:trans-Golgi	5/150	90/19659	0.000631	0.004873	0.003593	972/3113/5	5
GO:001000:endosome	11/150	462/19659	0.000854	0.006391	0.004712	51311/298/	11
GO:004661:anchored c	4/150	58/19659	0.001003	0.007288	0.005373	80328/2350	4
GO:010100:ficolin-1-ri	4/150	61/19659	0.001212	0.008556	0.006308	11314/229/	4
GO:001251:ER to Golg	4/150	62/19659	0.001288	0.00884	0.006517	972/3113/3	4
GO:003011:coated vesi	8/150	280/19659	0.001412	0.009424	0.006948	917/920/97	8
GO:003101:platelet alp	4/150	67/19659	0.001719	0.011173	0.008237	51571/347/	4
GO:000831:integrin coi	3/150	32/19659	0.001836	0.011629	0.008573	3684/3676/	3
GO:000571:vacuolar lu	6/150	171/19659	0.002022	0.012487	0.009207	6036/176/9	6
GO:009861:protein con	3/150	35/19659	0.002383	0.014355	0.010583	3684/3676/	3
GO:004531:phagocytic	5/150	124/19659	0.002631	0.015318	0.011294	51284/709/	5
GO:000571:late endosc	7/150	243/19659	0.002667	0.015318	0.011294	2149/972/5	7
GO:004301:NADPH ox	2/150	12/19659	0.00363	0.020378	0.015024	1536/4688	2
GO:006201:collagen-cc	8/150	332/19659	0.004029	0.022117	0.016306	7045/176/1	8
GO:000571:early endos	8/150	341/19659	0.004725	0.025372	0.018706	219285/21/	8
GO:003601:endolysoso	2/150	14/19659	0.004955	0.026042	0.0192	51311/512/	2
GO:003101:platelet alp	4/150	91/19659	0.005207	0.026795	0.019755	51571/347/	4
GO:000561:basement n	4/150	92/19659	0.005412	0.027282	0.020114	7045/176/3	4
GO:003011:COPII-coat	4/150	93/19659	0.005622	0.027775	0.020477	972/3113/3	4
GO:000571:primary lys	5/150	155/19659	0.006768	0.032148	0.023701	6036/8673/	5
GO:004251:azurophil g	5/150	155/19659	0.006768	0.032148	0.023701	6036/8673/	5
GO:003011:filopodium	4/150	100/19659	0.007249	0.033781	0.024906	10123/107/	4
GO:000581:trans-Golgi	6/150	225/19659	0.007683	0.035143	0.02591	7045/972/3	6
GO:003131:anchored c	2/150	19/19659	0.009082	0.04006	0.029535	2350/929	2
GO:004301:costamere	2/150	19/19659	0.009082	0.04006	0.029535	288/11314/	2
GO:003601:endolysoso	2/150	20/19659	0.010041	0.043513	0.03208	51311/512/	2
GO:003061:Golgi-assoc	4/150	111/19659	0.010384	0.044222	0.032603	972/3113/3	4

AMed GO MF

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:004221:MHC prote	6/141	36/17632	3.76E-07	9.98E-05	8.45E-05	51571/108/	6	
GO:001991:cytokine bi	9/141	125/17632	7.21E-07	9.98E-05	8.45E-05	3676/1524/	9	
GO:001981:immunoglc	5/141	23/17632	9.13E-07	9.98E-05	8.45E-05	2214/920/2	5	
GO:001981:IgG bindin	4/141	11/17632	1.24E-06	0.000102	8.6E-05	2214/2209/	4	
GO:000481:cytokine re	7/141	92/17632	8.95E-06	0.000587	0.000498	1524/920/3	7	
GO:000831:signaling p	4/141	20/17632	1.72E-05	0.000705	0.000597	51311/512/	4	
GO:002301:MHC prote	4/141	20/17632	1.72E-05	0.000705	0.000597	51571/972/	4	
GO:003811:pattern rec	4/141	20/17632	1.72E-05	0.000705	0.000597	51311/512/	4	
GO:000191:fibronectin	4/141	27/17632	5.96E-05	0.002172	0.001841	3676/7422/	4	
GO:002301:MHC class	3/141	16/17632	0.00026	0.00852	0.007218	972/3109/3	3	
GO:001981:growth fact	6/141	137/17632	0.000819	0.024433	0.020701	1277/658/3	6	
GO:003021:carbohydra	8/141	269/17632	0.001461	0.039922	0.033823	4973/1021/	8	
GO:004261:peptide ant	3/141	30/17632	0.001735	0.043778	0.037091	3113/3122/	3	
GO:000551:glycosamir	7/141	222/17632	0.002075	0.04567	0.038693	54209/176/	7	
GO:001991:chemokine	3/141	32/17632	0.002095	0.04567	0.038693	3676/1524/	3	
GO:001681:endoribonu	2/141	10/17632	0.00274	0.04567	0.038693	6036/6035	2	
GO:003161:G-protein t	2/141	10/17632	0.00274	0.04567	0.038693	2149/5433/	2	
GO:003231:MHC class	2/141	10/17632	0.00274	0.04567	0.038693	3113/3122	2	
GO:007171:lipopeptide	2/141	10/17632	0.00274	0.04567	0.038693	7096/929	2	
GO:000161:virus recep	4/141	74/17632	0.002924	0.04567	0.038693	920/23601/	4	
GO:010401:hijacked m	4/141	74/17632	0.002924	0.04567	0.038693	920/23601/	4	
GO:001611:superoxide	2/141	11/17632	0.003331	0.048943	0.041466	1536/4688	2	
GO:000511:integrin bir	5/141	126/17632	0.003432	0.048943	0.041466	3553/7045/	5	

