

**Supplementary Table S7. GO term analysis with differentially expressed genes between 4-1BB<sup>pos</sup> and 4-1BB<sup>neg</sup> PD-1<sup>high</sup> CD39<sup>+</sup> CD8 TILs**

<b>Enriched gene sets in 4-1BB<sup>pos</sup> cells</b>				
<b>GO term</b>	<b>Description</b>	<b>P-value</b>	<b>FDR q-value</b>	<b>Enrichment (N, B, n, b)</b>
<a href="#">GO:0022402</a>	cell cycle process	2.98E-58	4.61E-54	5.43 (17665,924,440,125)
<a href="#">GO:0051301</a>	cell division	1.95E-34	1.01E-30	6.67 (17665,385,440,64)
<a href="#">GO:0006260</a>	DNA replication	1.90E-26	3.27E-23	9.84 (17665,151,440,37)
<a href="#">GO:0046483</a>	heterocycle metabolic process	1.13E-20	8.74E-18	2.13 (17665,2746,440,146)
<a href="#">GO:0051716</a>	cellular response to stimulus	3.39E-13	9.56E-11	1.86 (17665,2790,440,129)
<a href="#">GO:1903047</a>	mitotic cell cycle process	3.77E-58	2.92E-54	6.90 (17665,605,440,104)
<a href="#">GO:0006259</a>	DNA metabolic process	2.84E-34	1.10E-30	4.69 (17665,736,440,86)
<a href="#">GO:0051276</a>	chromosome organization	4.57E-34	1.42E-30	6.86 (17665,363,440,62)
<a href="#">GO:0006974</a>	cellular response to DNA damage stimulus	4.94E-27	1.28E-23	4.25 (17665,708,440,75)
<a href="#">GO:0006996</a>	organelle organization	1.50E-26	3.32E-23	2.50 (17665,2263,440,141)
<a href="#">GO:0006281</a>	DNA repair	1.66E-26	3.22E-23	5.26 (17665,458,440,60)
<a href="#">GO:0051726</a>	regulation of cell cycle	2.99E-26	4.62E-23	3.35 (17665,1140,440,95)
<a href="#">GO:0010564</a>	regulation of cell cycle process	1.52E-25	2.14E-22	4.08 (17665,728,440,74)
<a href="#">GO:0007051</a>	spindle organization	6.25E-25	8.07E-22	10.19 (17665,134,440,34)
<a href="#">GO:0007059</a>	chromosome segregation	2.41E-24	2.87E-21	11.31 (17665,110,440,31)
<a href="#">GO:0007346</a>	regulation of mitotic cell cycle	1.08E-22	1.20E-19	4.18 (17665,614,440,64)
<a href="#">GO:1901990</a>	regulation of mitotic cell cycle phase transition	1.25E-22	1.29E-19	5.15 (17665,405,440,52)
<a href="#">GO:1901987</a>	regulation of cell cycle phase transition	5.57E-22	5.39E-19	4.89 (17665,435,440,53)
<a href="#">GO:0051983</a>	regulation of chromosome segregation	6.13E-21	5.58E-18	10.95 (17665,99,440,27)
<a href="#">GO:0034641</a>	cellular nitrogen compound metabolic process	8.51E-21	7.32E-18	2.05 (17665,3068,440,157)
<a href="#">GO:0071840</a>	cellular component organization or biogenesis	1.09E-20	8.92E-18	1.74 (17665,4974,440,215)
<a href="#">GO:0006725</a>	cellular aromatic compound metabolic process	1.99E-20	1.47E-17	2.11 (17665,2792,440,147)
<a href="#">GO:0006139</a>	nucleobase-containing compound metabolic process	3.98E-20	2.80E-17	2.17 (17665,2576,440,139)
<a href="#">GO:0007052</a>	mitotic spindle organization	4.00E-20	2.69E-17	12.35 (17665,78,440,24)
<a href="#">GO:0016043</a>	cellular component organization	5.24E-20	3.38E-17	1.73 (17665,4929,440,212)
<a href="#">GO:0090304</a>	nucleic acid metabolic process	2.85E-19	1.76E-16	2.32 (17665,2060,440,119)
<a href="#">GO:0000278</a>	mitotic cell cycle	3.65E-19	2.17E-16	8.56 (17665,136,440,29)
<a href="#">GO:1902850</a>	microtubule cytoskeleton organization involved in mitosis	7.95E-19	4.56E-16	9.76 (17665,107,440,26)
<a href="#">GO:1901360</a>	organic cyclic compound metabolic process	3.85E-18	2.13E-15	1.98 (17665,3014,440,149)
<a href="#">GO:0007017</a>	microtubule-based process	9.98E-18	5.33E-15	3.70 (17665,619,440,57)
<a href="#">GO:0044772</a>	mitotic cell cycle phase transition	1.59E-17	8.23E-15	5.76 (17665,251,440,36)
<a href="#">GO:0044770</a>	cell cycle phase transition	4.48E-17	2.24E-14	5.58 (17665,259,440,36)
<a href="#">GO:0090068</a>	positive regulation of cell cycle process	1.11E-16	5.37E-14	5.27 (17665,282,440,37)
<a href="#">GO:0000226</a>	microtubule cytoskeleton organization	1.28E-16	5.99E-14	4.50 (17665,384,440,43)
<a href="#">GO:0033554</a>	cellular response to stress	1.92E-16	8.73E-14	2.44 (17665,1546,440,94)
<a href="#">GO:0033045</a>	regulation of sister chromatid segregation	2.58E-16	1.14E-13	10.67 (17665,79,440,21)
<a href="#">GO:0007049</a>	cell cycle	2.90E-16	1.25E-13	4.21 (17665,429,440,45)

<a href="#">GO:0006271</a>	DNA strand elongation involved in DNA replication	7.97E-16	3.34E-13	26.77 (17665,18,440,12)
<a href="#">GO:1902749</a>	regulation of cell cycle G2/M phase transition	8.69E-16	3.54E-13	6.01 (17665,207,440,31)
<a href="#">GO:0071103</a>	DNA conformation change	9.88E-16	3.92E-13	7.08 (17665,153,440,27)
<a href="#">GO:0098813</a>	nuclear chromosome segregation	1.86E-15	7.21E-13	13.65 (17665,50,440,17)
<a href="#">GO:0010965</a>	regulation of mitotic sister chromatid separation	2.44E-15	9.23E-13	12.25 (17665,59,440,18)
<a href="#">GO:0034645</a>	cellular macromolecule biosynthetic process	5.47E-15	2.02E-12	2.92 (17665,894,440,65)
<a href="#">GO:0045787</a>	positive regulation of cell cycle	5.68E-15	2.05E-12	4.33 (17665,371,440,40)
<a href="#">GO:1905818</a>	regulation of chromosome separation	1.21E-14	4.27E-12	11.29 (17665,64,440,18)
<a href="#">GO:0009987</a>	cellular process	1.93E-14	6.65E-12	1.19 (17665,13415,440,396)
<a href="#">GO:0007088</a>	regulation of mitotic nuclear division	1.94E-14	6.52E-12	6.61 (17665,158,440,26)
<a href="#">GO:0006302</a>	double-strand break repair	2.32E-14	7.65E-12	6.27 (17665,173,440,27)
<a href="#">GO:0033047</a>	regulation of mitotic sister chromatid segregation	2.94E-14	9.49E-12	10.79 (17665,67,440,18)
<a href="#">GO:0010389</a>	regulation of G2/M transition of mitotic cell cycle	5.07E-14	1.60E-11	5.82 (17665,193,440,28)
<a href="#">GO:0022616</a>	DNA strand elongation	5.19E-14	1.61E-11	20.95 (17665,23,440,12)
<a href="#">GO:0010948</a>	negative regulation of cell cycle process	7.75E-14	2.35E-11	4.53 (17665,310,440,35)
<a href="#">GO:0045786</a>	negative regulation of cell cycle	9.34E-14	2.78E-11	3.48 (17665,543,440,47)
<a href="#">GO:0030071</a>	regulation of mitotic metaphase/anaphase transition	2.05E-13	5.98E-11	11.68 (17665,55,440,16)
<a href="#">GO:0009059</a>	macromolecule biosynthetic process	2.08E-13	5.96E-11	2.53 (17665,1141,440,72)
<a href="#">GO:1902099</a>	regulation of metaphase/anaphase transition of cell cycle	3.80E-13	1.05E-10	11.27 (17665,57,440,16)
<a href="#">GO:0051783</a>	regulation of nuclear division	5.97E-13	1.62E-10	5.74 (17665,182,440,26)
<a href="#">GO:0045930</a>	negative regulation of mitotic cell cycle	6.44E-13	1.72E-10	4.46 (17665,297,440,33)
<a href="#">GO:0071897</a>	DNA biosynthetic process	1.22E-12	3.19E-10	8.20 (17665,93,440,19)
<a href="#">GO:1901988</a>	negative regulation of cell cycle phase transition	1.95E-12	5.02E-10	5.04 (17665,223,440,28)
<a href="#">GO:0006807</a>	nitrogen compound metabolic process	2.41E-12	6.13E-10	1.44 (17665,6470,440,232)
<a href="#">GO:1901991</a>	negative regulation of mitotic cell cycle phase transition	2.77E-12	6.91E-10	5.16 (17665,210,440,27)
<a href="#">GO:0033044</a>	regulation of chromosome organization	3.47E-12	8.53E-10	4.09 (17665,334,440,34)
<a href="#">GO:0044843</a>	cell cycle G1/S phase transition	6.90E-12	1.67E-09	7.48 (17665,102,440,19)
<a href="#">GO:0006270</a>	DNA replication initiation	7.07E-12	1.68E-09	15.06 (17665,32,440,12)
<a href="#">GO:0000075</a>	cell cycle checkpoint	1.28E-11	3.00E-09	6.39 (17665,132,440,21)
<a href="#">GO:0007010</a>	cytoskeleton organization	1.36E-11	3.14E-09	2.66 (17665,860,440,57)
<a href="#">GO:0006310</a>	DNA recombination	1.53E-11	3.49E-09	5.20 (17665,193,440,25)
<a href="#">GO:0044260</a>	cellular macromolecule metabolic process	1.80E-11	4.05E-09	1.57 (17665,4426,440,173)
<a href="#">GO:0000724</a>	double-strand break repair via homologous recombination	3.80E-11	8.40E-09	7.30 (17665,99,440,18)
<a href="#">GO:0000725</a>	recombinational repair	4.53E-11	9.87E-09	7.23 (17665,100,440,18)
<a href="#">GO:0000082</a>	G1/S transition of mitotic cell cycle	4.53E-11	9.74E-09	7.23 (17665,100,440,18)
<a href="#">GO:0000727</a>	double-strand break repair via break-induced replication	6.31E-11	1.34E-08	26.77 (17665,12,440,8)
<a href="#">GO:0000819</a>	sister chromatid segregation	7.40E-11	1.55E-08	12.68 (17665,38,440,12)
<a href="#">GO:0044237</a>	cellular metabolic process	9.01E-11	1.86E-08	1.38 (17665,7066,440,242)
<a href="#">GO:0032392</a>	DNA geometric change	2.34E-10	4.77E-08	6.57 (17665,110,440,18)
<a href="#">GO:0043170</a>	macromolecule metabolic process	2.37E-10	4.77E-08	1.44 (17665,5683,440,204)
<a href="#">GO:0051383</a>	kinetochore organization	2.52E-10	5.00E-08	19.02 (17665,19,440,9)
<a href="#">GO:0051225</a>	spindle assembly	3.31E-10	6.48E-08	8.14 (17665,74,440,15)
<a href="#">GO:0000083</a>	regulation of transcription involved in G1/S transition of mitotic cell cycle	3.45E-10	6.68E-08	12.99 (17665,34,440,11)
<a href="#">GO:0044249</a>	cellular biosynthetic process	4.49E-10	8.59E-08	1.86 (17665,2137,440,99)

