

FET + FDR

	Go	samplenum	refnum	samplenoobs	refnoobs	FDR
269	extracellular matrix disassembly (GO:0022617)	6	79	86	20893	0.0098429
599	mitotic nuclear division (GO:0007067)	11	382	81	20590	0.0098429
1670	single-organism process (GO:0044699)	77	12622	15	8350	0.0098429
104	positive regulation of granulocyte chemotaxis (GO:0071624)	4	25	88	20947	0.0140845
573	chromosome segregation (GO:0007059)	9	294	83	20678	0.0140845
741	organelle fission (GO:0048285)	12	548	80	20424	0.0140845
862	cell migration (GO:0016477)	15	862	77	20110	0.0140845
1601	single-organism cellular process (GO:0044763)	65	9804	27	11168	0.0140845
707	cell division (GO:0051301)	11	474	81	20498	0.0145129
852	mitotic cell cycle (GO:0000278)	14	792	78	20180	0.0154038
759	nuclear division (GO:0000280)	11	517	81	20455	0.0221544
914	localization of cell (GO:0051674)	15	950	77	20022	0.0221544
915	cell motility (GO:0048870)	15	950	77	20022	0.0221544
308	antimicrobial humoral response (GO:0019730)	5	78	87	20894	0.0324439
872	mitotic cell cycle process (GO:1903047)	13	764	79	20208	0.0324439
176	regulation of granulocyte chemotaxis (GO:0071622)	4	39	88	20933	0.0349211
1761	cellular process (GO:0009987)	82	14854	10	6118	0.0382930
73	sequestering of metal ion (GO:0051238)	3	15	89	20957	0.0527612
1000	cell cycle process (GO:0022402)	15	1089	77	19883	0.0659500
9	neutrophil aggregation (GO:0070488)	2	2	90	20970	0.0852024
108	cellular zinc ion homeostasis (GO:0006882)	3	20	89	20952	0.0966103