AMed GO BP

ID	Descriptor	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:004211	T cell activation	76/958	451/18493	4.06E-20	2.12E-16	1.82E-16	8320/3445/	76
GO:000181	positive regulation of	71/958	422/18493	8.05E-19	2.1E-15	1.8E-15	64135/958/	71
GO:000711	leukocyte chemotaxis	59/958	327/18493	2.76E-17	4.8E-14	4.13E-14	84524/6413	59
GO:003005	lymphocyte chemotaxis	58/958	344/18493	1.26E-15	1.53E-12	1.32E-12	8320/3445/	58
GO:005084	regulation of chemotaxis	54/958	305/18493	1.47E-15	1.53E-12	1.32E-12	84524/6413	54
GO:002244	positive regulation of	48/958	251/18493	2.62E-15	2.27E-12	1.96E-12	4651/64127	48
GO:005124	regulation of chemotaxis	69/958	472/18493	4.49E-15	3.34E-12	2.87E-12	958/10464/	69
GO:004574	positive regulation of	62/958	397/18493	5.27E-15	3.43E-12	2.95E-12	4651/64127	62
GO:190307	positive regulation of	43/958	214/18493	1.22E-14	7.05E-12	6.06E-12	64127/51561/	43
GO:007066	leukocyte chemotaxis	50/958	283/18493	1.83E-14	8.65E-12	7.44E-12	958/3445/3	50
GO:190307	regulation of chemotaxis	51/958	293/18493	1.86E-14	8.65E-12	7.44E-12	84524/6413	51
GO:004664	lymphocyte chemotaxis	48/958	264/18493	1.99E-14	8.65E-12	7.44E-12	958/3445/3	48
GO:003294	mononuclear cell chemotaxis	48/958	266/18493	2.69E-14	1.08E-11	9.26E-12	958/3445/3	48
GO:002244	regulation of chemotaxis	59/958	388/18493	8.14E-14	3.03E-11	2.6E-11	4651/84524/	59
GO:005090	leukocyte chemotaxis	67/958	478/18493	8.94E-14	3.11E-11	2.67E-11	965/51561/	67
GO:005087	positive regulation of	40/958	202/18493	1.71E-13	5.56E-11	4.78E-11	64127/51561/	40
GO:003021	T cell differentiation	43/958	234/18493	3.17E-13	9.71E-11	8.34E-11	8320/84524/	43
GO:005084	positive regulation of	57/958	384/18493	6.1E-13	1.77E-10	1.52E-10	958/64127/	57
GO:000265	positive regulation of	55/958	372/18493	1.85E-12	5.06E-10	4.35E-10	958/64127/	55
GO:004211	B cell proliferation	24/958	91/18493	2.26E-11	5.9E-09	5.07E-09	958/3445/5	24
GO:003274	positive regulation of	20/958	63/18493	2.57E-11	6.39E-09	5.49E-09	51561/9460/	20
GO:005124	positive regulation of	49/958	333/18493	3.63E-11	8.6E-09	7.39E-09	958/64127/	49
GO:004664	alpha-beta T cell chemotaxis	29/958	134/18493	3.86E-11	8.75E-09	7.52E-09	8320/2000/	29
GO:004211	B cell activation	46/958	303/18493	4.97E-11	1.08E-08	9.27E-09	958/3445/6	46
GO:000264	negative regulation of	57/958	437/18493	1.21E-10	2.44E-08	2.09E-08	5987/10464/	57
GO:003266	interferon-gamma production	25/958	106/18493	1.22E-10	2.44E-08	2.09E-08	5987/8320/	25
GO:000264	regulation of chemotaxis	57/958	439/18493	1.44E-10	2.78E-08	2.39E-08	958/64127/	57
GO:003014	extracellular matrix organization	49/958	348/18493	1.76E-10	3.28E-08	2.82E-08	4327/3036/	49
GO:000274	immune response	57/958	445/18493	2.45E-10	4.4E-08	3.78E-08	958/4651/7	57
GO:000242	immune response	54/958	414/18493	3.75E-10	6.52E-08	5.6E-08	4651/7456/	54
GO:000274	regulation of chemotaxis	34/958	196/18493	4.81E-10	8.08E-08	6.95E-08	958/64127/	34
GO:004304	extracellular matrix organization	52/958	402/18493	1.07E-09	1.75E-07	1.5E-07	4327/3036/	52
GO:000754	blood coagulation	46/958	334/18493	1.33E-09	2.1E-07	1.8E-07	11216/958/	46
GO:005067	regulation of chemotaxis	34/958	205/18493	1.63E-09	2.49E-07	2.14E-07	958/51561/	34
GO:007066	regulation of chemotaxis	35/958	216/18493	1.78E-09	2.65E-07	2.28E-07	958/51561/	35
GO:003294	regulation of chemotaxis	34/958	206/18493	1.85E-09	2.68E-07	2.31E-07	958/51561/	34
GO:000754	hemostasis	46/958	339/18493	2.15E-09	3.03E-07	2.61E-07	11216/958/	46
GO:007066	positive regulation of	27/958	139/18493	2.32E-09	3.17E-07	2.72E-07	958/51561/	27
GO:005084	coagulation	46/958	340/18493	2.37E-09	3.17E-07	2.72E-07	11216/958/	46
GO:005077	negative regulation of	26/958	131/18493	2.83E-09	3.69E-07	3.17E-07	5987/9111/	26
GO:005067	positive regulation of	26/958	132/18493	3.36E-09	4.27E-07	3.67E-07	958/51561/	26
GO:003294	positive regulation of	26/958	133/18493	3.97E-09	4.93E-07	4.24E-07	958/51561/	26
GO:003084	regulation of chemotaxis	17/958	59/18493	4.28E-09	5.19E-07	4.46E-07	958/57162/	17
GO:000224	response to hypoxia	45/958	337/18493	5.36E-09	6.34E-07	5.45E-07	10068/958/	45
GO:005084	antigen recognition	38/958	259/18493	6.32E-09	7.32E-07	6.29E-07	7006/5933/	38
GO:000274	regulation of chemotaxis	27/958	146/18493	7.08E-09	8.02E-07	6.9E-07	958/9984/5	27
GO:004561	regulation of chemotaxis	29/958	166/18493	7.66E-09	8.49E-07	7.3E-07	84524/217/	29
GO:004504	regulation of chemotaxis	47/958	365/18493	7.94E-09	8.55E-07	7.35E-07	64135/9111/	47
GO:006032	cell chemotaxis	41/958	295/18493	8.04E-09	8.55E-07	7.35E-07	10850/1060/	41
GO:000281	regulation of chemotaxis	28/958	157/18493	8.65E-09	9.01E-07	7.75E-07	5987/958/9	28
GO:009752	myeloid leukocyte chemotaxis	32/958	199/18493	1.06E-08	1.09E-06	9.35E-07	51561/4920/	32
GO:005064	cytokine secretion	33/958	210/18493	1.13E-08	1.13E-06	9.74E-07	5987/6413/	33
GO:003264	regulation of chemotaxis	21/958	95/18493	1.28E-08	1.25E-06	1.08E-06	51561/9460/	21
GO:005071	positive regulation of	24/958	123/18493	1.63E-08	1.56E-06	1.34E-06	64135/6413/	24
GO:000190	leukocyte chemotaxis	22/958	105/18493	1.65E-08	1.56E-06	1.34E-06	3251/5156/	22
GO:003014	platelet activation	27/958	152/18493	1.74E-08	1.62E-06	1.39E-06	958/8526/7	27
GO:005074	regulation of chemotaxis	30/958	184/18493	2.21E-08	2.02E-06	1.74E-06	5987/6413/	30