<a href="#">GO:0000070</a>	mitotic sister chromatid segregation	4.92E-10	9.29E-08	12.62 (17665,35,440,11)
<a href="#">GO:0065004</a>	protein-DNA complex assembly	6.24E-10	1.16E-07	5.50 (17665,146,440,20)
<a href="#">GO:0044238</a>	primary metabolic process	6.44E-10	1.19E-07	1.36 (17665,6918,440,235)
<a href="#">GO:0032508</a>	DNA duplex unwinding	6.47E-10	1.18E-07	6.63 (17665,103,440,17)
<a href="#">GO:0022607</a>	cellular component assembly	1.13E-09	2.04E-07	1.84 (17665,2112,440,97)
<a href="#">GO:0045931</a>	positive regulation of mitotic cell cycle	1.29E-09	2.29E-07	5.28 (17665,152,440,20)
<a href="#">GO:0071704</a>	organic substance metabolic process	1.32E-09	2.32E-07	1.34 (17665,7276,440,243)
<a href="#">GO:0033043</a>	regulation of organelle organization	1.57E-09	2.72E-07	2.16 (17665,1244,440,67)
<a href="#">GO:1901576</a>	organic substance biosynthetic process	1.81E-09	3.12E-07	1.80 (17665,2255,440,101)
<a href="#">GO:1901989</a>	positive regulation of cell cycle phase transition	2.09E-09	3.56E-07	6.62 (17665,97,440,16)
<a href="#">GO:0009058</a>	biosynthetic process	2.97E-09	4.99E-07	1.78 (17665,2307,440,102)
<a href="#">GO:0000281</a>	mitotic cytokinesis	3.24E-09	5.39E-07	9.45 (17665,51,440,12)
<a href="#">GO:0007093</a>	mitotic cell cycle checkpoint	3.31E-09	5.46E-07	6.42 (17665,100,440,16)
<a href="#">GO:0006333</a>	chromatin assembly or disassembly	4.02E-09	6.55E-07	8.28 (17665,63,440,13)
<a href="#">GO:0051052</a>	regulation of DNA metabolic process	4.63E-09	7.46E-07	3.19 (17665,415,440,33)
<a href="#">GO:0000723</a>	telomere maintenance	4.92E-09	7.85E-07	6.77 (17665,89,440,15)
<a href="#">GO:0032200</a>	telomere organization	5.77E-09	9.12E-07	6.69 (17665,90,440,15)
<a href="#">GO:0072331</a>	signal transduction by p53 class mediator	6.37E-09	9.97E-07	5.74 (17665,119,440,17)
<a href="#">GO:0071824</a>	protein-DNA complex subunit organization	6.80E-09	1.05E-06	4.58 (17665,184,440,21)
<a href="#">GO:1901992</a>	positive regulation of mitotic cell cycle phase transition	1.15E-08	1.76E-06	6.94 (17665,81,440,14)
<a href="#">GO:0006950</a>	response to stress	1.26E-08	1.91E-06	1.63 (17665,2955,440,120)
<a href="#">GO:0070925</a>	organelle assembly	1.61E-08	2.42E-06	2.86 (17665,505,440,36)
<a href="#">GO:0051303</a>	establishment of chromosome localization	2.33E-08	3.47E-06	8.03 (17665,60,440,12)
<a href="#">GO:0042770</a>	signal transduction in response to DNA damage	2.54E-08	3.75E-06	6.02 (17665,100,440,15)
<a href="#">GO:0051984</a>	positive regulation of chromosome segregation	3.06E-08	4.47E-06	12.04 (17665,30,440,9)
<a href="#">GO:0030261</a>	chromosome condensation	3.06E-08	4.43E-06	12.04 (17665,30,440,9)
<a href="#">GO:0050000</a>	chromosome localization	3.44E-08	4.93E-06	7.77 (17665,62,440,12)
<a href="#">GO:0033046</a>	negative regulation of sister chromatid segregation	4.22E-08	5.99E-06	11.66 (17665,31,440,9)
<a href="#">GO:0000910</a>	cytokinesis	4.99E-08	7.03E-06	7.53 (17665,64,440,12)
<a href="#">GO:0061640</a>	cytoskeleton-dependent cytokinesis	4.99E-08	6.97E-06	7.53 (17665,64,440,12)
<a href="#">GO:0051985</a>	negative regulation of chromosome segregation	5.74E-08	7.93E-06	11.29 (17665,32,440,9)
<a href="#">GO:0030330</a>	DNA damage response, signal transduction by p53 class mediator	6.03E-08	8.26E-06	6.69 (17665,78,440,13)
<a href="#">GO:0000076</a>	DNA replication checkpoint	8.89E-08	1.21E-05	16.53 (17665,17,440,7)
<a href="#">GO:0032201</a>	telomere maintenance via semi-conservative replication	1.04E-07	1.40E-05	12.85 (17665,25,440,8)
<a href="#">GO:0031145</a>	anaphase-promoting complex-dependent catabolic process	1.11E-07	1.49E-05	6.36 (17665,82,440,13)
<a href="#">GO:2000816</a>	negative regulation of mitotic sister chromatid separation	1.46E-07	1.94E-05	12.35 (17665,26,440,8)
<a href="#">GO:0000086</a>	G2/M transition of mitotic cell cycle	1.68E-07	2.21E-05	4.90 (17665,131,440,16)
<a href="#">GO:0008152</a>	metabolic process	1.69E-07	2.19E-05	1.27 (17665,7781,440,247)
<a href="#">GO:0006323</a>	DNA packaging	1.76E-07	2.27E-05	10.04 (17665,36,440,9)
<a href="#">GO:0051310</a>	metaphase plate congression	1.88E-07	2.41E-05	8.54 (17665,47,440,10)
<a href="#">GO:0051302</a>	regulation of cell division	1.97E-07	2.50E-05	4.33 (17665,167,440,18)
<a href="#">GO:1905819</a>	negative regulation of chromosome separation	2.04E-07	2.56E-05	11.90 (17665,27,440,8)
<a href="#">GO:0044839</a>	cell cycle G2/M phase transition	2.08E-07	2.60E-05	4.83 (17665,133,440,16)

<a href="#">GO:0006334</a>	nucleosome assembly	2.66E-07	3.30E-05	6.51 (17665,74,440,12)
<a href="#">GO:0032465</a>	regulation of cytokinesis	3.00E-07	3.68E-05	5.86 (17665,89,440,13)
<a href="#">GO:0051988</a>	regulation of attachment of spindle microtubules to kinetochore	3.42E-07	4.16E-05	18.53 (17665,13,440,6)
<a href="#">GO:0033048</a>	negative regulation of mitotic sister chromatid segregation	3.77E-07	4.56E-05	11.08 (17665,29,440,8)
<a href="#">GO:1902299</a>	pre-replicative complex assembly involved in cell cycle DNA replication	4.93E-07	5.92E-05	25.09 (17665,8,440,5)
<a href="#">GO:0036388</a>	pre-replicative complex assembly	4.93E-07	5.88E-05	25.09 (17665,8,440,5)
<a href="#">GO:0006267</a>	pre-replicative complex assembly involved in nuclear cell cycle DNA replication	4.93E-07	5.83E-05	25.09 (17665,8,440,5)
<a href="#">GO:0051382</a>	kinetochore assembly	5.85E-07	6.86E-05	17.21 (17665,14,440,6)
<a href="#">GO:0051640</a>	organelle localization	6.60E-07	7.68E-05	2.59 (17665,512,440,33)
<a href="#">GO:0031055</a>	chromatin remodeling at centromere	6.63E-07	7.66E-05	10.36 (17665,31,440,8)
<a href="#">GO:0071173</a>	spindle assembly checkpoint	7.00E-07	8.02E-05	12.77 (17665,22,440,7)
<a href="#">GO:0071174</a>	mitotic spindle checkpoint	7.00E-07	7.97E-05	12.77 (17665,22,440,7)
<a href="#">GO:0007094</a>	mitotic spindle assembly checkpoint	7.00E-07	7.91E-05	12.77 (17665,22,440,7)
<a href="#">GO:0031577</a>	spindle checkpoint	7.00E-07	7.85E-05	12.77 (17665,22,440,7)
<a href="#">GO:0072422</a>	signal transduction involved in DNA damage checkpoint	8.63E-07	9.61E-05	6.49 (17665,68,440,11)
<a href="#">GO:0072401</a>	signal transduction involved in DNA integrity checkpoint	8.63E-07	9.55E-05	6.49 (17665,68,440,11)
<a href="#">GO:1902750</a>	negative regulation of cell cycle G2/M phase transition	9.35E-07	1.03E-04	5.33 (17665,98,440,13)
<a href="#">GO:0072395</a>	signal transduction involved in cell cycle checkpoint	1.00E-06	1.09E-04	6.40 (17665,69,440,11)
<a href="#">GO:0045841</a>	negative regulation of mitotic metaphase/anaphase transition	1.36E-06	1.47E-04	11.71 (17665,24,440,7)
<a href="#">GO:0051054</a>	positive regulation of DNA metabolic process	1.45E-06	1.55E-04	3.48 (17665,231,440,20)
<a href="#">GO:0045132</a>	meiotic chromosome segregation	1.50E-06	1.60E-04	15.06 (17665,16,440,6)
<a href="#">GO:2001251</a>	negative regulation of chromosome organization	1.57E-06	1.67E-04	4.72 (17665,119,440,14)
<a href="#">GO:0090307</a>	mitotic spindle assembly	1.81E-06	1.91E-04	9.18 (17665,35,440,8)
<a href="#">GO:1902100</a>	negative regulation of metaphase/anaphase transition of cell cycle	1.85E-06	1.93E-04	11.24 (17665,25,440,7)
<a href="#">GO:0010972</a>	negative regulation of G2/M transition of mitotic cell cycle	2.06E-06	2.14E-04	5.41 (17665,89,440,12)
<a href="#">GO:0019438</a>	aromatic compound biosynthetic process	2.61E-06	2.69E-04	1.99 (17665,1008,440,50)
<a href="#">GO:0006336</a>	DNA replication-independent nucleosome assembly	2.85E-06	2.92E-04	8.68 (17665,37,440,8)
<a href="#">GO:0006735</a>	NADH regeneration	3.27E-06	3.33E-04	10.41 (17665,27,440,7)
<a href="#">GO:0061718</a>	glucose catabolic process to pyruvate	3.27E-06	3.31E-04	10.41 (17665,27,440,7)
<a href="#">GO:0061621</a>	canonical glycolysis	3.27E-06	3.29E-04	10.41 (17665,27,440,7)
<a href="#">GO:0070507</a>	regulation of microtubule cytoskeleton organization	3.44E-06	3.43E-04	3.73 (17665,183,440,17)
<a href="#">GO:0071158</a>	positive regulation of cell cycle arrest	3.50E-06	3.48E-04	5.66 (17665,78,440,11)
<a href="#">GO:0034724</a>	DNA replication-independent nucleosome organization	3.53E-06	3.48E-04	8.45 (17665,38,440,8)
<a href="#">GO:0007062</a>	sister chromatid cohesion	3.53E-06	3.46E-04	8.45 (17665,38,440,8)
<a href="#">GO:0043933</a>	protein-containing complex subunit organization	3.76E-06	3.66E-04	1.77 (17665,1500,440,66)
<a href="#">GO:0034728</a>	nucleosome organization	3.90E-06	3.77E-04	4.70 (17665,111,440,13)
<a href="#">GO:0006275</a>	regulation of DNA replication	3.90E-06	3.75E-04	4.70 (17665,111,440,13)
<a href="#">GO:0044271</a>	cellular nitrogen compound biosynthetic process	3.97E-06	3.79E-04	1.84 (17665,1289,440,59)
<a href="#">GO:0061620</a>	glycolytic process through glucose-6-phosphate	4.27E-06	4.05E-04	10.04 (17665,28,440,7)
<a href="#">GO:0061615</a>	glycolytic process through fructose-6-phosphate	4.27E-06	4.03E-04	10.04 (17665,28,440,7)
<a href="#">GO:0045839</a>	negative regulation of mitotic nuclear division	4.34E-06	4.07E-04	8.24 (17665,39,440,8)
<a href="#">GO:0018130</a>	heterocycle biosynthetic process	4.51E-06	4.21E-04	1.97 (17665,999,440,49)
<a href="#">GO:0009124</a>	nucleoside monophosphate biosynthetic process	4.63E-06	4.29E-04	5.02 (17665,96,440,12)
<a href="#">GO:0031023</a>	microtubule organizing center organization	5.03E-06	4.64E-04	6.08 (17665,66,440,10)

