Extended Data Table 2

Up Regulated in APC^Pirc/++OX in relation to wild-type									
NAME	GS follow li	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
NUCLEOLAR PART	NUCLEOLAR P	Details ...	58	-0.6006561	-2.1327953	0	0.0525942	0.055	4810
PARTURITION	PARTURITION	Details ...	18	-0.76409274	-2.103174	0	0.043199193	0.088	1359
NEGATIVE REGULATION OF HORMONE SECRETION	NEGATIVE RE	Details ...	70	-0.5564646	-2.0809677	0	0.04139415	0.123	1315
TRANSLATIONAL ELONGATION	TRANSLATION	Details ...	106	-0.51414555	-2.071338	0	0.03434976	0.135	5412
REGULATION OF TYROSINE PHOSPHORYLATION OF STAT3 PROTEIN	REGULATION	Details ...	38	-0.61759853	-2.0574071	0	0.03441299	0.165	1359
ACUTE PHASE RESPONSE	ACUTE PHASE	Details ...	34	-0.6394826	-2.0536501	0	0.02992805	0.172	976
TRANSLATIONAL TERMINATION	TRANSLATION	Details ...	90	-0.5214301	-2.052021	0	0.026459541	0.178	5033
CELLULAR RESPONSE TO INTERLEUKIN 6	CELLULAR RE	Details ...	20	-0.71682686	-2.0428407	0	0.027400717	0.204	135
CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	CD4 POSITIVE	Details ...	29	-0.6542219	-2.0407088	0	0.025515366	0.212	1359
NEUROPEPTIDE HORMONE ACTIVITY	NEUROPEPTID	Details ...	25	-0.6644572	-2.0165114	0	0.030778589	0.271	3848
RESPONSE TO INTERLEUKIN 6	RESPONSE TO	Details ...	24	-0.6991114	-2.0083828	0	0.03079357	0.292	783
REGULATION OF CIRCADIAN SLEEP WAKE CYCLE	REGULATION	Details ...	23	-0.6778624	-1.9815817	0	0.041674998	0.401	1359
MITOCHONDRIAL TRANSLATION	MITOCHONDR	Details ...	103	-0.49125695	-1.9778397	0	0.040424347	0.416	5033
CELLULAR RESPONSE TO CORTICOSTEROID STIMULUS	CELLULAR RE	Details ...	55	-0.5542193	-1.9655665	0	0.04424591	0.477	459
RESPONSE TO INTERLEUKIN 1	RESPONSE TO	Details ...	91	-0.49679404	-1.9585394	0	0.045131046	0.516	1171
PRERIBOSOME	PRERIBOSOM	Details ...	52	-0.5536905	-1.9569926	0	0.04265956	0.518	5581
MONOCYTE CHEMOTAXIS	MONOCYTE C	Details ...	25	-0.66094345	-1.9483496	0	0.04529107	0.561	470
POSITIVE REGULATION OF T HELPER CELL DIFFERENTIATION	POSITIVE REG	Details ...	15	-0.7229009	-1.9468211	0.002105263	0.043553904	0.568	2
REGULATION OF VASODILATION	REGULATION	Details ...	42	-0.56943715	-1.9215052	0	0.057796985	0.694	2209
PEPTIDE SECRETION	PEPTIDE SECR	Details ...	55	-0.53095704	-1.9176296	0	0.05707113	0.703	319
MATURATION OF SSU RRNA	MATURATION	Details ...	39	-0.5764421	-1.9105362	0	0.058608096	0.724	4894
RIBOSOME BIOGENESIS	RIBOSOME BI	Details ...	280	-0.41458735	-1.9035401	0	0.06043072	0.753	4909
REGULATION OF T HELPER CELL DIFFERENTIATION	REGULATION	Details ...	19	-0.6855839	-1.9009429	0.002227172	0.0598399	0.764	2
POSITIVE REGULATION OF TYROSINE PHOSPHORYLATION OF STAT3 PR	POSITIVE REG	Details ...	31	-0.607626	-1.899474	0	0.05859747	0.771	1359
ARACHIDONIC ACID METABOLIC PROCESS	ARACHIDONIC	Details ...	30	-0.6091334	-1.8987209	0	0.05666881	0.772	1316
NEGATIVE REGULATION OF BEHAVIOR	NEGATIVE RE	Details ...	16	-0.7276433	-1.8984941	0	0.054633893	0.773	1359
RIBOSOME	RIBOSOME	Details ...	205	-0.43139622	-1.8959061	0	0.05382831	0.783	6908
NEUTROPHIL MEDIATED IMMUNITY	NEUTROPHIL	Details ...	15	-0.7247133	-1.8949344	0.002057613	0.05227384	0.785	275
SMALL NUCLEOLAR RIBONUCLEOPROTEIN COMPLEX	SMALL NUCLE	Details ...	18	-0.689783	-1.8903326	0	0.053187467	0.806	3711
REGULATION OF NEUROTRANSMITTER UPTAKE	REGULATION	Details ...	15	-0.7222038	-1.8896916	0	0.051758274	0.809	161
ARGININE METABOLIC PROCESS	ARGININE MET	Details ...	17	-0.68985146	-1.8859904	0.002192983	0.0527589	0.828	484
NEUROPEPTIDE SIGNALING PATHWAY	NEUROPEPTID	Details ...	76	-0.49999642	-1.8819045	0	0.053985182	0.843	2640
HORMONE ACTIVITY	HORMONE AC	Details ...	86	-0.48289585	-1.8786637	0	0.05448446	0.853	1128
RESPONSE TO DEXAMETHASONE	RESPONSE TO	Details ...	33	-0.58670306	-1.8772223	0	0.05401279	0.859	1038