GO:003134 positive re	51/958	427/18493	2.33E-08	2.09E-06	1.8E-06	64135/547	51
GO:005124 negative re	25/958	137/18493	3.35E-08	2.96E-06	2.55E-06	10464/845	25
GO:19021 regulation	37/958	265/18493	3.8E-08	3.3E-06	2.84E-06	84524/217	37
GO:00326 regulation	15/958	53/18493	4.56E-08	3.9E-06	3.35E-06	5987/5142	15
GO:00026 regulation	29/958	180/18493	4.95E-08	4.12E-06	3.54E-06	51561/634	29
GO:00181 peptidyl-ty	47/958	387/18493	4.98E-08	4.12E-06	3.54E-06	8444/8576	47
GO:00508 T cell rece	26/958	150/18493	5.34E-08	4.35E-06	3.74E-06	7006/5582	26
GO:00451 cellular ext	15/958	54/18493	6.02E-08	4.82E-06	4.15E-06	3695/3554	15
GO:00182 peptidyl-ty	47/958	390/18493	6.31E-08	4.98E-06	4.29E-06	8444/8576	47
GO:00026 negative re	27/958	164/18493	9.02E-08	7.01E-06	6.03E-06	10464/845	27
GO:00324 response to	41/958	324/18493	1.16E-07	8.9E-06	7.66E-06	10068/958	41
GO:00026 positive re	31/958	209/18493	1.21E-07	9.16E-06	7.87E-06	958/64127	31
GO:00455 regulation	24/958	137/18493	1.4E-07	1.05E-05	8.99E-06	84524/217	24
GO:00018 negative re	35/958	256/18493	1.49E-07	1.08E-05	9.33E-06	5987/6413	35
GO:00327 positive re	11/958	30/18493	1.5E-07	1.08E-05	9.33E-06	5142/5444	11
GO:00508 regulation	54/958	493/18493	1.66E-07	1.19E-05	1.02E-05	11216/958	54
GO:00024 adaptive in	43/958	354/18493	1.84E-07	1.29E-05	1.11E-05	10068/958	43
GO:00336 regulation	13/958	44/18493	2.07E-07	1.44E-05	1.24E-05	9270/9404	13
GO:00026 positive re	22/958	121/18493	2.36E-07	1.62E-05	1.39E-05	51561/634	22
GO:19035 regulation	23/958	131/18493	2.44E-07	1.65E-05	1.42E-05	5987/6413	23
GO:00305 leukocyte c	31/958	217/18493	2.86E-07	1.89E-05	1.62E-05	51561/634	31
GO:00508 negative re	28/958	184/18493	2.86E-07	1.89E-05	1.62E-05	10464/845	28
GO:00028 regulation	24/958	144/18493	3.67E-07	2.39E-05	2.05E-05	958/9984/5	24
GO:00717 tumor necr	23/958	135/18493	4.27E-07	2.75E-05	2.36E-05	5987/6413	23
GO:00326 interleukin	15/958	62/18493	4.38E-07	2.79E-05	2.4E-05	5987/5142	15
GO:00313 regulation	18/958	88/18493	4.78E-07	3E-05	2.58E-05	51561/555	18
GO:00507 positive re	33/958	246/18493	5.25E-07	3.25E-05	2.8E-05	64135/641	33
GO:00326 regulation	22/958	127/18493	5.64E-07	3.46E-05	2.98E-05	5987/6413	22
GO:00019 cell killing	25/958	158/18493	5.82E-07	3.51E-05	3.02E-05	3251/5156	25
GO:00024 lymphocyte	41/958	344/18493	5.87E-07	3.51E-05	3.02E-05	958/3251/9	41
GO:00450 T cell selec	13/958	48/18493	6.34E-07	3.75E-05	3.23E-05	51561/273	13
GO:00313 positive re	15/958	64/18493	6.82E-07	3.99E-05	3.43E-05	51561/555	15
GO:00450 positive re	38/958	309/18493	6.94E-07	4.02E-05	3.45E-05	64135/547	38
GO:00321 positive re	37/958	297/18493	7.06E-07	4.04E-05	3.47E-05	64127/515	37
GO:00326 tumor necr	22/958	129/18493	7.45E-07	4.22E-05	3.63E-05	5987/6413	22
GO:00336 cell adhesi	15/958	65/18493	8.44E-07	4.73E-05	4.07E-05	9270/9404	15
GO:00508 regulation	27/958	183/18493	8.69E-07	4.77E-05	4.1E-05	958/64127	27
GO:00508 regulation	14/958	57/18493	8.7E-07	4.77E-05	4.1E-05	9404/4067	14
GO:00433 positive T	11/958	35/18493	9.02E-07	4.89E-05	4.21E-05	51561/916	11
GO:00027 positive re	34/958	265/18493	1.01E-06	5.41E-05	4.65E-05	64135/641	34
GO:19021 positive re	23/958	142/18493	1.07E-06	5.68E-05	4.88E-05	51561/273	23
GO:00508 negative re	10/958	29/18493	1.08E-06	5.68E-05	4.88E-05	9984/4067	10
GO:00326 interleukin	22/958	132/18493	1.11E-06	5.78E-05	4.97E-05	64135/641	22
GO:00510 positive re	45/958	404/18493	1.13E-06	5.78E-05	4.97E-05	2668/6413	45
GO:00508 B cell rece	21/958	122/18493	1.13E-06	5.78E-05	4.97E-05	7006/5933	21
GO:19037 regulation	46/958	418/18493	1.2E-06	6.08E-05	5.22E-05	80349/845	46
GO:00450 positive re	7/958	13/18493	1.28E-06	6.4E-05	5.5E-05	5588/916/9	7
GO:00326 regulation	21/958	123/18493	1.3E-06	6.44E-05	5.54E-05	64135/641	21
GO:00456 positive re	18/958	94/18493	1.33E-06	6.48E-05	5.57E-05	51561/273	18
GO:00607 regulation	25/958	165/18493	1.33E-06	6.48E-05	5.57E-05	64135/547	25
GO:00019 regulation	16/958	76/18493	1.37E-06	6.61E-05	5.68E-05	51561/527	16
GO:00507 regulation	32/958	245/18493	1.41E-06	6.73E-05	5.79E-05	958/10464	32
GO:00027 positive re	19/958	105/18493	1.67E-06	7.79E-05	6.69E-05	958/51561	19
GO:00508 regulation	9/958	24/18493	1.67E-06	7.79E-05	6.69E-05	9404/4067	9
GO:00420 T cell proli	26/958	178/18493	1.67E-06	7.79E-05	6.69E-05	2000/5156	26
GO:19049 positive re	47/958	437/18493	1.76E-06	8.1E-05	6.96E-05	163882/55	47
GO:00488 homeostasi	32/958	248/18493	1.84E-06	8.38E-05	7.2E-05	2176/8444	32
GO:00072 positive re	37/958	309/18493	1.85E-06	8.38E-05	7.2E-05	8620/1066	37

