

FET + FDR

Author's published results

Go	samplenum	refnum	samplenoobs	refnoobs	FDR	ID	Term	Number of genes in category	Number of genes hit	pvalue
620 immune system process (GO:0002376)	16	2502	11	18470	0.000951	211	GO:0006952 defense response	835	13	2.5230470620967E-10
364 positive regulation of cell activation (GO:0050867)	7	372	20	20600	0.0029524	225	GO:0009607 response to biotic stimulus	872	13	4.33446460279027E-10
555 regulation of immune system process (GO:0002682)	11	1447	16	19525	0.0041192	239	GO:0006955 immune response	747	12	1.28472247681368E-9
517 defense response (GO:0006952)	10	1191	17	19781	0.0047799	252	GO:0050874 organismal physiological process	1771	13	2.31880326407752E-6
65 respiratory burst (GO:0045730)	3	16	24	20956	0.0055727	266	GO:0006922 cleavage of lamin	2	2	3.39137669157832E-6
157 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent (GO:0002479)	4	76	23	20896	0.0063485	269	GO:0006923 cleavage of cytoskeletal proteins	2	2	3.39137669157832E-6
168 antigen processing and presentation of exogenous peptide antigen via MHC class I (GO:0042593)	4	79	23	20893	0.0063485	272	GO:0050986 response to stimulus	1885	13	4.7855680402664E-6
360 regulation of T cell activation (GO:0050863)	6	315	21	20657	0.0063485	286	GO:0009605 response to external stimulus	472	7	1.63502873588694E-5
373 regulation of leukocyte cell-cell adhesion (GO:1903037)	6	330	21	20642	0.0063485	294	GO:0009613 response to pest, pathogen or parasite	495	7	2.22708492554493E-5
194 antigen processing and presentation of peptide antigen via MHC class I (GO:0002474)	4	94	23	20878	0.0080726	302	GO:0051707 response to other organism	521	7	3.10067995224182E-5
314 antigen processing and presentation (GO:0019882)	5	208	22	20764	0.0080726	310	GO:0009611 response to wounding	364	6	4.20165641002209E-5
390 positive regulation of leukocyte activation (GO:0002696)	6	362	21	20610	0.0080726	317	GO:0042110 T cell activation	45	3	7.80894733362938E-5
452 regulation of cell activation (GO:0050865)	7	562	20	20410	0.0080726	321	GO:0019882 antigen presentation	46	3	8.34362561117226E-5
669 cell surface receptor signaling pathway (GO:0007166)	12	2213	15	18759	0.0080726	325	GO:0006921 disassembly of cell structures during apoptosis	9	2	1.21120211632166E-4
323 positive regulation of T cell activation (GO:0050870)	5	219	22	20753	0.0090276	328	GO:0019835 cytolysis	17	2	4.53418047006444E-4
334 positive regulation of leukocyte cell-cell adhesion (GO:1903039)	5	228	22	20744	0.0102428	331	GO:0046469 lymphocyte activation	83	3	4.82849376699164E-4
414 regulation of cell-cell adhesion (GO:0022407)	6	406	21	20566	0.0103858	335	GO:0006968 cellular defense response	92	3	6.52775758161183E-4
108 positive regulation of leukocyte mediated cytotoxicity (GO:0001912)	3	34	24	20938	0.0122225	339	GO:0045321 immune cell activation	97	3	7.6177423364605E-4
482 innate immune response (GO:0045087)	7	655	20	20317	0.0124267	343	GO:0001775 cell activation	98	3	7.8487774282827E-4
248 cellular response to interferon-gamma (GO:0071346)	4	124	23	20848	0.0146832	347	GO:0019883 antigen presentation, endogenous antigen	27	2	0.00115698470215626
357 positive regulation of cell-cell adhesion (GO:0022409)	5	259	22	20713	0.0146832	350	GO:0019885 antigen processing, endogenous antigen via MHC class I	28	2	0.001244567824124
630 immune response (GO:0006955)	10	1638	17	19334	0.0146832	353	GO:0006950 response to stress	949	7	0.00128290868640215
445 regulation of lymphocyte activation (GO:0051249)	6	465	21	20507	0.0163569	361	GO:0030098 lymphocyte differentiation	34	2	0.00183454362706175
129 positive regulation of cell killing (GO:0031343)	3	43	24	20929	0.0177714	364	GO:0001773 dendritic cell activation	1	1	0.0018686919911932
535 regulation of immune response (GO:0050776)	8	1011	19	19961	0.0178862	366	GO:0030885 regulation of dendritic cell activation	1	1	0.0018686919911932
539 cell activation (GO:0001775)	8	1024	19	19948	0.0188358	368	GO:0030887 positive regulation of dendritic cell activation	1	1	0.0018686919911932
35 positive regulation of CD8-positive, alpha-beta T cell proliferation (GO:2000566)	2	5	25	20967	0.0189679	370	GO:0030333 antigen processing	38	2	0.00228847873380615
286 response to interferon-gamma (GO:0034341)	4	146	23	20826	0.0212143	373	GO:0006932 apoptotic program	47	2	0.00348320341059323
38 positive regulation of CD8-positive, alpha-beta T cell activation (GO:2001187)	2	6	25	20966	0.0227435	376	GO:0031580 lipid raft distribution	2	1	0.00377053260569671
43 regulation of CD8-positive, alpha-beta T cell proliferation (GO:2000564)	2	6	25	20966	0.0227435	378	GO:0031579 lipid raft organization and biogenesis	2	1	0.00377053260569671