DEFENSE RESPONSE TO GRAM POSITIVE BACTERIUM	DEFENSE RES	Details ...	45	-0.5426134	-1.8711301	0.002227172	0.05619107	0.877	360
CELLULAR RESPONSE TO DEXAMETHASONE STIMULUS	CELLULAR RE	Details ...	27	-0.6205979	-1.8705033	0	0.05502473	0.878	459
PEPTIDE HORMONE RECEPTOR BINDING	PEPTIDE HOR	Details ...	16	-0.71249783	-1.870344	0	0.05371582	0.878	1038
NEGATIVE REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS	NEGATIVE RE	Details ...	23	-0.6406753	-1.8698264	0	0.052722864	0.879	197
REGULATION OF NEUROLOGICAL SYSTEM PROCESS	REGULATION	Details ...	61	-0.51299596	-1.8697813	0	0.051370997	0.879	1373
RIBOSOME ASSEMBLY	RIBOSOME AS	Details ...	47	-0.54161465	-1.8631577	0.002375297	0.053890973	0.898	4181
RRNA METABOLIC PROCESS	RRNA METAB	Details ...	232	-0.42109925	-1.8628715	0	0.05273684	0.898	5924

ALPHA BETA T CELL ACTIVATION	ALPHA BETA T	Details ...	42	-0.551507	-1.8624436	0	0.051684488	0.9	1359
REGULATION OF RENAL SYSTEM PROCESS	REGULATION	Details ...	34	-0.5793682	-1.8566442	0	0.053712733	0.909	2943
90S PRERIBOSOME	90S PRERIBOS	Details ...	22	-0.6464757	-1.8565722	0.006564552	0.052556306	0.909	5017
POSITIVE REGULATION OF SMOOTH MUSCLE CONTRACTION	POSITIVE REG	Details ...	26	-0.6096725	-1.8508208	0.002020202	0.054939564	0.923	1023
REGULATION OF NITRIC OXIDE SYNTHASE BIOSYNTHETIC PROCESS	REGULATION	Details ...	16	-0.6895947	-1.8404835	0.00210084	0.060514305	0.944	1359
POSITIVE REGULATION OF VASODILATION	POSITIVE REG	Details ...	29	-0.59542114	-1.8394903	0	0.059689015	0.944	900
RESPONSE TO COLD	RESPONSE TO	Details ...	37	-0.5528324	-1.8353885	0.002192983	0.061184622	0.951	1150
POSITIVE REGULATION OF INFLAMMATORY RESPONSE	POSITIVE REG	Details ...	83	-0.46864662	-1.8312312	0	0.0628278	0.956	917
SMALL SUBUNIT PROCESSOME	SMALL SUBUN	Details ...	30	-0.58187366	-1.8272423	0.002145923	0.06401419	0.963	5765
VASCULAR PROCESS IN CIRCULATORY SYSTEM	VASCULAR PR	Details ...	152	-0.43414718	-1.8268363	0	0.06308989	0.964	2107
INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO ENDOPL	INTRINSIC AP	Details ...	29	-0.57496345	-1.8192376	0.002232143	0.06667311	0.969	2283
NCRNA PROCESSING	NCRNA PROC	Details ...	332	-0.3894126	-1.8188677	0	0.065573536	0.971	5935
POSITIVE REGULATION OF BLOOD CIRCULATION	POSITIVE REG	Details ...	87	-0.47386122	-1.8163941	0	0.066034235	0.975	1023
POSITIVE REGULATION OF IMMUNOGLOBULIN PRODUCTION	POSITIVE REG	Details ...	29	-0.5826723	-1.8153062	0.008810572	0.065484665	0.975	508
PORPHYRIN CONTAINING COMPOUND METABOLIC PROCESS	PORPHYRIN C	Details ...	34	-0.56016403	-1.81263	0.002392344	0.06625171	0.977	3591
ACUTE INFLAMMATORY RESPONSE	ACUTE INFLAM	Details ...	62	-0.49246898	-1.8090931	0	0.06716453	0.98	976
POSITIVE REGULATION OF VASOCONSTRICTION	POSITIVE REG	Details ...	35	-0.55808604	-1.8064594	0.004705882	0.06786971	0.983	1005
REGULATION OF BEHAVIOR	REGULATION	Details ...	55	-0.50086963	-1.8056107	0	0.067197666	0.983	1569
REGULATION OF EXCRETION	REGULATION	Details ...	27	-0.58789206	-1.801138	0.006741573	0.06911023	0.986	1359
LARGE RIBOSOMAL SUBUNIT	LARGE RIBOS	Details ...	85	-0.46640182	-1.799376	0	0.06899603	0.988	6761
REGULATION OF RENAL SODIUM EXCRETION	REGULATION	Details ...	22	-0.6254262	-1.7989463	0.010729614	0.06820163	0.988	2338
REGULATION OF SYNAPTIC TRANSMISSION DOPAMINERGIC	REGULATION	Details ...	16	-0.67172843	-1.7976642	0.006355932	0.068061754	0.989	138
RIBOSOMAL SUBUNIT	RIBOSOMAL S	Details ...	149	-0.41884616	-1.7883054	0	0.073387496	0.993	7124
RRNA TRANSCRIPTION	RRNA TRANS	Details ...	16	-0.6773662	-1.7872491	0.002061856	0.07292507	0.994	1062
SYNAPTIC TRANSMISSION CHOLINERGIC	SYNAPTIC TRA	Details ...	31	-0.562881	-1.7865131	0	0.07241493	0.995	4307