GO:00421	positive reg	18/958	97/18493	2.14E-06	9.6E-05	8.25E-05	51561/3718	18
GO:00017	leukocyte h	17/958	88/18493	2.29E-06	0.000102	8.76E-05	84524/309	17
GO:00512	positive reg	44/958	402/18493	2.36E-06	0.000104	8.96E-05	163882/64	44
GO:00509	leukocyte t	9/958	25/18493	2.49E-06	0.000109	9.38E-05	3695/3676	9
GO:00712	cellular res	30/958	229/18493	2.8E-06	0.000122	0.000105	958/64127	30
GO:00712	cellular res	28/958	206/18493	2.9E-06	0.000125	0.000107	958/64127	28
GO:00026	regulation	19/958	109/18493	2.99E-06	0.000128	0.00011	51561/6340	19
GO:00976	STAT casc	23/958	151/18493	3.19E-06	0.000135	0.000116	958/10464	23
GO:00509	positive reg	21/958	130/18493	3.26E-06	0.000137	0.000118	51561/6340	21
GO:00702	lymphocyte	15/958	72/18493	3.35E-06	0.00014	0.00012	84524/273	15
GO:00019	positive reg	13/958	55/18493	3.4E-06	0.000141	0.000121	51561/880	13
GO:00022	lymphocyte	25/958	174/18493	3.57E-06	0.000147	0.000126	8320/958/3	25
GO:00027	positive reg	21/958	131/18493	3.7E-06	0.00015	0.000129	958/64127	21
GO:00466	regulation	17/958	91/18493	3.71E-06	0.00015	0.000129	51561/273	17
GO:00507	positive reg	26/958	186/18493	3.85E-06	0.000154	0.000133	958/10464	26
GO:00466	alpha-beta	18/958	101/18493	3.9E-06	0.000155	0.000134	8320/5156	18
GO:00308	positive reg	11/958	40/18493	3.94E-06	0.000155	0.000134	958/57162	11
GO:00326	interleukin	10/958	33/18493	4.13E-06	0.000162	0.000139	114548/51	10
GO:00507	regulation	46/958	438/18493	4.3E-06	0.000166	0.000143	5987/6413	46
GO:00027	regulation	48/958	465/18493	4.3E-06	0.000166	0.000143	5987/6413	48
GO:00327	positive reg	7/958	15/18493	4.37E-06	0.000167	0.000144	64127/5150	7
GO:19902	neutrophil	19/958	112/18493	4.53E-06	0.000172	0.000148	51561/6340	19
GO:00326	regulation	9/958	27/18493	5.2E-06	0.000196	0.000169	114548/51	9
GO:00975	granulocyte	21/958	134/18493	5.34E-06	0.0002	0.000172	51561/6340	21
GO:00420	regulation	17/958	94/18493	5.87E-06	0.000218	0.000188	9111/5146	17
GO:00301	B cell diffe	20/958	125/18493	6.45E-06	0.000238	0.000205	3445/3718	20
GO:00023	cytokine pr	17/958	95/18493	6.8E-06	0.00025	0.000215	64127/114	17
GO:00028	positive reg	18/958	105/18493	6.9E-06	0.000251	0.000216	958/51561	18
GO:00072	JAK-STAT	22/958	147/18493	6.94E-06	0.000251	0.000216	958/10464	22
GO:00324	response to	6/958	11/18493	7.02E-06	0.000252	0.000217	64127/366	6
GO:19037	positive reg	25/958	183/18493	8.87E-06	0.000317	0.000272	51561/273	25
GO:00718	leukocyte a	18/958	107/18493	9.06E-06	0.000321	0.000276	84524/641	18
GO:19048	positive reg	16/958	88/18493	1.02E-05	0.00036	0.000309	958/10464	16
GO:00301	collagen fil	12/958	52/18493	1.05E-05	0.000368	0.000316	4017/1277	12
GO:19035	positive reg	40/958	373/18493	1.1E-05	0.000381	0.000328	2668/6413	40
GO:00509	regulation	27/958	210/18493	1.23E-05	0.000425	0.000365	51561/6340	27
GO:00421	neutrophil	49/958	498/18493	1.27E-05	0.000434	0.000374	5553/411/9	49
GO:00712	cellular res	26/958	199/18493	1.33E-05	0.000449	0.000386	958/64127	26
GO:00433	neutrophil	48/958	485/18493	1.33E-05	0.000449	0.000386	5553/411/9	48
GO:00024	neutrophil	49/958	499/18493	1.34E-05	0.000449	0.000386	5553/411/9	49
GO:00457	negative re	6/958	12/18493	1.34E-05	0.000449	0.000386	5027/3635	6
GO:00027	negative re	11/958	45/18493	1.36E-05	0.000452	0.000389	9984/5272	11
GO:00028	positive reg	17/958	100/18493	1.38E-05	0.000456	0.000392	958/51561	17
GO:00022	natural kill	13/958	62/18493	1.39E-05	0.000456	0.000392	5272/8807	13
GO:00022	neutrophil	48/958	488/18493	1.56E-05	0.00051	0.000438	5553/411/9	48
GO:00305	neutrophil	17/958	101/18493	1.58E-05	0.000513	0.000441	51561/6340	17
GO:00019	regulation	22/958	155/18493	1.64E-05	0.000529	0.000455	54726/604	22
GO:00027	regulation	20/958	133/18493	1.67E-05	0.00053	0.000456	958/64127	20
GO:19048	regulation	20/958	133/18493	1.67E-05	0.00053	0.000456	958/10464	20
GO:00458	negative re	11/958	46/18493	1.71E-05	0.000539	0.000463	9111/1121	11
GO:00071	negative re	32/958	276/18493	1.75E-05	0.00055	0.000473	55920/845	32
GO:00022	lymphocyte	13/958	64/18493	2E-05	0.000623	0.000536	84524/309	13
GO:00516	defense res	28/958	228/18493	2.03E-05	0.000628	0.00054	64135/958	28
GO:00455	positive reg	15/958	83/18493	2.07E-05	0.000638	0.000549	51561/273	15
GO:00450	positive thy	6/958	13/18493	2.38E-05	0.000731	0.000628	916/917/17	6
GO:00026	positive reg	15/958	84/18493	2.4E-05	0.000732	0.000629	51561/6340	15
GO:00105	regulation	9/958	32/18493	2.46E-05	0.000745	0.00064	3091/2321	9
GO:00025	tolerance ii	8/958	25/18493	2.47E-05	0.000745	0.00064	11213/406	8

GO:004208 cytokine bi	17/958	105/18493	2.67E-05	0.0008	0.000688	9111/51464	17
GO:004642 positive re	15/958	85/18493	2.78E-05	0.000827	0.000711	958/10464	15
GO:004211 positive re	12/958	57/18493	2.84E-05	0.000834	0.000717	51311/5588	12
GO:007022 regulation	12/958	57/18493	2.84E-05	0.000834	0.000717	84524/309	12
GO:004507 regulation	7/958	19/18493	2.85E-05	0.000834	0.000717	5588/916/9	7
GO:004211 cytokine m	17/958	106/18493	3.03E-05	0.000883	0.000759	9111/51464	17
GO:190355 positive re	14/958	76/18493	3.1E-05	0.000898	0.000772	64135/641	14
GO:005144 regulation	37/958	350/18493	3.17E-05	0.000914	0.000785	8620/1066	37
GO:005072 negative re	11/958	49/18493	3.23E-05	0.000926	0.000796	10464/228	11
GO:190262 positive re	8/958	26/18493	3.41E-05	0.000967	0.000831	51561/829	8
GO:004226 natural kill	12/958	58/18493	3.41E-05	0.000967	0.000831	5272/8807	12
GO:000271 regulation	14/958	77/18493	3.61E-05	0.001014	0.000872	64127/114	14
GO:004642 regulation	19/958	129/18493	3.62E-05	0.001014	0.000872	958/10464	19
GO:003264 regulation	11/958	50/18493	3.95E-05	0.001101	0.000947	958/10464	11
GO:004684 negative re	6/958	14/18493	3.99E-05	0.001106	0.000951	5027/3635	6
GO:003362 positive re	7/958	20/18493	4.19E-05	0.001151	0.000989	5777/8631	7
GO:001057 vascular en	9/958	34/18493	4.2E-05	0.001151	0.000989	3091/2321	9
GO:004208 T-helper 1	10/958	42/18493	4.29E-05	0.00117	0.001006	10068/515	10
GO:000961 response to	34/958	315/18493	4.31E-05	0.00117	0.001006	64135/958	34
GO:007162 granulocyte	18/958	120/18493	4.5E-05	0.001215	0.001044	51561/634	18
GO:003264 regulation	8/958	27/18493	4.63E-05	0.001237	0.001063	64127/515	8
GO:004557 regulation	8/958	27/18493	4.63E-05	0.001237	0.001063	3635/695/5	8
GO:005072 regulation	42/958	425/18493	4.71E-05	0.001252	0.001076	64127/217	42
GO:000221 activation	29/958	252/18493	4.9E-05	0.001296	0.001114	64135/547	29
GO:005072 positive re	19/958	133/18493	5.56E-05	0.001459	0.001255	64127/515	19
GO:000758 response to	26/958	216/18493	5.57E-05	0.001459	0.001255	54434/958	26
GO:004662 positive re	12/958	61/18493	5.78E-05	0.0015	0.001289	51561/273	12
GO:003261 interleukin	11/958	52/18493	5.81E-05	0.0015	0.001289	958/10464	11
GO:006076 positive re	11/958	52/18493	5.81E-05	0.0015	0.001289	64135/688	11
GO:004508 thymic T ce	7/958	21/18493	6E-05	0.001526	0.001312	2737/916/9	7
GO:005084 positive re	7/958	21/18493	6E-05	0.001526	0.001312	4067/3932	7
GO:000228 T cell activ	16/958	101/18493	6.01E-05	0.001526	0.001312	8320/3445	16
GO:003088 negative re	6/958	15/18493	6.36E-05	0.001601	0.001376	4067/3635	6
GO:003264 negative re	6/958	15/18493	6.36E-05	0.001601	0.001376	10464/112	6
GO:000271 regulation	10/958	44/18493	6.58E-05	0.001649	0.001418	5272/8807	10
GO:000242 T cell medi	16/958	102/18493	6.79E-05	0.001692	0.001455	3251/5156	16
GO:001972 calcium-me	26/958	220/18493	7.6E-05	0.001885	0.00162	5533/2274	26
GO:000272 innate imm	27/958	233/18493	7.82E-05	0.001923	0.001653	64135/547	27
GO:004644 phosphatid	27/958	233/18493	7.82E-05	0.001923	0.001653	8776/2840	27
GO:003125 T cell costi	11/958	54/18493	8.38E-05	0.002048	0.001761	4067/7409	11
GO:004208 interleukin	7/958	22/18493	8.41E-05	0.002048	0.001761	5588/916/9	7
GO:003276 positive re	13/958	73/18493	8.52E-05	0.002064	0.001775	64135/641	13
GO:003808 peptidyl-ty	9/958	37/18493	8.65E-05	0.002077	0.001786	7006/4067	9
GO:006174 leukocyte a	9/958	37/18493	8.65E-05	0.002077	0.001786	3695/3676	9
GO:000716 cell-matrix	26/958	222/18493	8.83E-05	0.002112	0.001816	55920/839	26
GO:004308 regulation	45/958	481/18493	9.48E-05	0.002253	0.001937	51256/202	45
GO:003434 response to	24/958	198/18493	9.51E-05	0.002253	0.001937	958/6672/9	24
GO:000242 mast cell r	10/958	46/18493	9.84E-05	0.002302	0.001979	4878/5710	10
GO:000271 positive re	10/958	46/18493	9.84E-05	0.002302	0.001979	51561/114	10
GO:004336 CD4-positi	13/958	74/18493	9.85E-05	0.002302	0.001979	51561/114	13
GO:003125 lymphocyte	11/958	55/18493	9.99E-05	0.002324	0.001998	4067/7409	11
GO:000178 B cell hom	8/958	30/18493	0.000106	0.002449	0.002106	3091/1001	8
GO:003272 positive re	8/958	30/18493	0.000106	0.002449	0.002106	10464/641	8
GO:005088 negative re	16/958	106/18493	0.000109	0.002495	0.002145	84524/273	16
GO:003412 regulation	12/958	65/18493	0.00011	0.002524	0.00217	54726/112	12
GO:003011 natural kill	14/958	85/18493	0.000111	0.002531	0.002176	10464/344	14
GO:003272 positive re	7/958	23/18493	0.000116	0.002606	0.00224	114548/54	7
GO:009002 positive re	7/958	23/18493	0.000116	0.002606	0.00224	51561/829	7