<a href="#">GO:0034080</a>	CENP-A containing nucleosome assembly	5.51E-06	5.04E-04	9.69 (17665,29,440,7)
<a href="#">GO:0006298</a>	mismatch repair	5.51E-06	5.01E-04	9.69 (17665,29,440,7)
<a href="#">GO:0031570</a>	DNA integrity checkpoint	5.77E-06	5.22E-04	5.39 (17665,82,440,11)
<a href="#">GO:0051255</a>	spindle midzone assembly	6.42E-06	5.78E-04	16.73 (17665,12,440,5)
<a href="#">GO:0008608</a>	attachment of spindle microtubules to kinetochore	6.65E-06	5.95E-04	12.04 (17665,20,440,6)
<a href="#">GO:0045840</a>	positive regulation of mitotic nuclear division	6.69E-06	5.95E-04	6.69 (17665,54,440,9)
<a href="#">GO:0032886</a>	regulation of microtubule-based process	6.79E-06	6.01E-04	3.39 (17665,213,440,18)
<a href="#">GO:1902751</a>	positive regulation of cell cycle G2/M phase transition	7.03E-06	6.18E-04	9.37 (17665,30,440,7)
<a href="#">GO:0006977</a>	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	7.83E-06	6.85E-04	6.57 (17665,55,440,9)
<a href="#">GO:1903046</a>	meiotic cell cycle process	7.84E-06	6.82E-04	3.89 (17665,155,440,15)
<a href="#">GO:0034654</a>	nucleobase-containing compound biosynthetic process	7.91E-06	6.84E-04	1.98 (17665,933,440,46)
<a href="#">GO:0006325</a>	chromatin organization	8.06E-06	6.93E-04	2.24 (17665,628,440,35)
<a href="#">GO:0071156</a>	regulation of cell cycle arrest	8.75E-06	7.48E-04	4.72 (17665,102,440,12)
<a href="#">GO:0006007</a>	glucose catabolic process	8.89E-06	7.56E-04	9.07 (17665,31,440,7)
<a href="#">GO:1902400</a>	intracellular signal transduction involved in G1 DNA damage checkpoint	9.12E-06	7.72E-04	6.45 (17665,56,440,9)
<a href="#">GO:1902403</a>	signal transduction involved in mitotic DNA integrity checkpoint	9.12E-06	7.68E-04	6.45 (17665,56,440,9)
<a href="#">GO:1902402</a>	signal transduction involved in mitotic DNA damage checkpoint	9.12E-06	7.63E-04	6.45 (17665,56,440,9)
<a href="#">GO:0072431</a>	signal transduction involved in mitotic G1 DNA damage checkpoint	9.12E-06	7.59E-04	6.45 (17665,56,440,9)
<a href="#">GO:0072413</a>	signal transduction involved in mitotic cell cycle checkpoint	9.12E-06	7.55E-04	6.45 (17665,56,440,9)
<a href="#">GO:0046605</a>	regulation of centrosome cycle	1.06E-05	8.73E-04	6.34 (17665,57,440,9)
<a href="#">GO:0043486</a>	histone exchange	1.12E-05	9.19E-04	7.30 (17665,44,440,8)
<a href="#">GO:0010032</a>	meiotic chromosome condensation	1.25E-05	1.02E-03	22.94 (17665,7,440,4)
<a href="#">GO:0071163</a>	DNA replication preinitiation complex assembly	1.54E-05	1.24E-03	40.15 (17665,3,440,3)
<a href="#">GO:0006297</a>	nucleotide-excision repair, DNA gap filling	1.63E-05	1.31E-03	10.47 (17665,23,440,6)
<a href="#">GO:0034622</a>	cellular protein-containing complex assembly	1.70E-05	1.36E-03	2.06 (17665,761,440,39)
<a href="#">GO:0010638</a>	positive regulation of organelle organization	1.86E-05	1.48E-03	2.21 (17665,599,440,33)
<a href="#">GO:0051784</a>	negative regulation of nuclear division	1.86E-05	1.48E-03	6.83 (17665,47,440,8)
<a href="#">GO:0009123</a>	nucleoside monophosphate metabolic process	2.07E-05	1.63E-03	3.58 (17665,168,440,15)
<a href="#">GO:0007076</a>	mitotic chromosome condensation	2.29E-05	1.80E-03	13.38 (17665,15,440,5)
<a href="#">GO:0065003</a>	protein-containing complex assembly	2.42E-05	1.89E-03	1.78 (17665,1215,440,54)
<a href="#">GO:0051256</a>	mitotic spindle midzone assembly	2.46E-05	1.91E-03	20.07 (17665,8,440,4)
<a href="#">GO:0006734</a>	NADH metabolic process	2.53E-05	1.96E-03	7.81 (17665,36,440,7)
<a href="#">GO:0009142</a>	nucleoside triphosphate biosynthetic process	2.58E-05	1.98E-03	5.08 (17665,79,440,10)
<a href="#">GO:0000731</a>	DNA synthesis involved in DNA repair	2.98E-05	2.29E-03	6.42 (17665,50,440,8)
<a href="#">GO:0006301</a>	postreplication repair	2.98E-05	2.27E-03	6.42 (17665,50,440,8)
<a href="#">GO:0007080</a>	mitotic metaphase plate congression	3.06E-05	2.32E-03	7.60 (17665,37,440,7)
<a href="#">GO:2001252</a>	positive regulation of chromosome organization	3.57E-05	2.70E-03	3.42 (17665,176,440,15)
<a href="#">GO:1901362</a>	organic cyclic compound biosynthetic process	3.58E-05	2.69E-03	1.79 (17665,1141,440,51)
<a href="#">GO:0009141</a>	nucleoside triphosphate metabolic process	3.66E-05	2.74E-03	3.60 (17665,156,440,14)
<a href="#">GO:0009435</a>	NAD biosynthetic process	4.00E-05	2.98E-03	6.18 (17665,52,440,8)
<a href="#">GO:1901293</a>	nucleoside phosphate biosynthetic process	4.49E-05	3.33E-03	2.95 (17665,245,440,18)
<a href="#">GO:0007019</a>	microtubule depolymerization	4.53E-05	3.34E-03	11.81 (17665,17,440,5)
<a href="#">GO:0051785</a>	positive regulation of nuclear division	4.56E-05	3.34E-03	5.31 (17665,68,440,9)
<a href="#">GO:0032467</a>	positive regulation of cytokinesis	5.19E-05	3.79E-03	7.03 (17665,40,440,7)

<a href="#">GO:0006096</a>	glycolytic process	5.19E-05	3.77E-03	7.03 (17665,40,440,7)
<a href="#">GO:0006272</a>	leading strand elongation	6.03E-05	4.36E-03	30.11 (17665,4,440,3)
<a href="#">GO:0007079</a>	mitotic chromosome movement towards spindle pole	6.03E-05	4.34E-03	30.11 (17665,4,440,3)
<a href="#">GO:0006757</a>	ATP generation from ADP	6.13E-05	4.39E-03	6.85 (17665,41,440,7)
<a href="#">GO:0048522</a>	positive regulation of cellular process	6.28E-05	4.48E-03	1.29 (17665,5162,440,166)
<a href="#">GO:0010639</a>	negative regulation of organelle organization	6.34E-05	4.50E-03	2.48 (17665,372,440,23)
<a href="#">GO:0031109</a>	microtubule polymerization or depolymerization	6.74E-05	4.76E-03	8.31 (17665,29,440,6)
<a href="#">GO:0033314</a>	mitotic DNA replication checkpoint	7.08E-05	4.98E-03	16.06 (17665,10,440,4)
<a href="#">GO:0034404</a>	nucleobase-containing small molecule biosynthetic process	7.50E-05	5.25E-03	3.57 (17665,146,440,13)
<a href="#">GO:0051656</a>	establishment of organelle localization	7.80E-05	5.44E-03	2.65 (17665,303,440,20)
<a href="#">GO:0006165</a>	nucleoside diphosphate phosphorylation	7.88E-05	5.47E-03	5.63 (17665,57,440,8)
<a href="#">GO:0062033</a>	positive regulation of mitotic sister chromatid segregation	8.16E-05	5.64E-03	10.57 (17665,19,440,5)
<a href="#">GO:0007063</a>	regulation of sister chromatid cohesion	8.16E-05	5.62E-03	10.57 (17665,19,440,5)
<a href="#">GO:2000045</a>	regulation of G1/S transition of mitotic cell cycle	9.24E-05	6.33E-03	3.50 (17665,149,440,13)
<a href="#">GO:0042866</a>	pyruvate biosynthetic process	9.79E-05	6.68E-03	6.39 (17665,44,440,7)
<a href="#">GO:0016572</a>	histone phosphorylation	1.00E-04	6.80E-03	7.77 (17665,31,440,6)
<a href="#">GO:0046939</a>	nucleotide phosphorylation	1.01E-04	6.85E-03	5.44 (17665,59,440,8)
<a href="#">GO:0009162</a>	deoxyribonucleoside monophosphate metabolic process	1.09E-04	7.34E-03	14.60 (17665,11,440,4)
<a href="#">GO:0006261</a>	DNA-dependent DNA replication	1.21E-04	8.09E-03	7.53 (17665,32,440,6)
<a href="#">GO:0009165</a>	nucleotide biosynthetic process	1.26E-04	8.41E-03	2.82 (17665,242,440,17)
<a href="#">GO:1901796</a>	regulation of signal transduction by p53 class mediator	1.36E-04	9.01E-03	3.19 (17665,176,440,14)
<a href="#">GO:0000915</a>	actomyosin contractile ring assembly	1.48E-04	9.78E-03	24.09 (17665,5,440,3)
<a href="#">GO:0000912</a>	assembly of actomyosin apparatus involved in cytokinesis	1.48E-04	9.74E-03	24.09 (17665,5,440,3)
<a href="#">GO:1902975</a>	mitotic DNA replication initiation	1.48E-04	9.70E-03	24.09 (17665,5,440,3)
<a href="#">GO:1902315</a>	nuclear cell cycle DNA replication initiation	1.48E-04	9.66E-03	24.09 (17665,5,440,3)
<a href="#">GO:1902292</a>	cell cycle DNA replication initiation	1.48E-04	9.62E-03	24.09 (17665,5,440,3)
<a href="#">GO:0044837</a>	actomyosin contractile ring organization	1.48E-04	9.58E-03	24.09 (17665,5,440,3)
<a href="#">GO:0008150</a>	biological_process	1.57E-04	1.01E-02	1.05 (17665,16319,440,425)
<a href="#">GO:0051315</a>	attachment of mitotic spindle microtubules to kinetochore	1.60E-04	1.03E-02	13.38 (17665,12,440,4)
<a href="#">GO:0035404</a>	histone-serine phosphorylation	1.60E-04	1.03E-02	13.38 (17665,12,440,4)
<a href="#">GO:1904029</a>	regulation of cyclin-dependent protein kinase activity	1.65E-04	1.05E-02	4.10 (17665,98,440,10)
<a href="#">GO:0006278</a>	RNA-dependent DNA biosynthetic process	1.74E-04	1.10E-02	9.12 (17665,22,440,5)
<a href="#">GO:0046031</a>	ADP metabolic process	1.97E-04	1.25E-02	5.74 (17665,49,440,7)
<a href="#">GO:0050896</a>	response to stimulus	2.08E-04	1.31E-02	1.26 (17665,5275,440,166)
<a href="#">GO:0048146</a>	positive regulation of fibroblast proliferation	2.25E-04	1.41E-02	5.62 (17665,50,440,7)
<a href="#">GO:0019320</a>	hexose catabolic process	2.25E-04	1.40E-02	5.62 (17665,50,440,7)
<a href="#">GO:0045842</a>	positive regulation of mitotic metaphase/anaphase transition	2.27E-04	1.41E-02	12.35 (17665,13,440,4)
<a href="#">GO:1901970</a>	positive regulation of mitotic sister chromatid separation	2.27E-04	1.41E-02	12.35 (17665,13,440,4)
<a href="#">GO:0051304</a>	chromosome separation	2.27E-04	1.40E-02	12.35 (17665,13,440,4)
<a href="#">GO:2000134</a>	negative regulation of G1/S transition of mitotic cell cycle	2.29E-04	1.41E-02	3.94 (17665,102,440,10)
<a href="#">GO:0032506</a>	cytokinetic process	2.38E-04	1.46E-02	6.69 (17665,36,440,6)
<a href="#">GO:0009201</a>	ribonucleoside triphosphate biosynthetic process	2.50E-04	1.53E-02	4.79 (17665,67,440,8)
<a href="#">GO:0006754</a>	ATP biosynthetic process	2.55E-04	1.55E-02	5.51 (17665,51,440,7)
<a href="#">GO:1902806</a>	regulation of cell cycle G1/S phase transition	2.56E-04	1.55E-02	3.16 (17665,165,440,13)
<a href="#">GO:0019674</a>	NAD metabolic process	2.78E-04	1.67E-02	4.72 (17665,68,440,8)