NCRNA METABOLIC PROCESS	NCRNA META	Details ...	451	-0.37245378	-1.7856072	0	0.07198153	0.995	5986
RESPONSE TO SALT	RESPONSE TO	Details ...	16	-0.67460734	-1.7760954	0.002087683	0.07748433	0.998	1359
POSITIVE REGULATION OF AMINE TRANSPORT	POSITIVE REG	Details ...	32	-0.55732644	-1.7756541	0.004310345	0.0766345	0.999	386
MATURATION OF SSU RRNA FROM TRICISTRONIC RRNA TRANSCRIPT	MATURATION	Details ...	32	-0.5586658	-1.7755531	0.006864989	0.0756209	0.999	4894
NEUROPEPTIDE RECEPTOR BINDING	NEUROPEPTID	Details ...	23	-0.6144161	-1.7745613	0.002132196	0.075324066	0.999	1038
POSITIVE REGULATION OF NEUROLOGICAL SYSTEM PROCESS	POSITIVE REG	Details ...	17	-0.65589446	-1.7711015	0.004273505	0.07657306	0.999	716
ALPHA BETA T CELL DIFFERENTIATION	ALPHA BETA T	Details ...	37	-0.54395115	-1.7666535	0.004672897	0.079118565	0.999	1359
DEATH RECEPTOR BINDING	DEATH RECEP	Details ...	17	-0.6517083	-1.7654413	0.00409836	0.07893731	0.999	4370
REGULATION OF RESPONSE TO INTERFERON GAMMA	REGULATION	Details ...	22	-0.6064194	-1.7622092	0.006410257	0.080279015	0.999	299
T CELL DIFFERENTIATION INVOLVED IN IMMUNE RESPONSE	T CELL DIFFER	Details ...	24	-0.5961816	-1.7616808	0.006535948	0.07964152	0.999	140
CELLULAR RESPONSE TO INTERLEUKIN 1	CELLULAR RES	Details ...	67	-0.47468987	-1.7604797	0.002525253	0.07932866	0.999	1359
POSITIVE REGULATION OF MUSCLE CONTRACTION	POSITIVE REG	Details ...	39	-0.5274248	-1.7587407	0.004926108	0.079649255	0.999	400
FERTILIZATION	FERTILIZATION	Details ...	90	-0.4426672	-1.7575744	0	0.079412885	0.999	3191
MATURATION OF 5 8S RRNA	MATURATION	Details ...	27	-0.5572005	-1.7552909	0.004728132	0.08021349	0.999	4716
NEGATIVE REGULATION OF COAGULATION	NEGATIVE REG	Details ...	41	-0.5172662	-1.7550461	0.002403846	0.07939759	0.999	1917
ORGAN OR TISSUE SPECIFIC IMMUNE RESPONSE	ORGAN OR TIS	Details ...	17	-0.656976	-1.7540039	0.010373444	0.079255655	0.999	44
RESPONSE TO AMINE	RESPONSE TO	Details ...	45	-0.51388276	-1.7515258	0.002283105	0.08031664	0.999	739
REACTIVE NITROGEN SPECIES METABOLIC PROCESS	REACTIVE NIT	Details ...	17	-0.6334953	-1.7510895	0.008385744	0.07971953	0.999	1839

NEGATIVE REGULATION OF FAT CELL DIFFERENTIATION	NEGATIVE REG	Details ...	36	-0.532201	-1.7431977	0.004444445	0.084675536	0.999	319
REGULATION OF IMMUNOGLOBULIN PRODUCTION	REGULATION O	Details ...	44	-0.50745904	-1.7398577	0.002386635	0.086245276	1	1368
REGULATION OF GLUCONEOGENESIS	REGULATION O	Details ...	32	-0.5385388	-1.7388082	0.006622517	0.08608628	1	52
RESPONSE TO IMMOBILIZATION STRESS	RESPONSE TO	Details ...	20	-0.6245355	-1.7342497	0.008849558	0.08880805	1	1401
HEME METABOLIC PROCESS	HEME METABO	Details ...	28	-0.5546032	-1.730616	0.004555809	0.0910437	1	3591
RIBONUCLEOPROTEIN COMPLEX BIOGENESIS	RIBONUCLEOP	Details ...	394	-0.36640283	-1.7248359	0	0.094531156	1	6143
LEUKOCYTE APOPTOTIC PROCESS	LEUKOCYTE AP	Details ...	19	-0.6230631	-1.7228842	0.006479482	0.09538452	1	531
NITRIC OXIDE METABOLIC PROCESS	NITRIC OXIDE	Details ...	15	-0.65519947	-1.7213454	0.008752735	0.095654845	1	1839
ORGANELLAR RIBOSOME	ORGANELLAR	Details ...	67	-0.46560308	-1.7185049	0.002583979	0.09717457	1	5033
CELLULAR PROTEIN COMPLEX DISASSEMBLY	CELLULAR PRO	Details ...	116	-0.41859972	-1.7181016	0.002941177	0.09644015	1	5033
RESPONSE TO MANGANESE ION	RESPONSE TO	Details ...	15	-0.6480533	-1.7172576	0.010141988	0.09606824	1	1597
PROSTANOID METABOLIC PROCESS	PROSTANOID M	Details ...	22	-0.58687353	-1.7170697	0.006564552	0.09528247	1	1316
POSITIVE REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC	POSITIVE REGU	Details ...	43	-0.51004577	-1.715787	0.007263923	0.0953731	1	198
QUINONE METABOLIC PROCESS	QUINONE MET	Details ...	24	-0.57202625	-1.7152073	0.006564552	0.094879024	1	3141