GO:004212:regulation of	20/958	153/18493	0.000127	0.00285	0.00245	51561/5710	20
GO:004506:negative th	5/958	11/18493	0.000131	0.002935	0.002524	2737/916/1	5
GO:003262:interleukin	8/958	31/18493	0.000137	0.003032	0.002606	64127/5156	8
GO:190262:regulation of	8/958	31/18493	0.000137	0.003032	0.002606	51561/829	8
GO:004557:mast cell ac	11/958	57/18493	0.00014	0.003094	0.00266	4878/5710	11
GO:003571:CD4-positi	14/958	87/18493	0.000144	0.003136	0.002696	51561/114	14
GO:200016:regulation of	14/958	87/18493	0.000144	0.003136	0.002696	84524/641	14
GO:005507:calcium ion	43/958	461/18493	0.000144	0.003136	0.002696	958/8620/1	43
GO:000222:pattern rec	22/958	179/18493	0.00015	0.003248	0.002792	64135/547	22
GO:004544:bone resor	11/958	58/18493	0.000165	0.00356	0.00306	760/1200/5	11
GO:000282:negative re	9/958	40/18493	0.000165	0.00356	0.00306	5987/9984/	9
GO:000722:integrin-me	15/958	99/18493	0.000169	0.003628	0.003119	55920/573	15
GO:003158:cell-substr	34/958	338/18493	0.000172	0.003681	0.003165	55920/570	34
GO:005121:cartilage de	24/958	206/18493	0.000176	0.003747	0.003221	8195/4017/	24
GO:004576:regulation of	37/958	381/18493	0.000186	0.003932	0.00338	958/6672/1	37
GO:000266:negative re	16/958	111/18493	0.000189	0.003983	0.003424	9984/1121	16
GO:007196:regulation of	45/958	496/18493	0.000191	0.004016	0.003453	1022/8812/	45
GO:003271:negative re	9/958	41/18493	0.000202	0.004231	0.003637	11213/114	9
GO:007022:T cell apop	10/958	50/18493	0.000206	0.00426	0.003662	84524/273	10
GO:005084:negative re	7/958	25/18493	0.000207	0.00426	0.003662	9404/5795/	7
GO:005092:positive re	7/958	25/18493	0.000207	0.00426	0.003662	7424/3603/	7
GO:007162:positive re	7/958	25/18493	0.000207	0.00426	0.003662	51561/829	7
GO:006032:interferon-	14/958	90/18493	0.000208	0.004269	0.003671	6672/9111/	14
GO:004338:negative T	5/958	12/18493	0.000215	0.004368	0.003755	2737/916/1	5
GO:004557:positive re	5/958	12/18493	0.000215	0.004368	0.003755	3635/695/3	5
GO:007252:T-helper 1	5/958	12/18493	0.000215	0.004368	0.003755	51561/356	5
GO:000228:alpha-beta	11/958	60/18493	0.000226	0.004544	0.003906	8320/5156	11
GO:000228:alpha-beta	11/958	60/18493	0.000226	0.004544	0.003906	8320/5156	11
GO:004226:regulation of	9/958	42/18493	0.000246	0.004904	0.004216	5272/8807/	9
GO:007167:regulation of	9/958	42/18493	0.000246	0.004904	0.004216	6346/4067/	9
GO:000252:acute infla	24/958	211/18493	0.000254	0.005044	0.004337	8620/1145	24
GO:000696:cellular de	11/958	61/18493	0.000263	0.005207	0.004476	135/5551/4	11
GO:005092:regulation of	7/958	26/18493	0.00027	0.005338	0.004589	7424/3603/	7
GO:003416:negative re	6/958	19/18493	0.000288	0.005668	0.004873	5027/3635/	6
GO:004352:positive re	38/958	405/18493	0.000305	0.005982	0.005143	51256/202	38
GO:004344:protein kin	27/958	253/18493	0.000307	0.005986	0.005146	117145/95	27
GO:004346:regulation of	33/958	335/18493	0.000313	0.006088	0.005234	958/11235/	33
GO:000726:tyrosine ph	13/958	83/18493	0.000324	0.006272	0.005392	958/10464/	13
GO:190132:regulation of	39/958	421/18493	0.000331	0.006385	0.005489	958/6672/1	39
GO:000242:complemer	5/958	13/18493	0.000335	0.00642	0.00552	1378/728/2	5
GO:000266:positive re	5/958	13/18493	0.000335	0.00642	0.00552	3554/7070/	5
GO:000276:negative re	8/958	35/18493	0.000339	0.006476	0.005567	9984/5272/	8
GO:003261:interleukin	12/958	73/18493	0.000345	0.006529	0.005613	64127/114	12
GO:003262:interleukin	12/958	73/18493	0.000345	0.006529	0.005613	64127/965/	12
GO:000282:regulation of	7/958	27/18493	0.000349	0.006564	0.005643	51561/946	7
GO:001057:positive re	7/958	27/18493	0.000349	0.006564	0.005643	3091/2321	7
GO:004333:mast cell d	9/958	44/18493	0.000356	0.00667	0.005734	4878/5710	9
GO:007132:cellular res	21/958	178/18493	0.000368	0.00688	0.005915	6672/9111/	21
GO:000961:response to	23/958	204/18493	0.000384	0.007143	0.006141	1111/958/8	23
GO:007256:cellular div	43/958	483/18493	0.000393	0.00729	0.006267	7782/958/8	43
GO:003264:regulation of	11/958	64/18493	0.000406	0.007496	0.006445	64127/114	11
GO:000274:MyD88-de	8/958	36/18493	0.000417	0.007671	0.006595	11213/513	8
GO:000227:mast cell ac	9/958	45/18493	0.000425	0.007709	0.006628	4878/5710	9
GO:003264:regulation of	9/958	45/18493	0.000425	0.007709	0.006628	10464/641	9
GO:003277:positive re	9/958	45/18493	0.000425	0.007709	0.006628	64127/114	9
GO:003598:endoderma	9/958	45/18493	0.000425	0.007709	0.006628	8320/3909/	9
GO:000222:toll-like rec	17/958	131/18493	0.000432	0.007825	0.006727	54726/112	17
GO:000267:positive re	7/958	28/18493	0.000445	0.007865	0.006762	9180/695/5	7