<a href="#">GO:0019363</a>	pyridine nucleotide biosynthetic process	2.78E-04	1.67E-02	4.72 (17665,68,440,8)
<a href="#">GO:0019359</a>	nicotinamide nucleotide biosynthetic process	2.78E-04	1.66E-02	4.72 (17665,68,440,8)
<a href="#">GO:0051781</a>	positive regulation of cell division	2.87E-04	1.71E-02	4.20 (17665,86,440,9)
<a href="#">GO:0090329</a>	regulation of DNA-dependent DNA replication	2.88E-04	1.71E-02	5.40 (17665,52,440,7)
<a href="#">GO:0006915</a>	apoptotic process	2.89E-04	1.71E-02	1.96 (17665,634,440,31)
<a href="#">GO:0009211</a>	pyrimidine deoxyribonucleoside triphosphate metabolic process	2.90E-04	1.71E-02	20.07 (17665,6,440,3)
<a href="#">GO:1902807</a>	negative regulation of cell cycle G1/S phase transition	2.90E-04	1.70E-02	3.82 (17665,105,440,10)
<a href="#">GO:0009166</a>	nucleotide catabolic process	2.90E-04	1.70E-02	3.82 (17665,105,440,10)
<a href="#">GO:2000573</a>	positive regulation of DNA biosynthetic process	3.07E-04	1.79E-02	4.65 (17665,69,440,8)
<a href="#">GO:1902101</a>	positive regulation of metaphase/anaphase transition of cell cycle	3.12E-04	1.81E-02	11.47 (17665,14,440,4)
<a href="#">GO:1903504</a>	regulation of mitotic spindle checkpoint	3.12E-04	1.80E-02	11.47 (17665,14,440,4)
<a href="#">GO:0090266</a>	regulation of mitotic cell cycle spindle assembly checkpoint	3.12E-04	1.79E-02	11.47 (17665,14,440,4)
<a href="#">GO:0090231</a>	regulation of spindle checkpoint	3.12E-04	1.79E-02	11.47 (17665,14,440,4)
<a href="#">GO:0009156</a>	ribonucleoside monophosphate biosynthetic process	3.13E-04	1.79E-02	4.15 (17665,87,440,9)
<a href="#">GO:0044282</a>	small molecule catabolic process	3.16E-04	1.80E-02	2.23 (17665,415,440,23)
<a href="#">GO:0045005</a>	DNA-dependent DNA replication maintenance of fidelity	3.24E-04	1.84E-02	6.34 (17665,38,440,6)
<a href="#">GO:2000278</a>	regulation of DNA biosynthetic process	3.39E-04	1.91E-02	3.75 (17665,107,440,10)
<a href="#">GO:0055086</a>	nucleobase-containing small molecule metabolic process	3.54E-04	1.99E-02	2.02 (17665,556,440,28)
<a href="#">GO:0051338</a>	regulation of transferase activity	3.61E-04	2.02E-02	1.74 (17665,971,440,42)
<a href="#">GO:0051347</a>	positive regulation of transferase activity	3.68E-04	2.05E-02	1.91 (17665,672,440,32)
<a href="#">GO:0007098</a>	centrosome cycle	3.75E-04	2.09E-02	6.18 (17665,39,440,6)
<a href="#">GO:0006753</a>	nucleoside phosphate metabolic process	3.82E-04	2.12E-02	2.11 (17665,475,440,25)
<a href="#">GO:0006760</a>	folic acid-containing compound metabolic process	4.00E-04	2.21E-02	7.72 (17665,26,440,5)
<a href="#">GO:0072525</a>	pyridine-containing compound biosynthetic process	4.12E-04	2.27E-02	4.46 (17665,72,440,8)
<a href="#">GO:0006268</a>	DNA unwinding involved in DNA replication	4.17E-04	2.29E-02	10.71 (17665,15,440,4)
<a href="#">GO:1905820</a>	positive regulation of chromosome separation	4.17E-04	2.28E-02	10.71 (17665,15,440,4)
<a href="#">GO:0009263</a>	deoxyribonucleotide biosynthetic process	4.17E-04	2.27E-02	10.71 (17665,15,440,4)
<a href="#">GO:0019985</a>	translesion synthesis	4.32E-04	2.35E-02	6.02 (17665,40,440,6)
<a href="#">GO:0009168</a>	purine ribonucleoside monophosphate biosynthetic process	4.53E-04	2.45E-02	4.40 (17665,73,440,8)
<a href="#">GO:1901292</a>	nucleoside phosphate catabolic process	4.55E-04	2.45E-02	3.62 (17665,111,440,10)
<a href="#">GO:0010971</a>	positive regulation of G2/M transition of mitotic cell cycle	4.81E-04	2.59E-02	7.43 (17665,27,440,5)
<a href="#">GO:0044818</a>	mitotic G2/M transition checkpoint	4.81E-04	2.58E-02	7.43 (17665,27,440,5)
<a href="#">GO:0002639</a>	positive regulation of immunoglobulin production	4.96E-04	2.65E-02	5.88 (17665,41,440,6)
<a href="#">GO:0010216</a>	maintenance of DNA methylation	4.99E-04	2.65E-02	17.21 (17665,7,440,3)
<a href="#">GO:0051305</a>	chromosome movement towards spindle pole	4.99E-04	2.64E-02	17.21 (17665,7,440,3)
<a href="#">GO:0009221</a>	pyrimidine deoxyribonucleotide biosynthetic process	4.99E-04	2.63E-02	17.21 (17665,7,440,3)
<a href="#">GO:1901137</a>	carbohydrate derivative biosynthetic process	5.19E-04	2.73E-02	2.15 (17665,430,440,23)
<a href="#">GO:0007099</a>	centriole replication	5.45E-04	2.86E-02	10.04 (17665,16,440,4)
<a href="#">GO:0043044</a>	ATP-dependent chromatin remodeling	5.45E-04	2.85E-02	4.28 (17665,75,440,8)
<a href="#">GO:0009127</a>	purine nucleoside monophosphate biosynthetic process	5.45E-04	2.84E-02	4.28 (17665,75,440,8)
<a href="#">GO:0000079</a>	regulation of cyclin-dependent protein serine/threonine kinase activity	5.57E-04	2.89E-02	3.84 (17665,94,440,9)
<a href="#">GO:0051128</a>	regulation of cellular component organization	5.65E-04	2.93E-02	1.41 (17665,2455,440,86)
<a href="#">GO:0051642</a>	centrosome localization	5.74E-04	2.96E-02	7.17 (17665,28,440,5)
<a href="#">GO:0019439</a>	aromatic compound catabolic process	5.98E-04	3.08E-02	2.09 (17665,462,440,24)
<a href="#">GO:0033567</a>	DNA replication, Okazaki fragment processing	6.19E-04	3.17E-02	40.15 (17665,2,440,2)

<a href="#">GO:0046271</a>	phenylpropanoid catabolic process	6.19E-04	3.16E-02	40.15 (17665,2,440,2)
<a href="#">GO:0046226</a>	coumarin catabolic process	6.19E-04	3.15E-02	40.15 (17665,2,440,2)
<a href="#">GO:0046365</a>	monosaccharide catabolic process	6.33E-04	3.21E-02	4.76 (17665,59,440,7)
<a href="#">GO:1901361</a>	organic cyclic compound catabolic process	6.76E-04	3.42E-02	2.03 (17665,494,440,25)
<a href="#">GO:0061842</a>	microtubule organizing center localization	6.79E-04	3.42E-02	6.92 (17665,29,440,5)
<a href="#">GO:0007096</a>	regulation of exit from mitosis	6.98E-04	3.51E-02	9.45 (17665,17,440,4)
<a href="#">GO:0051782</a>	negative regulation of cell division	6.98E-04	3.50E-02	9.45 (17665,17,440,4)
<a href="#">GO:0009200</a>	deoxyribonucleoside triphosphate metabolic process	6.98E-04	3.49E-02	9.45 (17665,17,440,4)
<a href="#">GO:0046653</a>	tetrahydrofolate metabolic process	6.98E-04	3.48E-02	9.45 (17665,17,440,4)
<a href="#">GO:0009117</a>	nucleotide metabolic process	7.17E-04	3.56E-02	2.06 (17665,468,440,24)
<a href="#">GO:0060249</a>	anatomical structure homeostasis	7.46E-04	3.69E-02	2.42 (17665,282,440,17)
<a href="#">GO:0009132</a>	nucleoside diphosphate metabolic process	7.73E-04	3.81E-02	4.07 (17665,79,440,8)
<a href="#">GO:0009206</a>	purine ribonucleoside triphosphate biosynthetic process	7.75E-04	3.81E-02	4.61 (17665,61,440,7)
<a href="#">GO:0009179</a>	purine ribonucleoside diphosphate metabolic process	7.75E-04	3.80E-02	4.61 (17665,61,440,7)
<a href="#">GO:0009135</a>	purine nucleoside diphosphate metabolic process	7.75E-04	3.79E-02	4.61 (17665,61,440,7)
<a href="#">GO:0048518</a>	positive regulation of biological process	7.82E-04	3.81E-02	1.22 (17665,5832,440,177)
<a href="#">GO:0034723</a>	DNA replication-dependent nucleosome organization	7.83E-04	3.80E-02	15.06 (17665,8,440,3)
<a href="#">GO:0006335</a>	DNA replication-dependent nucleosome assembly	7.83E-04	3.79E-02	15.06 (17665,8,440,3)
<a href="#">GO:1901993</a>	regulation of meiotic cell cycle phase transition	7.83E-04	3.78E-02	15.06 (17665,8,440,3)
<a href="#">GO:0075713</a>	establishment of integrated proviral latency	7.83E-04	3.76E-02	15.06 (17665,8,440,3)
<a href="#">GO:0090235</a>	regulation of metaphase plate congression	7.83E-04	3.75E-02	15.06 (17665,8,440,3)
<a href="#">GO:0051299</a>	centrosome separation	7.83E-04	3.74E-02	15.06 (17665,8,440,3)
<a href="#">GO:0009157</a>	deoxyribonucleoside monophosphate biosynthetic process	7.83E-04	3.73E-02	15.06 (17665,8,440,3)
<a href="#">GO:0006284</a>	base-excision repair	7.98E-04	3.79E-02	6.69 (17665,30,440,5)
<a href="#">GO:0031297</a>	replication fork processing	7.98E-04	3.78E-02	6.69 (17665,30,440,5)
<a href="#">GO:1901976</a>	regulation of cell cycle checkpoint	7.98E-04	3.77E-02	6.69 (17665,30,440,5)
<a href="#">GO:0046700</a>	heterocycle catabolic process	8.28E-04	3.89E-02	2.08 (17665,445,440,23)
<a href="#">GO:0009145</a>	purine nucleoside triphosphate biosynthetic process	8.56E-04	4.01E-02	4.53 (17665,62,440,7)
<a href="#">GO:0016445</a>	somatic diversification of immunoglobulins	9.33E-04	4.36E-02	6.48 (17665,31,440,5)
<a href="#">GO:0051321</a>	meiotic cell cycle	9.42E-04	4.39E-02	4.46 (17665,63,440,7)