REGULATION OF COLLATERAL SPROUTING	REGULATION O	Details ...	16	-0.64614403	-1.7150682	0.006263048	0.094015524	1	2374
MATURATION OF 5 8S RRNA FROM TRICISTRONIC RRNA TRANSCRIPT	MATURATION O	Details ...	19	-0.59864265	-1.713133	0.010729614	0.09474787	1	4716
GROWTH FACTOR ACTIVITY	GROWTH FACTOR ACTIVITY		138	-0.40393028	-1.7130457	0	0.09385669	1	1513
MYELOID LEUKOCYTE MEDIATED IMMUNITY	MYELOID LEUKOCYTE MEDIATE		33	-0.54154813	-1.7119161	0.006410257	0.093793936	1	275
OXIDOREDUCTASE ACTIVITY ACTING ON SINGLE DONORS WITH INCOR	OXIDOREDUCTASE ACTIVITY AC		22	-0.59569514	-1.7105917	0.013274336	0.09379449	1	975
REGULATION OF FATTY ACID BIOSYNTHETIC PROCESS	REGULATION OF FATTY ACID BI		33	-0.53827536	-1.7097352	0.015021459	0.0936153	1	2107
FATTY ACID DERIVATIVE METABOLIC PROCESS	FATTY ACID DERIVATIVE METAB		60	-0.47615	-1.7089449	0.005089059	0.093277216	1	316
FATTY ACID DERIVATIVE BIOSYNTHETIC PROCESS	FATTY ACID DERIVATIVE BIOSYN		34	-0.5260888	-1.7059797	0.007281554	0.094668284	1	216
REGULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR PRODUC	REGULATION OF VASCULAR EN		29	-0.54771656	-1.7005769	0.006818182	0.09857468	1	1150
RESPONSE TO AUDITORY STIMULUS	RESPONSE TO AUDITORY STIMU		22	-0.578965	-1.6962916	0.010706638	0.101665884	1	456
ACETYLCHOLINE RECEPTOR ACTIVITY	ACETYLCHOLINE RECEPTOR AC		26	-0.56859523	-1.6951098	0.010964912	0.10175026	1	3290
QUATERNARY AMMONIUM GROUP BINDING	QUATERNARY AMMONIUM GRO		42	-0.503441	-1.6921906	0.011709602	0.103321455	1	1860
POSITIVE REGULATION OF ADENYLATE CYCLASE ACTIVITY	POSITIVE REGULATION OF ADEN		43	-0.49576235	-1.6889213	0.006976744	0.104945175	1	922
ORGANELLAR LARGE RIBOSOMAL SUBUNIT	ORGANELLAR LARGE RIBOSOMA		29	-0.5487995	-1.6877773	0.011389522	0.104930736	1	5412
PTERIDINE CONTAINING COMPOUND BIOSYNTHETIC PROCESS	PTERIDINE CONTAINING COMPO		16	-0.6346818	-1.6873835	0.012526096	0.10433505	1	3247
MUSCLE CELL CELLULAR HOMEOSTASIS	MUSCLE CELL CELLULAR HOME		18	-0.61325896	-1.6870475	0.013186813	0.10376585	1	16
UNSATURATED FATTY ACID BIOSYNTHETIC PROCESS	UNSATURATED FATTY ACID BIO		41	-0.49552295	-1.686357	0.002427185	0.10348446	1	216
TRNA PROCESSING	TRNA PROCESSING		89	-0.42754707	-1.6849967	0.005434783	0.10371124	1	3736
DEFENSE RESPONSE TO GRAM NEGATIVE BACTERIUM	DEFENSE RESPONSE TO GRAM		28	-0.54311615	-1.6814405	0.013888889	0.10608895	1	349
POSITIVE REGULATION OF LYASE ACTIVITY	POSITIVE REGULATION OF LYAS		54	-0.4726829	-1.6809183	0.007407407	0.10574077	1	922
TRNA SPECIFIC RIBONUCLEASE ACTIVITY	TRNA SPECIFIC RIBONUCLEASE		15	-0.65101033	-1.6801977	0.008230452	0.1054935	1	3590
REGULATION OF TYROSINE PHOSPHORYLATION OF STAT PROTEIN	REGULATION OF TYROSINE PHO		58	-0.4617476	-1.6759759	0.004950495	0.10805049	1	1359
EATING BEHAVIOR	EATING BEHAVIOR		27	-0.54658437	-1.6738708	0.016587678	0.109152466	1	917
CYTOSOLIC LARGE RIBOSOMAL SUBUNIT	CYTOSOLIC LARGE RIBOSOMAL		54	-0.46377632	-1.6736087	0.007125891	0.10852884	1	7455
TRNA METABOLIC PROCESS	TRNA METABOLIC PROCESS		146	-0.39484602	-1.6662222	0	0.11458175	1	3736
CYTOKINE ACTIVITY	CYTOKINE ACTIVITY		148	-0.39194697	-1.6632221	0	0.11651573	1	1088
GLUTATHIONE METABOLIC PROCESS	GLUTATHIONE METABOLIC PRO		51	-0.46978927	-1.6630397	0.004938272	0.115741596	1	4241
REGULATION OF CELLULAR AMINO ACID METABOLIC PROCESS	REGULATION OF CELLULAR AM		61	-0.45803833	-1.6625749	0.004842615	0.115270555	1	5930
FEEDING BEHAVIOR	FEEDING BEHAVIOR		78	-0.44435227	-1.662473	0	0.11442946	1	917

NEGATIVE REGULATION OF CIRCADIAN RHYTHM	NEGATIVE REGULATION OF CIR	15	-0.6286619	-1.6611662	0.008196721	0.11481393	1	1359
RESPONSE TO DIETARY EXCESS	RESPONSE TO DIETARY EXCES	20	-0.5893722	-1.6533198	0.015384615	0.12180893	1	900
SMOOTH MUSCLE CONTRACTION	SMOOTH MUSCLE CONTRACTI	44	-0.47343296	-1.653036	0.007194245	0.12105345	1	814