GO:003264	regulation	7/958	28/18493	0.000445	0.007865	0.006762	64135/9111	7
GO:003502	positive reg	7/958	28/18493	0.000445	0.007865	0.006762	2828/21511	7
GO:007251	T-helper 1	7/958	28/18493	0.000445	0.007865	0.006762	51561/1141	7
GO:007261	interleukin	7/958	28/18493	0.000445	0.007865	0.006762	965/7097/2	7
GO:009002	regulation	7/958	28/18493	0.000445	0.007865	0.006762	51561/8291	7
GO:007061	negative re	12/958	75/18493	0.000445	0.007865	0.006762	57162/4061	12
GO:007045	interleukin	10/958	55/18493	0.000463	0.008151	0.007007	54726/6411	10
GO:003274	positive reg	9/958	46/18493	0.000504	0.008842	0.007601	64127/9651	9
GO:005082	regulation	8/958	37/18493	0.000508	0.008877	0.007632	5795/39321	8
GO:003261	interleukin	13/958	87/18493	0.000518	0.009021	0.007755	64127/1141	13
GO:003362	integrin act	6/958	21/18493	0.000527	0.00913	0.007849	9270/86311	6
GO:007022	negative re	6/958	21/18493	0.000527	0.00913	0.007849	3091/37181	6
GO:000225	T cell diffe	11/958	66/18493	0.000533	0.009141	0.007858	8320/51561	11
GO:000271	regulation	11/958	66/18493	0.000533	0.009141	0.007858	51561/1141	11
GO:003267	regulation	11/958	66/18493	0.000533	0.009141	0.007858	64127/9651	11
GO:003261	interferon-	7/958	29/18493	0.00056	0.009483	0.008152	64135/9111	7
GO:004594	positive reg	7/958	29/18493	0.00056	0.009483	0.008152	8807/74091	7
GO:005071	positive reg	7/958	29/18493	0.00056	0.009483	0.008152	64127/1141	7
GO:190302	negative re	16/958	122/18493	0.00056	0.009483	0.008152	84524/2731	16
GO:003015	regulation	12/958	77/18493	0.00057	0.009546	0.008207	7006/40671	12
GO:003262	regulation	12/958	77/18493	0.00057	0.009546	0.008207	64127/1141	12
GO:190002	regulation	12/958	77/18493	0.00057	0.009546	0.008207	7006/40671	12
GO:000682	cellular cal	40/958	448/18493	0.000584	0.009754	0.008385	958/8620/1	40
GO:000272	positive reg	9/958	47/18493	0.000595	0.009843	0.008463	64127/1141	9
GO:003261	interleukin	9/958	47/18493	0.000595	0.009843	0.008463	10464/6411	9
GO:015007	neuroinflar	9/958	47/18493	0.000595	0.009843	0.008463	135/513111	9
GO:003272	positive reg	8/958	38/18493	0.000614	0.010097	0.00868	64127/1141	8
GO:004512	regulation	8/958	38/18493	0.000614	0.010097	0.00868	760/5027/3	8
GO:200122	regulation	36/958	391/18493	0.000617	0.010118	0.008698	2668/66721	36
GO:004205	T-helper ce	10/958	57/18493	0.000622	0.010168	0.008742	51561/1141	10
GO:000282	regulation	7/958	30/18493	0.000698	0.011315	0.009727	64127/1141	7
GO:003281	regulation	7/958	30/18493	0.000698	0.011315	0.009727	10464/5151	7
GO:005071	interleukin	9/958	48/18493	0.000699	0.011315	0.009727	64127/1141	9
GO:003805	Fc receptor	21/958	187/18493	0.000711	0.011479	0.009868	4651/74561	21
GO:000282	positive reg	5/958	15/18493	0.000717	0.011495	0.009883	64127/1141	5
GO:200044	positive reg	5/958	15/18493	0.000717	0.011495	0.009883	965/7097/7	5
GO:000662	glyceropho	34/958	367/18493	0.000775	0.012389	0.010651	8776/28401	34
GO:003307	T cell diffe	11/958	69/18493	0.000786	0.012528	0.010771	84524/2731	11
GO:004801	vascular en	13/958	91/18493	0.000802	0.012736	0.010949	7424/22541	13
GO:004251	regulation	12/958	80/18493	0.00081	0.012833	0.011033	958/104641	12
GO:000225	CD4-positi	10/958	59/18493	0.000825	0.012986	0.011164	51561/1141	10
GO:003411	heterotypic	10/958	59/18493	0.000825	0.012986	0.011164	965/3695/3	10
GO:000271	positive reg	7/958	31/18493	0.000862	0.013368	0.011493	8807/74091	7
GO:004887	homeostasi	7/958	31/18493	0.000862	0.013368	0.011493	51542/1001	7
GO:005144	positive reg	7/958	31/18493	0.000862	0.013368	0.011493	2828/21511	7
GO:009871	response to	7/958	31/18493	0.000862	0.013368	0.011493	3718/695/3	7
GO:009871	cellular res	7/958	31/18493	0.000862	0.013368	0.011493	3718/695/3	7
GO:003292	negative re	11/958	70/18493	0.00089	0.013679	0.01176	57162/4061	11
GO:004252	positive reg	11/958	70/18493	0.00089	0.013679	0.01176	958/104641	11
GO:005067	negative re	11/958	70/18493	0.00089	0.013679	0.01176	57162/4061	11
GO:000265	regulation	6/958	23/18493	0.000898	0.013758	0.011828	3554/70701	6
GO:003274	positive reg	12/958	81/18493	0.000907	0.013863	0.011919	64135/6411	12
GO:000242	Fc receptor	17/958	140/18493	0.000932	0.014172	0.012184	4651/74561	17
GO:000722	I-kappaB k	26/958	258/18493	0.000933	0.014172	0.012184	958/641271	26
GO:000171	endoderm	19/958	50/18493	0.000952	0.01438	0.012363	8320/39091	9
GO:000191	T cell medi	9/958	50/18493	0.000952	0.01438	0.012363	3251/51561	9
GO:000225	T-helper ce	5/958	16/18493	0.000999	0.015039	0.01293	51561/3561	5
GO:200011	regulation	24/958	232/18493	0.001004	0.015071	0.012957	55081/1141	24