**Enriched gene sets in 4-1BB<sup>neg</sup> cells**

GO term	Description	P-value	FDR q-value	Enrichment (N, B, n, b)
<a href="#">GO:0010941</a>	<b>regulation of cell death</b>	3.98E-09	2.28E-06	1.85 (17665,1621,541,92)
<a href="#">GO:0042981</a>	<b>regulation of apoptotic process</b>	9.79E-09	4.89E-06	1.88 (17665,1479,541,85)
<a href="#">GO:0048585</a>	<b>negative regulation of response to stimulus</b>	1.04E-08	5.05E-06	1.84 (17665,1579,541,89)
<a href="#">GO:0031324</a>	<b>negative regulation of cellular metabolic process</b>	1.91E-08	7.76E-06	1.62 (17665,2502,541,124)
<a href="#">GO:0002698</a>	<b>negative regulation of immune effector process</b>	4.38E-06	6.40E-04	4.05 (17665,121,541,15)
<a href="#">GO:1902532</a>	negative regulation of intracellular signal transduction	1.14E-08	5.18E-06	2.67 (17665,501,541,41)
<a href="#">GO:0032269</a>	negative regulation of cellular protein metabolic process	2.30E-07	6.03E-05	1.99 (17665,1003,541,61)
<a href="#">GO:0048519</a>	negative regulation of biological process	7.96E-08	2.68E-05	1.36 (17665,5112,541,213)
<a href="#">GO:0019222</a>	regulation of metabolic process	1.90E-10	2.45E-07	1.36 (17665,6503,541,270)
<a href="#">GO:0043065</a>	positive regulation of apoptotic process	2.21E-10	2.63E-07	2.65 (17665,628,541,51)



<a href="#">GO:0065007</a>	biological regulation	2.27E-10	2.51E-07	1.19 (17665,11627,541,422)
<a href="#">GO:0001817</a>	regulation of cytokine production	2.75E-10	2.84E-07	2.55 (17665,692,541,54)
<a href="#">GO:0043068</a>	positive regulation of programmed cell death	3.09E-10	2.99E-07	2.63 (17665,634,541,51)
<a href="#">GO:0031323</a>	regulation of cellular metabolic process	3.13E-10	2.85E-07	1.38 (17665,6006,541,253)
<a href="#">GO:0050794</a>	regulation of cellular process	3.24E-10	2.78E-07	1.22 (17665,10323,541,385)
<a href="#">GO:0010942</a>	positive regulation of cell death	5.52E-10	4.50E-07	2.53 (17665,685,541,53)
<a href="#">GO:0032268</a>	regulation of cellular protein metabolic process	6.82E-10	5.28E-07	1.68 (17665,2552,541,131)
<a href="#">GO:0080090</a>	regulation of primary metabolic process	1.17E-09	8.65E-07	1.37 (17665,5865,541,246)
<a href="#">GO:0065009</a>	regulation of molecular function	1.49E-09	1.05E-06	1.61 (17665,2904,541,143)
<a href="#">GO:0051246</a>	regulation of protein metabolic process	1.73E-09	1.16E-06	1.63 (17665,2722,541,136)
<a href="#">GO:0046649</a>	lymphocyte activation	3.53E-09	2.28E-06	3.15 (17665,352,541,34)
<a href="#">GO:0043067</a>	regulation of programmed cell death	3.73E-09	2.31E-06	1.90 (17665,1497,541,87)
<a href="#">GO:0051171</a>	regulation of nitrogen compound metabolic process	3.87E-09	2.31E-06	1.37 (17665,5689,541,238)
<a href="#">GO:0002376</a>	immune system process	6.12E-21	9.47E-17	2.20 (17665,2133,541,144)
<a href="#">GO:0045321</a>	leukocyte activation	6.74E-14	5.22E-10	2.63 (17665,882,541,71)
<a href="#">GO:0001775</a>	cell activation	1.28E-13	6.63E-10	2.49 (17665,996,541,76)
<a href="#">GO:0007166</a>	cell surface receptor signaling pathway	1.59E-13	6.15E-10	1.92 (17665,2142,541,126)
<a href="#">GO:0002682</a>	regulation of immune system process	4.66E-13	1.44E-09	2.12 (17665,1506,541,98)
<a href="#">GO:0002252</a>	immune effector process	6.87E-13	1.77E-09	2.51 (17665,925,541,71)
<a href="#">GO:0048583</a>	regulation of response to stimulus	1.42E-12	3.15E-09	1.57 (17665,4043,541,195)
<a href="#">GO:0050789</a>	regulation of biological process	2.43E-11	4.71E-08	1.21 (17665,10991,541,408)
<a href="#">GO:1902531</a>	regulation of intracellular signal transduction	3.19E-11	5.48E-08	1.90 (17665,1836,541,107)
<a href="#">GO:0050776</a>	regulation of immune response	7.59E-11	1.17E-07	2.30 (17665,980,541,69)
<a href="#">GO:0048518</a>	positive regulation of biological process	1.19E-10	1.67E-07	1.39 (17665,5832,541,249)
<a href="#">GO:0048522</a>	positive regulation of cellular process	2.46E-08	9.75E-06	1.37 (17665,5162,541,217)
<a href="#">GO:0031399</a>	regulation of protein modification process	3.02E-08	1.17E-05	1.75 (17665,1791,541,96)
<a href="#">GO:0042110</a>	T cell activation	3.71E-08	1.40E-05	3.70 (17665,212,541,24)
<a href="#">GO:0002521</a>	leukocyte differentiation	3.73E-08	1.38E-05	3.20 (17665,296,541,29)
<a href="#">GO:0050900</a>	leukocyte migration	5.01E-08	1.80E-05	3.16 (17665,300,541,29)
<a href="#">GO:0030217</a>	T cell differentiation	6.79E-08	2.39E-05	4.87 (17665,114,541,17)
<a href="#">GO:0009896</a>	positive regulation of catabolic process	7.74E-08	2.66E-05	2.69 (17665,437,541,36)
<a href="#">GO:0007165</a>	signal transduction	8.11E-08	2.67E-05	1.39 (17665,4607,541,196)
<a href="#">GO:0050896</a>	response to stimulus	9.77E-08	3.15E-05	1.35 (17665,5275,541,218)
<a href="#">GO:0043549</a>	regulation of kinase activity	9.86E-08	3.11E-05	2.11 (17665,865,541,56)
<a href="#">GO:0009966</a>	regulation of signal transduction	9.93E-08	3.07E-05	1.52 (17665,3013,541,140)
<a href="#">GO:0042325</a>	regulation of phosphorylation	1.02E-07	3.09E-05	1.78 (17665,1558,541,85)

<a href="#">GO:0009892</a>	negative regulation of metabolic process	1.17E-07	3.49E-05	1.54 (17665,2828,541,133)
<a href="#">GO:0030155</a>	regulation of cell adhesion	1.35E-07	3.96E-05	2.25 (17665,696,541,48)
<a href="#">GO:0030098</a>	lymphocyte differentiation	1.43E-07	4.11E-05	3.56 (17665,211,541,23)
<a href="#">GO:0048523</a>	negative regulation of cellular process	1.47E-07	4.14E-05	1.38 (17665,4583,541,194)
<a href="#">GO:0080134</a>	regulation of response to stress	1.51E-07	4.16E-05	1.78 (17665,1522,541,83)
<a href="#">GO:0051248</a>	negative regulation of protein metabolic process	1.56E-07	4.25E-05	1.97 (17665,1062,541,64)
<a href="#">GO:0070887</a>	cellular response to chemical stimulus	2.20E-07	5.88E-05	1.73 (17665,1662,541,88)
<a href="#">GO:0009968</a>	negative regulation of signal transduction	2.31E-07	5.95E-05	1.88 (17665,1217,541,70)
<a href="#">GO:0051716</a>	cellular response to stimulus	2.93E-07	7.43E-05	1.52 (17665,2790,541,130)
<a href="#">GO:0071310</a>	cellular response to organic substance	2.94E-07	7.33E-05	1.82 (17665,1347,541,75)
<a href="#">GO:0019220</a>	regulation of phosphate metabolic process	3.03E-07	7.45E-05	1.70 (17665,1751,541,91)
<a href="#">GO:0051174</a>	regulation of phosphorus metabolic process	3.11E-07	7.52E-05	1.70 (17665,1752,541,91)
<a href="#">GO:0031329</a>	regulation of cellular catabolic process	3.61E-07	8.60E-05	2.05 (17665,877,541,55)
<a href="#">GO:0006955</a>	immune response	4.36E-07	1.02E-04	1.98 (17665,975,541,59)
<a href="#">GO:0001819</a>	positive regulation of cytokine production	5.20E-07	1.20E-04	2.57 (17665,432,541,34)
<a href="#">GO:1902105</a>	regulation of leukocyte differentiation	5.79E-07	1.32E-04	3.02 (17665,281,541,26)
<a href="#">GO:0010646</a>	regulation of cell communication	5.82E-07	1.31E-04	1.45 (17665,3386,541,150)
<a href="#">GO:0031347</a>	regulation of defense response	6.30E-07	1.39E-04	2.08 (17665,801,541,51)
<a href="#">GO:0001932</a>	regulation of protein phosphorylation	6.35E-07	1.38E-04	1.77 (17665,1399,541,76)
<a href="#">GO:0051172</a>	negative regulation of nitrogen compound metabolic process	6.71E-07	1.44E-04	1.56 (17665,2339,541,112)
<a href="#">GO:0045859</a>	regulation of protein kinase activity	7.67E-07	1.63E-04	2.10 (17665,761,541,49)
<a href="#">GO:0035556</a>	intracellular signal transduction	7.74E-07	1.62E-04	1.71 (17665,1583,541,83)
<a href="#">GO:0002764</a>	immune response-regulating signaling pathway	7.91E-07	1.63E-04	2.52 (17665,440,541,34)
<a href="#">GO:0031325</a>	positive regulation of cellular metabolic process	8.87E-07	1.81E-04	1.45 (17665,3239,541,144)
<a href="#">GO:0002683</a>	negative regulation of immune system process	9.24E-07	1.86E-04	2.51 (17665,443,541,34)
<a href="#">GO:0002757</a>	immune response-activating signal transduction	1.09E-06	2.17E-04	2.57 (17665,406,541,32)
<a href="#">GO:0002274</a>	myeloid leukocyte activation	1.10E-06	2.16E-04	2.28 (17665,572,541,40)
<a href="#">GO:0002697</a>	regulation of immune effector process	1.14E-06	2.22E-04	2.62 (17665,387,541,31)
<a href="#">GO:0023051</a>	regulation of signaling	1.19E-06	2.27E-04	1.43 (17665,3426,541,150)
<a href="#">GO:0051249</a>	regulation of lymphocyte activation	1.21E-06	2.28E-04	2.52 (17665,428,541,33)
<a href="#">GO:0010508</a>	positive regulation of autophagy	1.23E-06	2.30E-04	4.21 (17665,124,541,16)
<a href="#">GO:0006950</a>	response to stress	1.42E-06	2.62E-04	1.47 (17665,2955,541,133)
<a href="#">GO:0006952</a>	defense response	1.49E-06	2.71E-04	1.84 (17665,1133,541,64)
<a href="#">GO:0010506</a>	regulation of autophagy	1.56E-06	2.81E-04	2.74 (17665,334,541,28)
<a href="#">GO:0045637</a>	regulation of myeloid cell differentiation	1.72E-06	3.05E-04	3.19 (17665,225,541,22)
<a href="#">GO:0010648</a>	negative regulation of cell communication	1.74E-06	3.07E-04	1.77 (17665,1311,541,71)