148 regulation of leukocyte mediated cytotoxicity (GO:0001910)	3	52	24	20920	0.0232401	380	GO:0051665 lipid raft localization	2	1	0.00377053260569671
467 regulation of leukocyte activation (GO:0002694)	6	526	21	20446	0.0232401	382	GO:0045059 positive thymic T cell selection	2	1	0.00377053260569671
413 positive regulation of lymphocyte activation (GO:0051251)	5	335	22	20637	0.0303250	384	GO:0001766 lipid raft polarization	2	1	0.00377053260569671
316 antigen processing and presentation of exogenous peptide antigen (GO:0002478)	4	169	23	20803	0.0304586	386	GO:0045061 thymic T cell selection	3	1	0.00565071763448033
174 positive regulation of tumor necrosis factor production (GO:0032760)	3	62	24	20910	0.0335520	388	GO:0006954 inflammatory response	200	3	0.00598954977819568
326 antigen processing and presentation of exogenous antigen (GO:0019884)	4	176	23	20796	0.0335520	392	GO:0006874 calcium ion homeostasis	72	2	0.00800574181898028
56 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent (GO:0002480)	2	9	25	20963	0.0342834	395	GO:0051668 localization within membrane	5	1	0.00940095405195562
179 positive regulation of tumor necrosis factor superfamily cytokine production (GO:1903557)	3	64	24	20908	0.0342834	397	GO:0019735 antimicrobial humoral response (sensu Vertebrata)	80	2	0.00980828402935984
328 antigen processing and presentation of peptide antigen (GO:0048002)	4	179	23	20793	0.0342834	400	GO:0030097 hemopoiesis	81	2	0.010045216297965
180 regulation of cell killing (GO:0031341)	3	65	24	20907	0.0345455	403	GO:0048534 hemopoietic or lymphoid organ development	82	2	0.0102846976579692
531 leukocyte activation (GO:0045321)	7	877	20	20095	0.0363751	406	GO:0019730 antimicrobial humoral response	82	2	0.0102846976579692
58 regulation of CD8-positive, alpha-beta T cell activation (GO:2001185)	2	10	25	20962	0.0381712	409	GO:0045058 T cell selection	6	1	0.0112710169758061
200 vascular endothelial growth factor receptor signaling pathway (GO:0048010)	3	74	24	20898	0.0454872	411	GO:0007708 plasma membrane organization and biogenesis	7	1	0.013137717384284
446 positive regulation of cytokine production (GO:0001819)	5	388	22	20584	0.0454872	413	GO:0030005 di-, tri-valent inorganic cation homeostasis	95	2	0.0136256297299144
451 positive regulation of cell adhesion (GO:0045785)	5	401	22	20571	0.0511982	416	GO:0006875 metal ion homeostasis	102	2	0.0155951675960223
505 regulation of cell adhesion (GO:0030155)	6	665	21	20307	0.0567841	419	GO:0045580 regulation of T cell differentiation	9	1	0.0168610536229175
695 positive regulation of response to stimulus (GO:0048584)	10	2099	17	18873	0.0567841	421	GO:0030003 cation homeostasis	108	2	0.0173752850646516
72 superoxide anion generation (GO:0042554)	2	14	25	20958	0.0605344	424	GO:0016064 humoral defense mechanism (sensu Vertebrata)	109	2	0.0176800756392694
377 T cell activation (GO:0042110)	4	225	23	20747	0.0623082	427	GO:0006873 cell ion homeostasis	114	2	0.0192362822889773
241 positive regulation of leukocyte chemotaxis (GO:0002690)	3	87	24	20885	0.0635751	430	GO:0006935 chemotaxis	117	2	0.020200162716105
75 positive regulation of T cell cytokine production (GO:0002729)	2	15	25	20957	0.0645189	433	GO:0042330 taxis	117	2	0.020200162716105
584 positive regulation of immune system process (GO:0002684)	7	1003	20	19969	0.0656313	436	GO:0045619 regulation of lymphocyte differentiation	11	1	0.0205710086105458
85 positive regulation of T cell mediated cytotoxicity (GO:0001916)	2	17	25	20955	0.0751039	438	GO:0007626 locomotory behavior	122	2	0.0218477024171166
86 positive regulation of monocyte chemotaxis (GO:0090026)	2	17	25	20955	0.0751039	441	GO:0050801 ion homeostasis	127	2	0.0235497023464554
253 regulation of interferon-gamma production (GO:0032649)	3	95	24	20877	0.0751039	444	GO:0030101 natural killer cell activation	13	1	0.0242676280415554
813 positive regulation of cellular process (GO:0048522)	15	4846	12	16126	0.0753557	446	GO:0006801 superoxide metabolism	14	1	0.0261109511623843
485 cytokine-mediated signaling pathway (GO:0019221)	5	476	22	20496	0.0886607	448	GO:0019725 cell homeostasis	135	2	0.0263835248031855
278 regulation of leukocyte chemotaxis (GO:0002688)	3	106	24	20866	0.0963572	451	GO:0030217 T cell differentiation	17	1	0.03162104227246
280 regulation of tumor necrosis factor production (GO:0032680)	3	108	24	20864	0.0999136	453	GO:0006959 humoral immune response	150	2	0.0320504983005711
						456	GO:0042592 homeostasis	171	2	0.0407142552000209
						459	GO:0050867 positive regulation of cell activation	24	1	0.0443626898038781
						461	GO:0016066 cellular defense response (sensu Vertebrata)	25	1	0.046169832517954
						463	GO:0007610 behavior	187	2	0.0478470088625235