GO:00458 positive reg 17/958	141/18493	0.00101	0.015117	0.012996	8867/5533/	17
GO:00508 regulation 12/958	82/18493	0.001014	0.015134	0.013011	7006/4067/	12
GO:00468 bone remoc 12/958	83/18493	0.00113	0.016827	0.014467	760/1200/5	12
GO:00017 formation 15/958	118/18493	0.00114	0.016901	0.01453	8320/7403/	15
GO:00020 positive reg 6/958	24/18493	0.001145	0.016901	0.01453	54806/4908	6
GO:20004 regulation 6/958	24/18493	0.001145	0.016901	0.01453	965/7097/2	6
GO:00300 myeloid ce 36/958	405/18493	0.001162	0.017112	0.014711	8444/23054	36
GO:00024 dendritic c 4/958	10/18493	0.001169	0.017156	0.014749	64127/508	4
GO:19908 response to 13/958	95/18493	0.001206	0.017609	0.015139	3720/1123	13
GO:19908 cellular res 13/958	95/18493	0.001206	0.017609	0.015139	3720/1123	13
GO:00614 connective 26/958	263/18493	0.001234	0.017815	0.015316	8195/4017/	26
GO:00108 positive reg 8/958	42/18493	0.001234	0.017815	0.015316	9170/5330/	8
GO:00507 regulation 8/958	42/18493	0.001234	0.017815	0.015316	64127/114	8
GO:00716 regulation 8/958	42/18493	0.001234	0.017815	0.015316	51561/829	8
GO:20012 negative re 23/958	222/18493	0.00124	0.017853	0.015348	2668/2140/	23
GO:00508 positive reg 17/958	144/18493	0.001277	0.018317	0.015747	958/64127/	17
GO:00702 negative re 7/958	33/18493	0.001279	0.018317	0.015747	3091/3718/	7
GO:00224 negative re 19/958	170/18493	0.001322	0.018875	0.016227	84524/273	19
GO:00433 CD4-positi 5/958	17/18493	0.001355	0.019289	0.016583	51561/356	5
GO:00466 regulation 10/958	63/18493	0.001392	0.019767	0.016994	51561/273	10
GO:00199 second-me 38/958	439/18493	0.001397	0.019787	0.017011	5533/2274/	38
GO:00215 subpallium 6/958	25/18493	0.001441	0.020352	0.017497	8195/3251/	6
GO:00327 positive reg 9/958	53/18493	0.001466	0.020589	0.017701	3091/7097/	9
GO:00465 positive reg 9/958	53/18493	0.001466	0.020589	0.017701	26053/282	9
GO:00507 positive reg 7/958	34/18493	0.00154	0.021516	0.018498	64127/114	7
GO:20005 positive reg 7/958	34/18493	0.00154	0.021516	0.018498	51561/114	7
GO:00024 production 26/958	268/18493	0.001615	0.022438	0.019291	958/64127/	26
GO:00062 DNA replic 26/958	268/18493	0.001615	0.022438	0.019291	5985/7907	26
GO:00066 phospholip 40/958	473/18493	0.001636	0.022669	0.019489	8776/2840	40
GO:00467 protein aut 23/958	227/18493	0.001666	0.023028	0.019798	8576/5175	23
GO:00468 regulation 8/958	44/18493	0.001691	0.023255	0.019992	760/5027/3	8
GO:19002 regulation 8/958	44/18493	0.001691	0.023255	0.019992	9170/5330/	8
GO:00336 regulation 4/958	11/18493	0.001762	0.024031	0.02066	8631/916/5	4
GO:00425 negative re 4/958	11/18493	0.001762	0.024031	0.02066	10464/228	4
GO:00706 response to 4/958	11/18493	0.001762	0.024031	0.02066	10068/880	4
GO:00434 negative re 11/958	76/18493	0.001777	0.024128	0.020743	11072/112	11
GO:00023 T cell linea 6/958	26/18493	0.001792	0.024128	0.020743	51561/3574	6
GO:00509 detection o 6/958	26/18493	0.001792	0.024128	0.020743	8195/3815/	6
GO:00725 T-helper 1 6/958	26/18493	0.001792	0.024128	0.020743	51561/114	6
GO:00027 positive reg 5/958	18/18493	0.001796	0.024128	0.020743	114548/54	5
GO:00702 thymocyte 5/958	18/18493	0.001796	0.024128	0.020743	84524/273	5
GO:00069 phagocytos 31/958	342/18493	0.001827	0.02448	0.021046	4651/7456/	31
GO:00726 interleukin 7/958	35/18493	0.00184	0.02459	0.02114	64135/513	7
GO:00714 cellular res 30/958	328/18493	0.001871	0.02494	0.021441	54434/111	30
GO:00140 regulation 14/958	112/18493	0.001932	0.025687	0.022083	8867/2293	14
GO:00509 positive ch 10/958	66/18493	0.001999	0.026499	0.022782	8846/2668/	10
GO:00066 membrane 21/958	203/18493	0.002014	0.026644	0.022906	284098/64	21
GO:00506 epithelial c 36/958	420/18493	0.002175	0.028523	0.024522	11235/273	36
GO:00019 negative re 9/958	56/18493	0.002182	0.028523	0.024522	54726/112	9
GO:00507 interleukin 9/958	56/18493	0.002182	0.028523	0.024522	64127/114	9
GO:00420 type 2 imm 7/958	36/18493	0.002184	0.028523	0.024522	64127/114	7
GO:00702 regulation 7/958	36/18493	0.002184	0.028523	0.024522	84524/309	7
GO:00712 cellular res 11/958	78/18493	0.002197	0.028626	0.024611	1111/958/4	11
GO:00019 positive reg 8/958	46/18493	0.002273	0.029536	0.025392	3091/5462	8
GO:00705 response to 17/958	152/18493	0.002298	0.029794	0.025615	958/54726/	17
GO:00023 alpha-beta 5/958	19/18493	0.002335	0.03012	0.025895	51561/356	5
GO:00217 striatum de 5/958	19/18493	0.002335	0.03012	0.025895	8195/3251/	5
GO:20005 regulation 9/958	57/18493	0.002474	0.031836	0.02737	51561/114	9

GO:003024lipid modif	27/958	291/18493	0.002518	0.032059	0.027562	10478/8776	27
GO:000274positive re	12/958	91/18493	0.002524	0.032059	0.027562	958/64127	12
GO:200011negative re	12/958	91/18493	0.002524	0.032059	0.027562	135/5272/2	12
GO:003362regulation	4/958	12/18493	0.002535	0.032059	0.027562	8631/5341/	4
GO:005112NK T cell	4/958	12/18493	0.002535	0.032059	0.027562	2000/5156	4
GO:005192regulation	4/958	12/18493	0.002535	0.032059	0.027562	55920/229	4
GO:007042thrombin-a	4/958	12/18493	0.002535	0.032059	0.027562	2151/2149/	4
GO:000282negative re	7/958	37/18493	0.002575	0.032491	0.027933	9984/3718/	7
GO:000692acute-phase	8/958	47/18493	0.002617	0.032861	0.028251	3630/3569/	8
GO:004332regulation	8/958	47/18493	0.002617	0.032861	0.028251	51561/114	8
GO:005074regulation	11/958	80/18493	0.002695	0.033762	0.029025	8291/5795/	11
GO:004312positive re	19/958	181/18493	0.002729	0.034108	0.029323	958/64127/	19
GO:000722smoothene	15/958	129/18493	0.002786	0.034735	0.029863	26005/558	15
GO:001052positive re	9/958	58/18493	0.002797	0.034785	0.029905	9170/5330/	9
GO:005252regulation	37/958	442/18493	0.002847	0.035319	0.030364	55081/114	37
GO:004322regulation	21/958	209/18493	0.002865	0.035463	0.030488	55081/114	21
GO:000282positive re	5/958	20/18493	0.002982	0.036566	0.031436	51561/946	5
GO:003242response to	5/958	20/18493	0.002982	0.036566	0.031436	64127/366	5
GO:004252tumor necr	5/958	20/18493	0.002982	0.036566	0.031436	51465/709	5
GO:004252regulation	5/958	20/18493	0.002982	0.036566	0.031436	51465/709	5
GO:000282regulation	15/958	130/18493	0.003003	0.036733	0.03158	22933/515	15
GO:005512digestive sy	16/958	143/18493	0.003035	0.037016	0.031823	2735/2737/	16
GO:004642glycerolipi	38/958	459/18493	0.00304	0.037016	0.031823	8776/2840	38
GO:007262T cell migr	9/958	59/18493	0.003152	0.038286	0.032915	3695/1880/	9
GO:004852digestive tr	15/958	131/18493	0.003233	0.039182	0.033686	2735/2737/	15
GO:003292collagen m	13/958	106/18493	0.003266	0.039488	0.033948	4327/1306/	13
GO:004392regulation	32/958	371/18493	0.003382	0.04079	0.035068	8812/5987/	32
GO:004312regulation	22/958	226/18493	0.003406	0.040984	0.035235	958/64127/	22
GO:005074regulation	8/958	49/18493	0.003427	0.041047	0.035289	64127/114	8
GO:006032face develc	8/958	49/18493	0.003427	0.041047	0.035289	8195/5933	8
GO:000172immunolog	4/958	13/18493	0.003512	0.041366	0.035563	5551/8486	4
GO:003162regulation	4/958	13/18493	0.003512	0.041366	0.035563	8862/3553/	4
GO:003232prostaglanc	4/958	13/18493	0.003512	0.041366	0.035563	10257/502	4
GO:003572interleukin	4/958	13/18493	0.003512	0.041366	0.035563	3718/920/3	4
GO:006002regulation	4/958	13/18493	0.003512	0.041366	0.035563	11314/367	4
GO:007132cellular res	4/958	13/18493	0.003512	0.041366	0.035563	3718/920/3	4
GO:200032regulation	4/958	13/18493	0.003512	0.041366	0.035563	2735/5529	4
GO:004302T cell hom	7/958	39/18493	0.003517	0.041366	0.035563	84524/100	7
GO:005102positive re	9/958	60/18493	0.003541	0.041471	0.035653	26053/282	9
GO:006072negative re	9/958	60/18493	0.003541	0.041471	0.035653	54726/112	9
GO:003132negative re	20/958	199/18493	0.003551	0.04149	0.03567	9111/2293	20
GO:000702cell-substr	12/958	95/18493	0.003622	0.042041	0.036144	55920/839	12
GO:199082response to	12/958	95/18493	0.003622	0.042041	0.036144	10936/106	12
GO:199082cellular res	12/958	95/18493	0.003622	0.042041	0.036144	10936/106	12
GO:000662phosphatid	16/958	146/18493	0.003734	0.043226	0.037162	8776/2840	16
GO:003572CD4-positi	5/958	21/18493	0.003749	0.043226	0.037162	114548/88	5
GO:004332CD4-positi	5/958	21/18493	0.003749	0.043226	0.037162	51561/356	5
GO:005182regulation	22/958	228/18493	0.003787	0.043567	0.037456	117145/22	22
GO:000232B cell activ	10/958	72/18493	0.003844	0.04389	0.037733	958/9984/9	10
GO:000642protein N-I	10/958	72/18493	0.003844	0.04389	0.037733	79868/537	10
GO:000172myeloid de	6/958	30/18493	0.003874	0.04389	0.037733	84868/814	6
GO:000722activation	6/958	30/18493	0.003874	0.04389	0.037733	9170/5330/	6
GO:001052regulation	6/958	30/18493	0.003874	0.04389	0.037733	7006/4067/	6
GO:003812interleukin	6/958	30/18493	0.003874	0.04389	0.037733	3718/3574/	6
GO:004332positive re	6/958	30/18493	0.003874	0.04389	0.037733	51561/114	6
GO:200122negative re	12/958	96/18493	0.00395	0.044648	0.038384	3630/6880/	12
GO:005172positive re	11/958	84/18493	0.003963	0.044668	0.038402	22933/844	11
GO:004672viral entry	14/958	121/18493	0.003969	0.044668	0.038402	51193/369	14