<a href="#">GO:0051056</a>	regulation of small GTPase mediated signal transduction	1.77E-06	3.08E-04	2.78 (17665,317,541,27)
<a href="#">GO:0051338</a>	regulation of transferase activity	1.81E-06	3.12E-04	1.92 (17665,971,541,57)
<a href="#">GO:0023057</a>	negative regulation of signaling	1.89E-06	3.22E-04	1.76 (17665,1314,541,71)
<a href="#">GO:0002366</a>	leukocyte activation involved in immune response	1.95E-06	3.28E-04	2.21 (17665,607,541,41)
<a href="#">GO:0010605</a>	negative regulation of macromolecule metabolic process	2.01E-06	3.35E-04	1.50 (17665,2584,541,119)
<a href="#">GO:0002263</a>	cell activation involved in immune response	2.21E-06	3.63E-04	2.19 (17665,610,541,41)
<a href="#">GO:0009893</a>	positive regulation of metabolic process	2.34E-06	3.81E-04	1.41 (17665,3523,541,152)
<a href="#">GO:0050863</a>	regulation of T cell activation	2.39E-06	3.85E-04	2.74 (17665,322,541,27)
<a href="#">GO:0046632</a>	alpha-beta T cell differentiation	2.60E-06	4.15E-04	7.35 (17665,40,541,9)
<a href="#">GO:0009615</a>	response to virus	2.69E-06	4.25E-04	2.85 (17665,286,541,25)
<a href="#">GO:0009894</a>	regulation of catabolic process	2.91E-06	4.55E-04	1.89 (17665,986,541,57)
<a href="#">GO:0010033</a>	response to organic substance	2.97E-06	4.59E-04	1.56 (17665,2113,541,101)
<a href="#">GO:1903037</a>	regulation of leukocyte cell-cell adhesion	3.44E-06	5.28E-04	2.75 (17665,309,541,26)
<a href="#">GO:0009967</a>	positive regulation of signal transduction	3.81E-06	5.79E-04	1.66 (17665,1596,541,81)
<a href="#">GO:0002253</a>	activation of immune response	4.14E-06	6.23E-04	2.34 (17665,474,541,34)
<a href="#">GO:0009628</a>	response to abiotic stimulus	4.18E-06	6.22E-04	1.85 (17665,1022,541,58)
<a href="#">GO:0002831</a>	regulation of response to biotic stimulus	4.23E-06	6.23E-04	3.84 (17665,136,541,16)
<a href="#">GO:0006986</a>	response to unfolded protein	4.69E-06	6.79E-04	5.44 (17665,66,541,11)
<a href="#">GO:0045785</a>	positive regulation of cell adhesion	4.89E-06	7.00E-04	2.44 (17665,415,541,31)
<a href="#">GO:0022407</a>	regulation of cell-cell adhesion	5.13E-06	7.29E-04	2.43 (17665,416,541,31)
<a href="#">GO:0042221</a>	response to chemical	6.20E-06	8.72E-04	1.47 (17665,2616,541,118)
<a href="#">GO:0050865</a>	regulation of cell activation	6.83E-06	9.53E-04	2.20 (17665,550,541,37)
<a href="#">GO:1903039</a>	positive regulation of leukocyte cell-cell adhesion	7.04E-06	9.74E-04	3.02 (17665,227,541,21)
<a href="#">GO:0042119</a>	neutrophil activation	7.41E-06	1.02E-03	2.28 (17665,487,541,34)
<a href="#">GO:0002694</a>	regulation of leukocyte activation	7.90E-06	1.07E-03	2.24 (17665,510,541,35)
<a href="#">GO:0009987</a>	cellular process	7.97E-06	1.07E-03	1.10 (17665,13415,541,452)
<a href="#">GO:0036230</a>	granulocyte activation	9.21E-06	1.23E-03	2.26 (17665,492,541,34)
<a href="#">GO:0001776</a>	leukocyte homeostasis	9.29E-06	1.23E-03	5.63 (17665,58,541,10)
<a href="#">GO:0009607</a>	response to biotic stimulus	1.02E-05	1.34E-03	1.89 (17665,883,541,51)
<a href="#">GO:0090084</a>	negative regulation of inclusion body assembly	1.05E-05	1.36E-03	14.84 (17665,11,541,5)
<a href="#">GO:0050688</a>	regulation of defense response to virus	1.12E-05	1.44E-03	4.99 (17665,72,541,11)
<a href="#">GO:1903706</a>	regulation of hemopoiesis	1.19E-05	1.52E-03	2.30 (17665,455,541,32)
<a href="#">GO:0051251</a>	positive regulation of lymphocyte activation	1.38E-05	1.76E-03	2.73 (17665,275,541,23)
<a href="#">GO:0071901</a>	negative regulation of protein serine/threonine kinase activity	1.41E-05	1.77E-03	3.68 (17665,133,541,15)
<a href="#">GO:0002761</a>	regulation of myeloid leukocyte differentiation	1.52E-05	1.89E-03	3.87 (17665,118,541,14)
<a href="#">GO:0051239</a>	regulation of multicellular organismal process	1.60E-05	1.98E-03	1.41 (17665,3066,541,132)
<a href="#">GO:0035966</a>	response to topologically incorrect protein	1.67E-05	2.05E-03	4.79 (17665,75,541,11)

<a href="#">GO:0031400</a>	negative regulation of protein modification process	1.76E-05	2.15E-03	2.10 (17665,574,541,37)
<a href="#">GO:0032479</a>	regulation of type I interferon production	1.84E-05	2.23E-03	3.81 (17665,120,541,14)
<a href="#">GO:0019538</a>	protein metabolic process	1.85E-05	2.22E-03	1.34 (17665,3888,541,160)
<a href="#">GO:1900034</a>	regulation of cellular response to heat	1.90E-05	2.26E-03	4.73 (17665,76,541,11)
<a href="#">GO:0010638</a>	positive regulation of organelle organization	1.93E-05	2.29E-03	2.07 (17665,599,541,38)
<a href="#">GO:0032101</a>	regulation of response to external stimulus	1.94E-05	2.28E-03	1.88 (17665,832,541,48)
<a href="#">GO:0010647</a>	positive regulation of cell communication	1.96E-05	2.28E-03	1.57 (17665,1748,541,84)
<a href="#">GO:0043207</a>	response to external biotic stimulus	2.06E-05	2.38E-03	1.86 (17665,858,541,49)
<a href="#">GO:0050870</a>	positive regulation of T cell activation	2.28E-05	2.62E-03	2.98 (17665,208,541,19)
<a href="#">GO:1902107</a>	positive regulation of leukocyte differentiation	2.44E-05	2.78E-03	3.35 (17665,156,541,16)
<a href="#">GO:0043299</a>	leukocyte degranulation	2.48E-05	2.80E-03	2.18 (17665,494,541,33)
<a href="#">GO:0046631</a>	alpha-beta T cell activation	2.52E-05	2.83E-03	5.65 (17665,52,541,9)
<a href="#">GO:0016239</a>	positive regulation of macroautophagy	2.63E-05	2.93E-03	5.02 (17665,65,541,10)
<a href="#">GO:0001816</a>	cytokine production	2.67E-05	2.96E-03	3.69 (17665,124,541,14)
<a href="#">GO:0043312</a>	neutrophil degranulation	2.67E-05	2.94E-03	2.20 (17665,474,541,32)
<a href="#">GO:0002832</a>	negative regulation of response to biotic stimulus	2.88E-05	3.14E-03	6.37 (17665,41,541,8)
<a href="#">GO:0022409</a>	positive regulation of cell-cell adhesion	2.99E-05	3.24E-03	2.67 (17665,269,541,22)
<a href="#">GO:0060337</a>	type I interferon signaling pathway	3.02E-05	3.24E-03	4.95 (17665,66,541,10)
<a href="#">GO:0002283</a>	neutrophil activation involved in immune response	3.15E-05	3.36E-03	2.19 (17665,478,541,32)
<a href="#">GO:0051336</a>	regulation of hydrolase activity	3.19E-05	3.38E-03	1.68 (17665,1247,541,64)
<a href="#">GO:0046634</a>	regulation of alpha-beta T cell activation	3.26E-05	3.44E-03	4.12 (17665,95,541,12)
<a href="#">GO:0071900</a>	regulation of protein serine/threonine kinase activity	3.28E-05	3.43E-03	2.15 (17665,501,541,33)
<a href="#">GO:0002819</a>	regulation of adaptive immune response	3.34E-05	3.47E-03	3.27 (17665,160,541,16)
<a href="#">GO:0010604</a>	positive regulation of macromolecule metabolic process	3.51E-05	3.63E-03	1.37 (17665,3231,541,136)
<a href="#">GO:0051173</a>	positive regulation of nitrogen compound metabolic process	3.52E-05	3.61E-03	1.39 (17665,3087,541,131)
<a href="#">GO:0050867</a>	positive regulation of cell activation	3.52E-05	3.59E-03	2.46 (17665,332,541,25)
<a href="#">GO:0051704</a>	multi-organism process	3.54E-05	3.58E-03	1.60 (17665,1511,541,74)
<a href="#">GO:0051607</a>	defense response to virus	3.72E-05	3.74E-03	2.98 (17665,197,541,18)
<a href="#">GO:1901652</a>	response to peptide	3.80E-05	3.79E-03	2.35 (17665,375,541,27)
<a href="#">GO:0023056</a>	positive regulation of signaling	3.99E-05	3.96E-03	1.54 (17665,1756,541,83)
<a href="#">GO:0061077</a>	chaperone-mediated protein folding	4.02E-05	3.96E-03	5.34 (17665,55,541,9)
<a href="#">GO:0002768</a>	immune response-regulating cell surface receptor signaling pathway	4.29E-05	4.20E-03	2.43 (17665,336,541,25)
<a href="#">GO:0006464</a>	cellular protein modification process	4.29E-05	4.18E-03	1.40 (17665,2899,541,124)
<a href="#">GO:0036211</a>	protein modification process	4.29E-05	4.15E-03	1.40 (17665,2899,541,124)
<a href="#">GO:1902533</a>	positive regulation of intracellular signal transduction	4.61E-05	4.43E-03	1.73 (17665,1059,541,56)
<a href="#">GO:0002275</a>	myeloid cell activation involved in immune response	4.65E-05	4.45E-03	2.11 (17665,510,541,33)
<a href="#">GO:0050777</a>	negative regulation of immune response	5.00E-05	4.75E-03	3.31 (17665,148,541,15)