Author's published results

ID	Term	Number.of.genes.in.category	Number.of.genes.hit	pvalue
190	GO:0007059 chromosome segregation	35	6	5.36202746576449E-8
197	GO:0000279 M phase	189	7	1.34095775672848E-4
205	GO:0050926 regulation of positive chemotaxis	4	2	2.12573033887526E-4
217	GO:0050927 positive regulation of positive chemotaxis	4	2	2.12573033887526E-4
229	GO:0050918 positive chemotaxis	4	2	2.12573033887526E-4
241	GO:0050930 induction of positive chemotaxis	4	2	2.12573033887526E-4
253	GO:0007067 mitosis	148	6	2.55803464574941E-4
260	GO:0000087 M phase of mitotic cell cycle	150	6	2.75048605293038E-4
267	GO:0050920 regulation of chemotaxis	5	2	3.52909810082872E-4
279	GO:0050921 positive regulation of chemotaxis	5	2	3.52909810082872E-4
291	GO:0051301 cell division	160	6	3.89033488213736E-4
298	GO:0000270 peptidoglycan metabolism	25	3	4.36309556489712E-4
302	GO:0065996 polyamine biosynthesis	7	2	7.3535792801318E-4
305	GO:0000278 mitotic cell cycle	195	6	0.00110075537106273
312	GO:0065995 polyamine metabolism	10	2	0.00155747478335576
315	GO:0007588 excretion	42	3	0.00202442457818816
319	GO:0065976 biogenic amine metabolism	44	3	0.00231556422418221
323	GO:0030595 immune cell chemotaxis	14	2	0.00310097820066174
335	GO:0050900 immune cell migration	14	2	0.00310097820066174
347	GO:0065975 amino acid derivative metabolism	50	3	0.00333993541941618
351	GO:0030574 collagen catabolism	17	2	0.00458079072064237
354	GO:0007049 cell cycle	653	10	0.00538838169729787
365	GO:0000070 mitotic sister chromatid segregation	19	2	0.00571519131444641
368	GO:0009935 nutrient import	1	1	0.00602030730523861
370	GO:0006701 progesterone biosynthesis	1	1	0.00602030730523861
372	GO:0006597 spermine biosynthesis	1	1	0.00602030730523861
374	GO:0008215 spermine metabolism	1	1	0.00602030730523861
376	GO:0015855 pyrimidine transport	1	1	0.00602030730523861
378	GO:0045132 meiotic chromosome segregation	1	1	0.00602030730523861
380	GO:0042127 regulation of cell proliferation	277	6	0.006308801615306
396	GO:0007051 spindle organization and biogenesis	20	2	0.00632566105631813
399	GO:0000819 sister chromatid segregation	20	2	0.00632566105631813
402	GO:0042401 biogenic amine biosynthesis	21	2	0.00696450086180834
405	GO:0006954 inflammatory response	200	5	0.00699179819908507
420	GO:0019722 calcium-mediated signaling	23	2	0.00832588079437378
423	GO:0042398 amino acid derivative biosynthesis	24	2	0.00904772374882653
426	GO:0006863 purine transport	2	1	0.012004908258739
428	GO:0006569 tryptophan catabolism	2	1	0.012004908258739
430	GO:0046218 indolalkylamine catabolism	2	1	0.012004908258739
432	GO:0045090 retroviral genome replication	2	1	0.012004908258739
434	GO:0045091 regulation of retroviral genome replication	2	1	0.012004908258739
436	GO:0015791 polyol transport	2	1	0.012004908258739
438	GO:0046689 response to mercury ion	2	1	0.012004908258739
440	GO:0042448 progesterone metabolism	2	1	0.012004908258739
442	GO:0042436 indole derivative catabolism	2	1	0.012004908258739
444	GO:0051382 kinetochore assembly	2	1	0.012004908258739
446	GO:0051383 kinetochore organization and biogenesis	2	1	0.012004908258739
448	GO:0007242 intracellular signaling cascade	995	12	0.0146885903671481
461	GO:0008054 cyclin catabolism	3	1	0.0179540114443831
463	GO:0006970 response to osmotic stress	3	1	0.0179540114443831
465	GO:0008295 spermidine biosynthesis	3	1	0.0179540114443831
467	GO:0030104 water homeostasis	3	1	0.0179540114443831
469	GO:0030502 negative regulation of bone mineralization	3	1	0.0179540114443831
480	GO:0042119 neutrophil activation	3	1	0.0179540114443831
482	GO:0009611 response to wounding	364	6	0.0219587919320345
498	GO:0000085 G2 phase of mitotic cell cycle	4	1	0.0238678242462189
500	GO:0008216 spermidine metabolism	4	1	0.0238678242462189
502	GO:0046851 negative regulation of bone remodeling	4	1	0.0238678242462189
513	GO:0030279 negative regulation of ossification	4	1	0.0238678242462189
524	GO:0015851 nucleobase transport	4	1	0.0238678242462189
526	GO:0051310 metaphase plate congression	4	1	0.0238678242462189
528	GO:0051319 G2 phase	4	1	0.0238678242462189
530	GO:0000075 cell cycle checkpoint	41	2	0.0251771787800968
533	GO:0019932 second-messenger-mediated signaling	187	4	0.0260419551001039
538	GO:0008015 circulation	109	3	0.027844360338472
542	GO:0031577 spindle checkpoint	5	1	0.0297465528552524
544	GO:0006568 tryptophan metabolism	5	1	0.0297465528552524
546	GO:0050000 chromosome localization	5	1	0.0297465528552524
548	GO:0007094 mitotic spindle checkpoint	5	1	0.0297465528552524
550	GO:0006072 glycerol-3-phosphate metabolism	5	1	0.0297465528552524
552	GO:0042402 biogenic amine catabolism	5	1	0.0297465528552524
554	GO:0051303 establishment of chromosome localization	5	1	0.0297465528552524
556	GO:0008283 cell proliferation	500	7	0.0301408768439179
573	GO:0007126 meiosis	47	2	0.0324364841655954
576	GO:0051321 meiotic cell cycle	47	2	0.0324364841655954
579	GO:0051327 M phase of meiotic cell cycle	47	2	0.0324364841655954
582	GO:0006935 chemotaxis	117	3	0.0333591447266675
595	GO:0042330 taxis	117	3	0.0333591447266675
608	GO:0000226 microtubule cytoskeleton organization and biogenesis	49	2	0.0350181380687131
611	GO:0019674 NAD metabolism	6	1	0.0355904022762081
613	GO:0046580 negative regulation of Ras protein signal transduction	6	1	0.0355904022762081
615	GO:0030593 neutrophil chemotaxis	6	1	0.0355904022762081
617	GO:0009435 NAD biosynthesis	6	1	0.0355904022762081
619	GO:0050684 regulation of mRNA processing	6	1	0.0355904022762081
621	GO:0019229 regulation of vasoconstriction	6	1	0.0355904022762081
623	GO:0042219 amino acid derivative catabolism	6	1	0.0355904022762081
625	GO:0007626 locomotory behavior	122	3	0.0370742005258308
638	GO:0008284 positive regulation of cell proliferation	125	3	0.0394013721313521
651	GO:0006833 water transport	7	1	0.0413995763342399
653	GO:0006586 indolalkylamine metabolism	7	1	0.0413995763342399
655	GO:0010038 response to metal ion	7	1	0.0413995763342399
657	GO:0045069 regulation of viral genome replication	7	1	0.0413995763342399
659	GO:0030500 regulation of bone mineralization	7	1	0.0413995763342399
670	GO:0042044 fluid transport	7	1	0.0413995763342399
672	GO:0051058 negative regulation of smali GTPase mediated signal transduction	7	1	0.0413995763342399
674	GO:0051084 postranslational protein folding	7	1	0.0413995763342399
676	GO:0042430 indole and derivative metabolism	7	1	0.0413995763342399
678	GO:0042434 indole derivative metabolism	7	1	0.0413995763342399
680	GO:0031589 cell-substrate adhesion	54	2	0.0418054334552816
692	GO:0007160 cell-matrix adhesion	54	2	0.0418054334552816
704	GO:0000074 regulation of progression through cell cycle	430	6	0.0442566433010616
711	GO:0051726 regulation of cell cycle	431	6	0.0446748486408944
718	GO:0051656 establishment of organelle localization	8	1	0.0471742776816237
720	GO:0016998 cell wall catabolism	8	1	0.0471742776816237
722	GO:0046578 regulation of Ras protein signal transduction	8	1	0.0471742776816237
724	GO:0042221 response to chemical stimulus	328	5	0.0472060220094024
739	GO:0001525 angiogenesis	58	2	0.0475604030737719