GO:00719	negative re	15/958	134/18493	0.004013	0.045065	0.038743	5570/1107	15
GO:20012	regulation	17/958	161/18493	0.004186	0.046908	0.040328	10059/3630	17
GO:00024	immune re	15/958	135/18493	0.004304	0.047926	0.041203	4651/7456	15
GO:00027	negative re	15/958	135/18493	0.004304	0.047926	0.041203	5987/8620	15
GO:00380	Fc-gamma	15/958	135/18493	0.004304	0.047926	0.041203	4651/7456	15
GO:01200	regulation	18/958	175/18493	0.00432	0.047999	0.041266	54434/512	18
GO:00109	positive re	19/958	189/18493	0.004404	0.048728	0.041892	55081/114	19
GO:19011	carbohydr	19/958	189/18493	0.004404	0.048728	0.041892	411/8930/1	19
GO:20001	negative re	8/958	51/18493	0.004418	0.048772	0.04193	64127/309	8
GO:00190	viral life cy	26/958	289/18493	0.004514	0.049733	0.042757	8812/5987	26

AMed GO CC

ID	Descriptor	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:00098	external sic	51/1002	359/19659	3.1E-11	1.78E-08	1.68E-08	958/3762/1	51
GO:00620	collagen-cc	48/1002	332/19659	6.38E-11	1.83E-08	1.73E-08	5553/2345	48
GO:00310	extracellul	57/1002	490/19659	5.24E-09	1E-06	9.48E-07	5553/2345	57
GO:00444	extracellul	15/1002	49/19659	1.13E-08	1.62E-06	1.53E-06	1306/1282	15
GO:00017	immunolog	11/1002	34/19659	5.53E-07	6.35E-05	6.01E-05	3001/5795	11
GO:00421	T cell recep	8/1002	17/19659	7.13E-07	6.82E-05	6.46E-05	5777/8631	8
GO:00056	basement n	17/1002	92/19659	3.5E-06	0.000287	0.000272	4017/1306	17
GO:00306	secretory g	34/1002	295/19659	7.9E-06	0.000567	0.000536	84519/685	34
GO:00986	complex of	7/1002	19/19659	2.57E-05	0.001638	0.00155	1282/1277	7
GO:00988	membrane	33/1002	305/19659	3.9E-05	0.002241	0.00212	153129/82	33
GO:00057	endoplasm	32/1002	301/19659	7.13E-05	0.003461	0.003275	9601/411/7	32
GO:00426	mast cell g	7/1002	22/19659	7.6E-05	0.003461	0.003275	4878/4067	7
GO:00985	membrane	33/1002	316/19659	7.84E-05	0.003461	0.003275	153129/82	33
GO:00451	membrane	32/1002	304/19659	8.61E-05	0.003529	0.003339	153129/35	32
GO:00055	fibrillar col	5/1002	11/19659	0.000122	0.004362	0.004127	1277/1278	5
GO:00986	banded col	5/1002	11/19659	0.000122	0.004362	0.004127	1277/1278	5
GO:00432	receptor co	38/1002	396/19659	0.000142	0.004798	0.00454	958/12612	38
GO:00988	plasma me	22/1002	184/19659	0.000179	0.005692	0.005387	958/12612	22
GO:00708	tertiary gra	19/1002	164/19659	0.00071	0.021456	0.020303	965/8836/4	19
GO:00055	collagen tri	12/1002	87/19659	0.001497	0.042957	0.040649	1306/1282	12
GO:00986	protein con	7/1002	35/19659	0.001678	0.045866	0.043401	3695/4067	7

AMed GO MF

ID	Descriptor	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:00052	extracellul	31/970	155/17632	3.07E-10	2.64E-07	2.43E-07	5553/1306	31
GO:00048	cytokine re	17/970	92/17632	9.55E-06	0.004114	0.003783	10936/106	17
GO:00047	non-memb	11/970	46/17632	2.98E-05	0.007627	0.007013	8576/7006	11
GO:00055	glycosamir	28/970	222/17632	3.61E-05	0.007627	0.007013	5553/6412	28
GO:00199	cytokine bi	19/970	125/17632	5.21E-05	0.007627	0.007013	10068/106	19
GO:00051	integrin bir	19/970	126/17632	5.82E-05	0.007627	0.007013	9270/3695	19
GO:00055	collagen bi	13/970	67/17632	6.19E-05	0.007627	0.007013	7045/9806	13
GO:00300	extracellul	9/970	37/17632	0.000137	0.014742	0.013556	1306/1282	9
GO:00198	growth fact	19/970	137/17632	0.000182	0.017439	0.016036	9702/2031	19
GO:00082	heparin bin	20/970	163/17632	0.000643	0.048109	0.044238	5553/1706	20
GO:00016	virus recep	12/970	74/17632	0.00067	0.048109	0.044238	3695/290/9	12
GO:01040	hijacked m	12/970	74/17632	0.00067	0.048109	0.044238	3695/290/9	12