<a href="#">GO:0002696</a>	positive regulation of leukocyte activation	5.10E-05	4.81E-03	2.46 (17665,319,541,24)
<a href="#">GO:0045332</a>	phospholipid translocation	5.19E-05	4.87E-03	8.52 (17665,23,541,6)
<a href="#">GO:0030334</a>	regulation of cell migration	5.36E-05	5.00E-03	1.82 (17665,842,541,47)
<a href="#">GO:0051058</a>	negative regulation of small GTPase mediated signal transduction	5.38E-05	4.99E-03	5.16 (17665,57,541,9)
<a href="#">GO:2000271</a>	positive regulation of fibroblast apoptotic process	5.52E-05	5.09E-03	16.33 (17665,8,541,4)
<a href="#">GO:0040012</a>	regulation of locomotion	6.15E-05	5.63E-03	1.75 (17665,970,541,52)
<a href="#">GO:0002429</a>	immune response-activating cell surface receptor signaling pathway	6.35E-05	5.79E-03	2.48 (17665,303,541,23)
<a href="#">GO:0001818</a>	negative regulation of cytokine production	6.75E-05	6.11E-03	2.60 (17665,264,541,21)
<a href="#">GO:1901698</a>	response to nitrogen compound	7.23E-05	6.50E-03	1.79 (17665,877,541,48)
<a href="#">GO:0002431</a>	Fc receptor mediated stimulatory signaling pathway	7.33E-05	6.56E-03	4.47 (17665,73,541,10)
<a href="#">GO:0046578</a>	regulation of Ras protein signal transduction	7.39E-05	6.57E-03	2.94 (17665,189,541,17)
<a href="#">GO:0048872</a>	homeostasis of number of cells	7.93E-05	7.02E-03	3.54 (17665,120,541,13)
<a href="#">GO:0090083</a>	regulation of inclusion body assembly	8.73E-05	7.68E-03	10.20 (17665,16,541,5)
<a href="#">GO:2000514</a>	regulation of CD4-positive, alpha-beta T cell activation	9.31E-05	8.14E-03	4.82 (17665,61,541,9)
<a href="#">GO:0046635</a>	positive regulation of alpha-beta T cell activation	9.31E-05	8.10E-03	4.82 (17665,61,541,9)
<a href="#">GO:0010243</a>	response to organonitrogen compound	9.43E-05	8.15E-03	1.81 (17665,813,541,45)
<a href="#">GO:0042127</a>	regulation of cell proliferation	9.53E-05	8.20E-03	1.55 (17665,1585,541,75)
<a href="#">GO:0009266</a>	response to temperature stimulus	9.85E-05	8.42E-03	3.12 (17665,157,541,15)
<a href="#">GO:0033043</a>	regulation of organelle organization	9.91E-05	8.43E-03	1.63 (17665,1244,541,62)
<a href="#">GO:0016192</a>	vesicle-mediated transport	9.96E-05	8.42E-03	1.54 (17665,1614,541,76)
<a href="#">GO:0043434</a>	response to peptide hormone	1.02E-04	8.56E-03	2.46 (17665,292,541,22)
<a href="#">GO:0009605</a>	response to external stimulus	1.03E-04	8.66E-03	1.56 (17665,1509,541,72)
<a href="#">GO:0044093</a>	positive regulation of molecular function	1.06E-04	8.80E-03	1.51 (17665,1752,541,81)
<a href="#">GO:0034204</a>	lipid translocation	1.10E-04	9.07E-03	7.54 (17665,26,541,6)
<a href="#">GO:0034157</a>	positive regulation of toll-like receptor 7 signaling pathway	1.12E-04	9.20E-03	24.49 (17665,4,541,3)
<a href="#">GO:0006458</a>	'de novo' protein folding	1.13E-04	9.22E-03	6.18 (17665,37,541,7)
<a href="#">GO:0043900</a>	regulation of multi-organism process	1.13E-04	9.22E-03	2.20 (17665,400,541,27)
<a href="#">GO:0009725</a>	response to hormone	1.15E-04	9.32E-03	1.89 (17665,675,541,39)
<a href="#">GO:0046637</a>	regulation of alpha-beta T cell differentiation	1.20E-04	9.70E-03	4.66 (17665,63,541,9)
<a href="#">GO:1903708</a>	positive regulation of hemopoiesis	1.23E-04	9.88E-03	2.82 (17665,197,541,17)
<a href="#">GO:0002250</a>	adaptive immune response	1.27E-04	1.01E-02	2.63 (17665,236,541,19)
<a href="#">GO:0006954</a>	inflammatory response	1.27E-04	1.01E-02	2.12 (17665,447,541,29)
<a href="#">GO:0042326</a>	negative regulation of phosphorylation	1.39E-04	1.09E-02	2.14 (17665,427,541,28)
<a href="#">GO:0070098</a>	chemokine-mediated signaling pathway	1.44E-04	1.13E-02	4.13 (17665,79,541,10)
<a href="#">GO:0043085</a>	positive regulation of catalytic activity	1.45E-04	1.13E-02	1.56 (17665,1419,541,68)
<a href="#">GO:0031327</a>	negative regulation of cellular biosynthetic process	1.46E-04	1.13E-02	1.54 (17665,1526,541,72)
<a href="#">GO:0009890</a>	negative regulation of biosynthetic process	1.46E-04	1.13E-02	1.53 (17665,1553,541,73)
<a href="#">GO:0046580</a>	negative regulation of Ras protein signal transduction	1.47E-04	1.13E-02	5.12 (17665,51,541,8)

<a href="#">GO:0016032</a>	viral process	1.61E-04	1.23E-02	1.86 (17665,686,541,39)
<a href="#">GO:0044403</a>	symbiont process	1.61E-04	1.23E-02	1.86 (17665,686,541,39)
<a href="#">GO:0042026</a>	protein refolding	1.63E-04	1.24E-02	9.07 (17665,18,541,5)
<a href="#">GO:0051240</a>	positive regulation of multicellular organismal process	1.80E-04	1.36E-02	1.50 (17665,1699,541,78)
<a href="#">GO:0001933</a>	negative regulation of protein phosphorylation	1.91E-04	1.44E-02	2.17 (17665,391,541,26)
<a href="#">GO:0040017</a>	positive regulation of locomotion	2.01E-04	1.50E-02	1.96 (17665,551,541,33)
<a href="#">GO:0045671</a>	negative regulation of osteoclast differentiation	2.09E-04	1.56E-02	6.76 (17665,29,541,6)
<a href="#">GO:0051085</a>	chaperone cofactor-dependent protein refolding	2.09E-04	1.55E-02	6.76 (17665,29,541,6)
<a href="#">GO:0045944</a>	positive regulation of transcription by RNA polymerase II	2.11E-04	1.56E-02	1.61 (17665,1174,541,58)
<a href="#">GO:0002440</a>	production of molecular mediator of immune response	2.21E-04	1.62E-02	5.57 (17665,41,541,7)
<a href="#">GO:0051345</a>	positive regulation of hydrolase activity	2.30E-04	1.68E-02	1.79 (17665,747,541,41)
<a href="#">GO:0043254</a>	regulation of protein complex assembly	2.31E-04	1.68E-02	2.05 (17665,463,541,29)
<a href="#">GO:0002699</a>	positive regulation of immune effector process	2.37E-04	1.71E-02	2.67 (17665,208,541,17)
<a href="#">GO:2000106</a>	regulation of leukocyte apoptotic process	2.41E-04	1.74E-02	3.89 (17665,84,541,10)
<a href="#">GO:0070213</a>	protein auto-ADP-ribosylation	2.42E-04	1.73E-02	11.87 (17665,11,541,4)
<a href="#">GO:0032870</a>	cellular response to hormone stimulus	2.47E-04	1.76E-02	2.26 (17665,332,541,23)
<a href="#">GO:0043408</a>	regulation of MAPK cascade	2.56E-04	1.82E-02	1.81 (17665,702,541,39)
<a href="#">GO:2000145</a>	regulation of cell motility	2.61E-04	1.85E-02	1.70 (17665,901,541,47)
<a href="#">GO:1902106</a>	negative regulation of leukocyte differentiation	2.65E-04	1.86E-02	3.56 (17665,101,541,11)
<a href="#">GO:0051130</a>	positive regulation of cellular component organization	2.72E-04	1.90E-02	1.58 (17665,1238,541,60)
<a href="#">GO:0034155</a>	regulation of toll-like receptor 7 signaling pathway	2.73E-04	1.90E-02	19.59 (17665,5,541,3)
<a href="#">GO:0001780</a>	neutrophil homeostasis	2.73E-04	1.89E-02	19.59 (17665,5,541,3)
<a href="#">GO:0002433</a>	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis	2.74E-04	1.89E-02	4.20 (17665,70,541,9)
<a href="#">GO:0038096</a>	Fc-gamma receptor signaling pathway involved in phagocytosis	2.74E-04	1.88E-02	4.20 (17665,70,541,9)
<a href="#">GO:0010629</a>	negative regulation of gene expression	2.79E-04	1.91E-02	1.48 (17665,1723,541,78)
<a href="#">GO:0016241</a>	regulation of macroautophagy	2.88E-04	1.97E-02	2.83 (17665,173,541,15)
<a href="#">GO:0044267</a>	cellular protein metabolic process	2.97E-04	2.02E-02	1.32 (17665,3206,541,130)
<a href="#">GO:0070663</a>	regulation of leukocyte proliferation	2.98E-04	2.01E-02	2.53 (17665,232,541,18)
<a href="#">GO:0032480</a>	negative regulation of type I interferon production	3.01E-04	2.02E-02	5.32 (17665,43,541,7)
<a href="#">GO:0045936</a>	negative regulation of phosphate metabolic process	3.01E-04	2.02E-02	1.93 (17665,540,541,32)
<a href="#">GO:1901700</a>	response to oxygen-containing compound	3.02E-04	2.02E-02	1.55 (17665,1349,541,64)
<a href="#">GO:0050727</a>	regulation of inflammatory response	3.06E-04	2.03E-02	2.11 (17665,403,541,26)
<a href="#">GO:0010563</a>	negative regulation of phosphorus metabolic process	3.11E-04	2.06E-02	1.93 (17665,541,541,32)
<a href="#">GO:0045055</a>	regulated exocytosis	3.19E-04	2.10E-02	1.83 (17665,661,541,37)
<a href="#">GO:0050821</a>	protein stabilization	3.26E-04	2.14E-02	2.80 (17665,175,541,15)
<a href="#">GO:0043412</a>	macromolecule modification	3.35E-04	2.19E-02	1.33 (17665,3098,541,126)
<a href="#">GO:0060326</a>	cell chemotaxis	3.42E-04	2.23E-02	2.68 (17665,195,541,16)
<a href="#">GO:0061515</a>	myeloid cell development	3.48E-04	2.26E-02	5.19 (17665,44,541,7)