POSITIVE REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PR	POSITIVE REGULATION OF REA	75	-0.43552506	-1.652058	0.002617801	0.12109735	1	598
REGULATION OF NITRIC OXIDE BIOSYNTHETIC PROCESS	REGULATION OF NITRIC OXIDE	48	-0.47477174	-1.6506666	0	0.121520564	1	198
CLEAVAGE INVOLVED IN RRNA PROCESSING	CLEAVAGE INVOLVED IN RRNA	18	-0.5905455	-1.6486639	0.012765957	0.122551434	1	4716
POSITIVE REGULATION OF CD4 POSITIVE ALPHA BETA T CELL ACTIVATI	POSITIVE REGULATION OF CD4	23	-0.5691609	-1.645629	0.009433962	0.12467408	1	373
BRANCHING INVOLVED IN SALIVARY GLAND MORPHOGENESIS	BRANCHING INVOLVED IN SALIV	16	-0.62353224	-1.6439987	0.018367346	0.12552686	1	795
REGULATION OF CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	REGULATION OF CD4 POSITIVE	30	-0.52706844	-1.643717	0.01369863	0.124831036	1	373
RIBOSOMAL LARGE SUBUNIT ASSEMBLY	RIBOSOMAL LARGE SUBUNIT AS	21	-0.5774823	-1.6411891	0.024096385	0.12622117	1	4181
NEGATIVE REGULATION OF LIPASE ACTIVITY	NEGATIVE REGULATION OF LIPA	15	-0.63404745	-1.6391689	0.008714597	0.12722947	1	1385
REGULATION OF AMINE TRANSPORT	REGULATION OF AMINE TRANS	70	-0.43591616	-1.6386166	0.005208334	0.12688187	1	1038
REGULATION OF IMMUNOGLOBULIN SECRETION	REGULATION OF IMMUNOGLOB	16	-0.62391645	-1.636391	0.01793722	0.12847202	1	691
SPLICEOSOMAL TRI SNRNP COMPLEX	SPLICEOSOMAL TRI SNRNP CO	25	-0.53115964	-1.6363146	0.018867925	0.12764752	1	5771
BINDING OF SPERM TO ZONA PELLUCIDA	BINDING OF SPERM TO ZONA P	23	-0.5628001	-1.6347451	0.010869565	0.12852176	1	3191
SINGLE FERTILIZATION	SINGLE FERTILIZATION	67	-0.4402325	-1.6337653	0.004854369	0.12873393	1	3191
REGULATION OF RESPONSE TO FOOD	REGULATION OF RESPONSE TO	18	-0.58248925	-1.6330615	0.025751073	0.12855853	1	310
CELLULAR MODIFIED AMINO ACID BIOSYNTHETIC PROCESS	CELLULAR MODIFIED AMINO AC	47	-0.46783745	-1.6313294	0.007246377	0.12936743	1	3247
REGULATION OF MULTICELLULAR ORGANISMAL METABOLIC PROCESS	REGULATION OF MULTICELLULA	34	-0.5088341	-1.6286978	0.016470589	0.13101038	1	299
POSITIVE T CELL SELECTION	POSITIVE T CELL SELECTION	16	-0.60686964	-1.6283677	0.027600849	0.13058516	1	2
DNA TEMPLATED TRANSCRIPTION ELONGATION	DNA TEMPLATED TRANSCRIPTI	83	-0.42352492	-1.6268209	0	0.13147178	1	5690
REGULATION OF TYPE 2 IMMUNE RESPONSE	REGULATION OF TYPE 2 IMMUN	22	-0.57637864	-1.6261991	0.013015185	0.13114494	1	1301
AMMONIUM TRANSMEMBRANE TRANSPORTER ACTIVITY	AMMONIUM TRANSMEMBRANE	21	-0.56804526	-1.6256189	0.021598272	0.13086532	1	1620
GROWTH FACTOR RECEPTOR BINDING	GROWTH FACTOR RECEPTOR	112	-0.39742866	-1.625026	0.005747126	0.13072167	1	1069
REGULATION OF POTASSIUM ION TRANSPORT	REGULATION OF POTASSIUM IO	79	-0.4276063	-1.6245054	0	0.13035122	1	2209
HORMONE TRANSPORT	HORMONE TRANSPORT	70	-0.43659323	-1.6206479	0	0.13350533	1	319
NIK NF KAPPAB SIGNALING	NIK NF KAPPAB SIGNALING	73	-0.42508337	-1.6174443	0.005263158	0.13604534	1	5893
ACETYLCHOLINE BINDING	ACETYLCHOLINE BINDING	19	-0.59618646	-1.6172688	0.022779044	0.13534378	1	3290
BLOOD COAGULATION INTRINSIC PATHWAY	BLOOD COAGULATION INTRINS	16	-0.6224568	-1.6152682	0.020876827	0.13657106	1	363
CORNIFIED ENVELOPE	CORNIFIED ENVELOPE	17	-0.58943444	-1.6142095	0.019480519	0.13686062	1	2297
FIBROBLAST GROWTH FACTOR RECEPTOR BINDING	FIBROBLAST GROWTH FACTOR	27	-0.5294301	-1.6138088	0.010845987	0.13639387	1	1286
T CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	T CELL ACTIVATION INVOLVED I	37	-0.50091046	-1.6131631	0	0.13616934	1	287
MYELOID CELL HOMEOSTASIS	MYELOID CELL HOMEOSTASIS	79	-0.4252156	-1.6124978	0.011049724	0.1360367	1	887
NEGATIVE REGULATION OF SECRETION	NEGATIVE REGULATION OF SEC	172	-0.3727858	-1.6122775	0	0.13542643	1	1359
RIBOSOMAL SMALL SUBUNIT BIOGENESIS	RIBOSOMAL SMALL SUBUNIT BI	53	-0.4526313	-1.610597	0.012106538	0.1363033	1	5920
REGULATION OF BLOOD PRESSURE	REGULATION OF BLOOD PRESS	145	-0.38046545	-1.6102413	0.002976191	0.13581362	1	900
COFACTOR CATABOLIC PROCESS	COFACTOR CATABOLIC PROCE	17	-0.60583204	-1.607994	0.016393442	0.13738987	1	397
U2 SNRNP	U2 SNRNP	17	-0.59511024	-1.6068072	0.025695931	0.13776828	1	3660
ER NUCLEUS SIGNALING PATHWAY	ER NUCLEUS SIGNALING PATHW	32	-0.5070384	-1.6048927	0.019002376	0.138942	1	2310
REGULATION OF REACTIVE OXYGEN SPECIES BIOSYNTHETIC PROCES	REGULATION OF REACTIVE OXY	59	-0.45101976	-1.6048838	0.00255102	0.1381382	1	198
POSITIVE REGULATION OF STAT CASCADE	POSITIVE REGULATION OF STAT	60	-0.4406852	-1.6045489	0.005037783	0.13772956	1	1359
EXOSOME RNASE COMPLEX	EXOSOME RNASE COMPLEX	18	-0.57818687	-1.6033396	0.033783782	0.13822304	1	3708
NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS EXONUCLEOLYT	NUCLEAR TRANSCRIBED MRNA	27	-0.52313024	-1.603106	0.017699115	0.13764825	1	5285

NCRNA CATABOLIC PROCESS	NCRNA CATABOLIC PROCESS	17	-0.593871	-1.6019275	0.020576132	0.1380717	1	3708
AMMONIUM ION BINDING	AMMONIUM ION BINDING	60	-0.43422395	-1.5990611	0.007142857	0.14021803	1	1860
POSITIVE REGULATION OF RESPONSE TO WOUNDING	POSITIVE REGULATION OF RES	128	-0.388692	-1.5982804	0	0.14037856	1	413
REGULATION OF SYSTEM PROCESS	REGULATION OF SYSTEM PRO	471	-0.32834715	-1.5977186	0	0.14027888	1	1401
SPERM EGG RECOGNITION	SPERM EGG RECOGNITION	25	-0.53195333	-1.5963802	0.027083334	0.14095286	1	5018
RESPONSE TO CADMIUM ION	RESPONSE TO CADMIUM ION	34	-0.49306765	-1.5960038	0.009708738	0.14052154	1	1654
MOTILE CILIUM	MOTILE CILIUM	71	-0.41637227	-1.5956029	0.007633588	0.14020576	1	3097
RNA POLYMERASE ACTIVITY	RNA POLYMERASE ACTIVITY	38	-0.49662656	-1.5951614	0.015189873	0.13996711	1	5690
SNORNA BINDING	SNORNA BINDING	26	-0.53463733	-1.594063	0.014799154	0.1404181	1	6050
LOW DENSITY LIPOPROTEIN PARTICLE RECEPTOR BINDING	LOW DENSITY LIPOPROTEIN PA	16	-0.59347206	-1.5927765	0.026258206	0.14101017	1	1860
PROSTANOID BIOSYNTHETIC PROCESS	PROSTANOID BIOSYNTHETIC P	16	-0.594672	-1.5922258	0.03285421	0.14076108	1	1316
REGULATION OF SYNAPTIC TRANSMISSION GLUTAMATERGIC	REGULATION OF SYNAPTIC TRA	47	-0.4545024	-1.5918436	0.010050251	0.14042085	1	598
OVARIAN FOLLICLE DEVELOPMENT	OVARIAN FOLLICLE DEVELOPME	51	-0.45193514	-1.5914117	0.014423077	0.14018342	1	1239
RIBONUCLEASE ACTIVITY	RIBONUCLEASE ACTIVITY	75	-0.42091265	-1.5893621	0.005361931	0.14168935	1	4930
POSITIVE REGULATION OF LIGASE ACTIVITY	POSITIVE REGULATION OF LIGA	101	-0.39748314	-1.5874932	0	0.14287776	1	5893
POSITIVE REGULATION OF NEUROTRANSMITTER TRANSPORT	POSITIVE REGULATION OF NEU	15	-0.60377467	-1.5867558	0.014314928	0.14304805	1	1359
NEGATIVE REGULATION OF POTASSIUM ION TRANSPORT	NEGATIVE REGULATION OF POT	29	-0.52382517	-1.5860679	0.034632035	0.14311473	1	1782
CELLULAR RESPONSE TO FLUID SHEAR STRESS	CELLULAR RESPONSE TO FLUID	18	-0.5846185	-1.5859574	0.029227557	0.14245403	1	1639
FEMALE GAMETE GENERATION	FEMALE GAMETE GENERATION	66	-0.42609072	-1.5857458	0.010282776	0.1418895	1	2444
TRIGLYCERIDE CATABOLIC PROCESS	TRIGLYCERIDE CATABOLIC PR	21	-0.56020814	-1.5855138	0.024229076	0.14142999	1	1860
REGULATION OF URINE VOLUME	REGULATION OF URINE VOLUM	20	-0.5639464	-1.5825925	0.020361992	0.14379206	1	1359
REGULATION OF ENDOPLASMIC RETICULUM STRESS INDUCED INTRIN	REGULATION OF ENDOPLASMI	26	-0.5308047	-1.5815501	0.02764977	0.14410391	1	1753
OVULATION CYCLE PROCESS	OVULATION CYCLE PROCESS	76	-0.4114712	-1.5788108	0.010526316	0.14632742	1	1239
U12 TYPE SPLICEOSOMAL COMPLEX	U12 TYPE SPLICEOSOMAL COM	24	-0.53203005	-1.5753808	0.019955654	0.14938174	1	3660
RESPONSE TO PAIN	RESPONSE TO PAIN	26	-0.52137536	-1.5750811	0.025229357	0.14895347	1	1215