<a href="#">GO:0032944</a>	regulation of mononuclear cell proliferation	3.49E-04	2.25E-02	2.58 (17665,215,541,17)
<a href="#">GO:0030154</a>	cell differentiation	3.57E-04	2.29E-02	1.45 (17665,1875,541,83)
<a href="#">GO:0065008</a>	regulation of biological quality	3.68E-04	2.35E-02	1.29 (17665,3636,541,144)
<a href="#">GO:0038094</a>	Fc-gamma receptor signaling pathway	3.77E-04	2.40E-02	4.03 (17665,73,541,9)
<a href="#">GO:0030335</a>	positive regulation of cell migration	3.88E-04	2.46E-02	1.96 (17665,501,541,30)
<a href="#">GO:0009409</a>	response to cold	4.02E-04	2.54E-02	5.08 (17665,45,541,7)
<a href="#">GO:0030162</a>	regulation of proteolysis	4.04E-04	2.54E-02	1.76 (17665,743,541,40)
<a href="#">GO:0033673</a>	negative regulation of kinase activity	4.06E-04	2.54E-02	2.47 (17665,238,541,18)
<a href="#">GO:0048870</a>	cell motility	4.10E-04	2.56E-02	1.66 (17665,945,541,48)
<a href="#">GO:0044419</a>	interspecies interaction between organisms	4.23E-04	2.63E-02	1.69 (17665,870,541,45)
<a href="#">GO:0032652</a>	regulation of interleukin-1 production	4.25E-04	2.63E-02	3.63 (17665,90,541,10)
<a href="#">GO:0051084</a>	'de novo' posttranslational protein folding	4.39E-04	2.71E-02	5.94 (17665,33,541,6)
<a href="#">GO:0043901</a>	negative regulation of multi-organism process	4.42E-04	2.71E-02	2.84 (17665,161,541,14)
<a href="#">GO:0051270</a>	regulation of cellular component movement	4.43E-04	2.71E-02	1.64 (17665,974,541,49)
<a href="#">GO:0030225</a>	macrophage differentiation	4.52E-04	2.75E-02	7.42 (17665,22,541,5)
<a href="#">GO:0050687</a>	negative regulation of defense response to virus	4.52E-04	2.74E-02	7.42 (17665,22,541,5)
<a href="#">GO:0048869</a>	cellular developmental process	4.59E-04	2.78E-02	1.35 (17665,2714,541,112)
<a href="#">GO:0043407</a>	negative regulation of MAP kinase activity	4.62E-04	2.78E-02	3.92 (17665,75,541,9)
<a href="#">GO:0016477</a>	cell migration	4.82E-04	2.89E-02	1.69 (17665,850,541,44)
<a href="#">GO:0032270</a>	positive regulation of cellular protein metabolic process	4.97E-04	2.97E-02	1.48 (17665,1564,541,71)
<a href="#">GO:0043255</a>	regulation of carbohydrate biosynthetic process	5.07E-04	3.02E-02	3.55 (17665,92,541,10)
<a href="#">GO:1901564</a>	organonitrogen compound metabolic process	5.12E-04	3.03E-02	1.23 (17665,4935,541,186)
<a href="#">GO:0032940</a>	secretion by cell	5.13E-04	3.03E-02	1.65 (17665,929,541,47)
<a href="#">GO:0045089</a>	positive regulation of innate immune response	5.19E-04	3.05E-02	2.19 (17665,328,541,22)
<a href="#">GO:2000516</a>	positive regulation of CD4-positive, alpha-beta T cell activation	5.20E-04	3.05E-02	5.76 (17665,34,541,6)
<a href="#">GO:0071495</a>	cellular response to endogenous stimulus	5.20E-04	3.04E-02	1.76 (17665,703,541,38)
<a href="#">GO:0032648</a>	regulation of interferon-beta production	5.28E-04	3.07E-02	4.86 (17665,47,541,7)
<a href="#">GO:0043370</a>	regulation of CD4-positive, alpha-beta T cell differentiation	5.28E-04	3.06E-02	4.86 (17665,47,541,7)
<a href="#">GO:0051247</a>	positive regulation of protein metabolic process	5.32E-04	3.07E-02	1.46 (17665,1650,541,74)
<a href="#">GO:0070432</a>	regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway	5.33E-04	3.07E-02	16.33 (17665,6,541,3)
<a href="#">GO:1903753</a>	negative regulation of p38MAPK cascade	5.33E-04	3.06E-02	16.33 (17665,6,541,3)
<a href="#">GO:0009597</a>	detection of virus	5.33E-04	3.05E-02	16.33 (17665,6,541,3)
<a href="#">GO:1901701</a>	cellular response to oxygen-containing compound	5.36E-04	3.05E-02	1.69 (17665,829,541,43)
<a href="#">GO:0043170</a>	macromolecule metabolic process	5.40E-04	3.06E-02	1.21 (17665,5683,541,210)
<a href="#">GO:0051726</a>	regulation of cell cycle	5.50E-04	3.11E-02	1.58 (17665,1140,541,55)
<a href="#">GO:0097530</a>	granulocyte migration	5.53E-04	3.11E-02	3.51 (17665,93,541,10)
<a href="#">GO:0002262</a>	myeloid cell homeostasis	5.63E-04	3.16E-02	7.10 (17665,23,541,5)
<a href="#">GO:0050860</a>	negative regulation of T cell receptor signaling pathway	5.63E-04	3.15E-02	7.10 (17665,23,541,5)
<a href="#">GO:0043409</a>	negative regulation of MAPK cascade	5.66E-04	3.15E-02	2.77 (17665,165,541,14)

<a href="#">GO:0061024</a>	membrane organization	5.74E-04	3.19E-02	1.77 (17665,682,541,37)
<a href="#">GO:0043550</a>	regulation of lipid kinase activity	5.80E-04	3.21E-02	4.21 (17665,62,541,8)
<a href="#">GO:0045580</a>	regulation of T cell differentiation	5.96E-04	3.29E-02	2.89 (17665,147,541,13)
<a href="#">GO:0051250</a>	negative regulation of lymphocyte activation	5.96E-04	3.27E-02	2.89 (17665,147,541,13)
<a href="#">GO:0051272</a>	positive regulation of cellular component movement	5.97E-04	3.27E-02	1.88 (17665,538,541,31)
<a href="#">GO:0010468</a>	regulation of gene expression	6.00E-04	3.27E-02	1.25 (17665,4369,541,167)
<a href="#">GO:0097191</a>	extrinsic apoptotic signaling pathway	6.02E-04	3.27E-02	3.47 (17665,94,541,10)
<a href="#">GO:0002260</a>	lymphocyte homeostasis	6.02E-04	3.26E-02	4.76 (17665,48,541,7)
<a href="#">GO:1901699</a>	cellular response to nitrogen compound	6.10E-04	3.29E-02	1.95 (17665,468,541,28)
<a href="#">GO:0045622</a>	regulation of T-helper cell differentiation	6.11E-04	3.29E-02	5.60 (17665,35,541,6)
<a href="#">GO:1901214</a>	regulation of neuron death	6.32E-04	3.39E-02	2.20 (17665,311,541,21)
<a href="#">GO:0097237</a>	cellular response to toxic substance	6.47E-04	3.45E-02	3.21 (17665,112,541,11)
<a href="#">GO:0019219</a>	regulation of nucleobase-containing compound metabolic process	6.59E-04	3.51E-02	1.26 (17665,3954,541,153)
<a href="#">GO:0002762</a>	negative regulation of myeloid leukocyte differentiation	6.84E-04	3.63E-02	4.66 (17665,49,541,7)
<a href="#">GO:0001782</a>	B cell homeostasis	6.93E-04	3.66E-02	6.80 (17665,24,541,5)
<a href="#">GO:0031348</a>	negative regulation of defense response	6.96E-04	3.67E-02	2.51 (17665,208,541,16)
<a href="#">GO:0006887</a>	exocytosis	6.98E-04	3.66E-02	1.72 (17665,739,541,39)
<a href="#">GO:0002702</a>	positive regulation of production of molecular mediator of immune response	7.11E-04	3.72E-02	3.40 (17665,96,541,10)
<a href="#">GO:0019216</a>	regulation of lipid metabolic process	7.29E-04	3.80E-02	2.02 (17665,404,541,25)
<a href="#">GO:0006457</a>	protein folding	7.33E-04	3.81E-02	2.50 (17665,209,541,16)
<a href="#">GO:0071214</a>	cellular response to abiotic stimulus	7.38E-04	3.82E-02	2.23 (17665,293,541,20)
<a href="#">GO:0104004</a>	cellular response to environmental stimulus	7.38E-04	3.81E-02	2.23 (17665,293,541,20)
<a href="#">GO:0042542</a>	response to hydrogen peroxide	7.51E-04	3.86E-02	3.15 (17665,114,541,11)
<a href="#">GO:2000116</a>	regulation of cysteine-type endopeptidase activity	7.54E-04	3.86E-02	2.41 (17665,230,541,17)
<a href="#">GO:0043069</a>	negative regulation of programmed cell death	7.60E-04	3.88E-02	1.65 (17665,869,541,44)
<a href="#">GO:0009612</a>	response to mechanical stimulus	7.76E-04	3.95E-02	2.58 (17665,190,541,15)
<a href="#">GO:0051707</a>	response to other organism	7.79E-04	3.96E-02	1.77 (17665,644,541,35)
<a href="#">GO:2000147</a>	positive regulation of cell motility	7.83E-04	3.96E-02	1.87 (17665,523,541,30)
<a href="#">GO:0044260</a>	cellular macromolecule metabolic process	8.04E-04	4.05E-02	1.24 (17665,4426,541,168)
<a href="#">GO:0071236</a>	cellular response to antibiotic	8.08E-04	4.06E-02	3.12 (17665,115,541,11)
<a href="#">GO:2000113</a>	negative regulation of cellular macromolecule biosynthetic process	8.15E-04	4.08E-02	1.49 (17665,1401,541,64)
<a href="#">GO:0050851</a>	antigen receptor-mediated signaling pathway	8.19E-04	4.09E-02	2.56 (17665,191,541,15)
<a href="#">GO:2001235</a>	positive regulation of apoptotic signaling pathway	8.53E-04	4.25E-02	2.66 (17665,172,541,14)
<a href="#">GO:0032946</a>	positive regulation of mononuclear cell proliferation	8.57E-04	4.25E-02	2.92 (17665,134,541,12)
<a href="#">GO:0010822</a>	positive regulation of mitochondrion organization	8.68E-04	4.29E-02	3.10 (17665,116,541,11)
<a href="#">GO:0045670</a>	regulation of osteoclast differentiation	8.86E-04	4.37E-02	3.96 (17665,66,541,8)
<a href="#">GO:0009719</a>	response to endogenous stimulus	8.97E-04	4.41E-02	1.58 (17665,1032,541,50)

<a href="#">GO:0050670</a>	regulation of lymphocyte proliferation	8.98E-04	4.40E-02	2.45 (17665,213,541,16)
<a href="#">GO:2000345</a>	regulation of hepatocyte proliferation	9.07E-04	4.43E-02	8.71 (17665,15,541,4)
<a href="#">GO:0034097</a>	response to cytokine	9.09E-04	4.43E-02	1.83 (17665,552,541,31)
<a href="#">GO:1901098</a>	positive regulation of autophagosome maturation	9.12E-04	4.43E-02	13.99 (17665,7,541,3)
<a href="#">GO:0031349</a>	positive regulation of defense response	9.15E-04	4.43E-02	1.93 (17665,457,541,27)
<a href="#">GO:0010558</a>	negative regulation of macromolecule biosynthetic process	9.16E-04	4.42E-02	1.47 (17665,1462,541,66)
<a href="#">GO:0043066</a>	negative regulation of apoptotic process	9.28E-04	4.46E-02	1.65 (17665,852,541,43)
<a href="#">GO:0032621</a>	interleukin-18 production	9.36E-04	4.49E-02	32.65 (17665,2,541,2)
<a href="#">GO:0010868</a>	negative regulation of triglyceride biosynthetic process	9.36E-04	4.47E-02	32.65 (17665,2,541,2)
<a href="#">GO:0072110</a>	glomerular mesangial cell proliferation	9.36E-04	4.46E-02	32.65 (17665,2,541,2)
<a href="#">GO:1903378</a>	positive regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway	9.36E-04	4.45E-02	32.65 (17665,2,541,2)
<a href="#">GO:0006914</a>	autophagy	9.57E-04	4.53E-02	2.36 (17665,235,541,17)
<a href="#">GO:0061919</a>	process utilizing autophagic mechanism	9.57E-04	4.52E-02	2.36 (17665,235,541,17)
<a href="#">GO:0060548</a>	negative regulation of cell death	9.64E-04	4.54E-02	1.60 (17665,957,541,47)
<a href="#">GO:0002718</a>	regulation of cytokine production involved in immune response	9.74E-04	4.57E-02	3.54 (17665,83,541,9)
<a href="#">GO:0040011</a>	locomotion	9.75E-04	4.56E-02	1.58 (17665,1036,541,50)
<a href="#">GO:0045088</a>	regulation of innate immune response	9.89E-04	4.61E-02	1.95 (17665,436,541,26)