STAT CASCADE	STAT CASCADE	41	-0.47006744	-1.5745685	0.01724138	0.14872192	1	1225
G PROTEIN COUPLED AMINE RECEPTOR ACTIVITY	G PROTEIN COUPLED AMINE R	33	-0.49774063	-1.5713376	0.025943397	0.15160136	1	3570
CARBOHYDRATE KINASE ACTIVITY	CARBOHYDRATE KINASE ACTIV	17	-0.58471954	-1.5704219	0.025806451	0.1517331	1	3635
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX ASSEMBLY	MITOCHONDRIAL RESPIRATOR	59	-0.43436483	-1.5685818	0.02189781	0.15316984	1	7283
VASODILATION	VASODILATION	25	-0.52359414	-1.5659082	0.018099548	0.15555234	1	236
NEGATIVE REGULATION OF LIPID STORAGE	NEGATIVE REGULATION OF LIP	17	-0.58307207	-1.5657965	0.018907564	0.1549042	1	299
CARBOHYDRATE PHOSPHORYLATION	CARBOHYDRATE PHOSPHORYL	18	-0.5642845	-1.5629354	0.031712472	0.15734911	1	4008
POSITIVE REGULATION OF BEHAVIOR	POSITIVE REGULATION OF BEH	20	-0.55216634	-1.5621771	0.03267974	0.15745832	1	1359
POSITIVE REGULATION OF FATTY ACID BIOSYNTHETIC PROCESS	POSITIVE REGULATION OF FATT	17	-0.57834524	-1.5612104	0.03267974	0.15776668	1	2540
POSITIVE REGULATION OF ACUTE INFLAMMATORY RESPONSE	POSITIVE REGULATION OF ACU	25	-0.5271728	-1.5610977	0.031042129	0.15712583	1	413
NEGATIVE REGULATION OF PEPTIDASE ACTIVITY	NEGATIVE REGULATION OF PE	177	-0.36526406	-1.559287	0	0.15845431	1	1148
PRERIBOSOME LARGE SUBUNIT PRECURSOR	PRERIBOSOME LARGE SUBUNIT	17	-0.5781355	-1.5587263	0.029535865	0.15838346	1	3389
CYTOSOLIC RIBOSOME	CYTOSOLIC RIBOSOME	101	-0.3920506	-1.5578437	0.007936508	0.15861148	1	7455
DEFENSE RESPONSE TO BACTERIUM	DEFENSE RESPONSE TO BACT	116	-0.38081437	-1.5575876	0.003003003	0.15820447	1	1673
RRNA BINDING	RRNA BINDING	53	-0.43375117	-1.5560036	0.016786572	0.15931103	1	5089
NEUROMUSCULAR SYNAPTIC TRANSMISSION	NEUROMUSCULAR SYNAPTIC T	26	-0.51192206	-1.5529352	0.035955057	0.16224465	1	867
NEUTRAL LIPID CATABOLIC PROCESS	NEUTRAL LIPID CATABOLIC PR	25	-0.5175395	-1.552355	0.034136545	0.16214025	1	1860
REGULATION OF HORMONE SECRETION	REGULATION OF HORMONE SE	239	-0.34401748	-1.5522618	0	0.16145867	1	2412

REGULATION OF PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	REGULATION OF PROTEIN IMPO	19	-0.5631081	-1.5520402	0.047210302	0.1609801	1	541
WATER TRANSPORT	WATER TRANSPORT	18	-0.5436702	-1.5511686	0.06511628	0.16127412	1	2153
RNA PHOSPHODIESTER BOND HYDROLYSIS	RNA PHOSPHODIESTER BOND H	97	-0.39572355	-1.5497491	0.005540166	0.16221403	1	4930
NEGATIVE REGULATION OF INTERFERON GAMMA PRODUCTION	NEGATIVE REGULATION OF INT	24	-0.51790345	-1.5490801	0.027459955	0.1623412	1	2961
RIBOSOMAL LARGE SUBUNIT BIOGENESIS	RIBOSOMAL LARGE SUBUNIT BIO	44	-0.4594868	-1.5490752	0.013513514	0.16160087	1	5071
PHASIC SMOOTH MUSCLE CONTRACTION	PHASIC SMOOTH MUSCLE CON	15	-0.5848662	-1.5470359	0.044444446	0.1632779	1	716
ANAPHASE PROMOTING COMPLEX DEPENDENT CATABOLIC PROCESS	ANAPHASE PROMOTING COMPL	73	-0.40845042	-1.5441308	0.00530504	0.16619964	1	7670
PROTEIN HOMOTETRAMERIZATION	PROTEIN HOMOTETRAMERIZAT	55	-0.4339742	-1.5435418	0.015306123	0.16611451	1	4241
POSITIVE REGULATION OF FATTY ACID METABOLIC PROCESS	POSITIVE REGULATION OF FATT	33	-0.47876945	-1.5426396	0.01978022	0.16635132	1	2107
RESPONSE TO HEAT	RESPONSE TO HEAT	77	-0.4095533	-1.5418661	0.016853932	0.16659059	1	1590
CYTOKINE RECEPTOR BINDING	CYTOKINE RECEPTOR BINDING	202	-0.34807688	-1.5379907	0	0.17050132	1	1088
SPLICEOSOMAL SNRNP ASSEMBLY	SPLICEOSOMAL SNRNP ASSEM	34	-0.4754643	-1.5379537	0.021413276	0.16977246	1	4322
TETRAPYRROLE METABOLIC PROCESS	TETRAPYRROLE METABOLIC PR	53	-0.44046834	-1.5346752	0.016548464	0.17310183	1	3591
NUCLEASE ACTIVITY	NUCLEASE ACTIVITY	157	-0.3662824	-1.5335778	0.003030303	0.17373148	1	4957
POSITIVE REGULATION OF INTERLEUKIN 6 PRODUCTION	POSITIVE REGULATION OF INTE	56	-0.43621257	-1.5320773	0.014457831	0.17493683	1	319
INNER MITOCHONDRIAL MEMBRANE PROTEIN COMPLEX	INNER MITOCHONDRIAL MEMB	93	-0.38588896	-1.5320398	0.010526316	0.17421031	1	7329
HEME BIOSYNTHETIC PROCESS	HEME BIOSYNTHETIC PROCESS	20	-0.54336375	-1.5315003	0.033264033	0.17422497	1	5772
U5 SNRNP	U5 SNRNP	16	-0.57524556	-1.5302283	0.046025105	0.17492884	1	3660
ACTIVATION OF ADENYLATE CYCLASE ACTIVITY	ACTIVATION OF ADENYLATE CY	36	-0.4672132	-1.5300931	0.029612755	0.1743691	1	2369
RESPONSE TO TUMOR NECROSIS FACTOR	RESPONSE TO TUMOR NECROS	182	-0.34968266	-1.527638	0.003257329	0.17670485	1	1341
UNSATURATED FATTY ACID METABOLIC PROCESS	UNSATURATED FATTY ACID ME	71	-0.40398467	-1.5274428	0.010471204	0.17615965	1	316
MITOCHONDRIAL RESPIRATORY CHAIN COMPLEX I BIOGENESIS	MITOCHONDRIAL RESPIRATORY	48	-0.44593737	-1.526048	0.029339854	0.17707443	1	7283
REGULATION OF APPETITE	REGULATION OF APPETITE	22	-0.5292496	-1.5251846	0.046413504	0.17741995	1	310
SIGNAL RELEASE	SIGNAL RELEASE	154	-0.36110792	-1.5248322	0	0.17714715	1	1753
POSITIVE REGULATION OF ERK1 AND ERK2 CASCADE	POSITIVE REGULATION OF ERK1	133	-0.366752	-1.522887	0.006116208	0.17876211	1	887
TETRAPYRROLE BIOSYNTHETIC PROCESS	TETRAPYRROLE BIOSYNTHETIC	26	-0.5052387	-1.5222982	0.029478459	0.17886777	1	3430
CALCIUM ION REGULATED EXOCYTOSIS OF NEUROTRANSMITTER	CALCIUM ION REGULATED EXOC	28	-0.49877366	-1.5220474	0.03524229	0.17845209	1	2246
PROTEASOME COMPLEX	PROTEASOME COMPLEX	70	-0.40572596	-1.5220261	0.017676767	0.17774692	1	7481
RESPONSE TO ANTIBIOTIC	RESPONSE TO ANTIBIOTIC	43	-0.4493413	-1.5186414	0.009367681	0.18140796	1	316
ESTROUS CYCLE	ESTROUS CYCLE	18	-0.5489115	-1.5183762	0.050955415	0.18103981	1	1081
CELL REDOX HOMEOSTASIS	CELL REDOX HOMEOSTASIS	54	-0.42965674	-1.5171634	0.02173913	0.18186167	1	352
PEPTIDE TRANSPORT	PEPTIDE TRANSPORT	66	-0.4128453	-1.5167581	0.012285012	0.18158329	1	1753
MITOCHONDRIAL PROTEIN COMPLEX	MITOCHONDRIAL PROTEIN COM	119	-0.37327826	-1.5149662	0.00617284	0.18314807	1	7369
CELLULAR RESPONSE TO ALCOHOL	CELLULAR RESPONSE TO ALCO	105	-0.38075763	-1.5142857	0.008333334	0.1834359	1	1128
TRANSFERASE ACTIVITY TRANSFERRING AMINO ACYL GROUPS	TRANSFERASE ACTIVITY TRANS	15	-0.5744686	-1.5133828	0.04	0.18381685	1	884
REGULATION OF DIGESTIVE SYSTEM PROCESS	REGULATION OF DIGESTIVE SYS	33	-0.47896248	-1.513037	0.029411765	0.18351287	1	2667
RESPONSE TO MOLECULE OF BACTERIAL ORIGIN	RESPONSE TO MOLECULE OF B	280	-0.32937184	-1.5129856	0	0.18283932	1	1153
OXYGEN BINDING	OXYGEN BINDING	24	-0.5129608	-1.5128042	0.030042918	0.18238054	1	2184
SENSORY PERCEPTION OF PAIN	SENSORY PERCEPTION OF PAIN	69	-0.4025032	-1.5122916	0.026666667	0.1823285	1	1505
ADENYLATE CYCLASE ACTIVATING G PROTEIN COUPLED RECEPTOR SI	ADENYLATE CYCLASE ACTIVATI	54	-0.43051577	-1.5121413	0.020512821	0.1817751	1	900
REGULATION OF KERATINOCYTE PROLIFERATION	REGULATION OF KERATINOCYT	23	-0.508729	-1.5119845	0.030567685	0.18129219	1	1664
RESPONSE TO HYDROGEN PEROXIDE	RESPONSE TO HYDROGEN PER	100	-0.37693194	-1.5110351	0.005617978	0.18181239	1	216
MATERNAL PROCESS INVOLVED IN FEMALE PREGNANCY	MATERNAL PROCESS INVOLVED	53	-0.42667273	-1.5107136	0.017632242	0.18148367	1	983

PSEUDOURIDINE SYNTHESIS	PSEUDOURIDINE SYNTHESIS	15	-0.581652	-1.5093158	0.042372882	0.18249226	1	2986
NEGATIVE REGULATION OF NEURON DEATH	NEGATIVE REGULATION OF NEU	152	-0.3553655	-1.5091907	0	0.1819384	1	2000
INTRINSIC APOPTOTIC SIGNALING PATHWAY	INTRINSIC APOPTOTIC SIGNALI	134	-0.364631	-1.508536	0.005780347	0.18210009	1	1597
RNA PHOSPHODIESTER BOND HYDROLYSIS ENDONUCLEOLYTIC	RNA PHOSPHODIESTER BOND	52	-0.42352653	-1.5078399	0.024271844	0.18224119	1	4909
REGULATION OF AMINO ACID TRANSPORT	REGULATION OF AMINO ACID T	25	-0.4915542	-1.5073988	0.05463183	0.18216921	1	917
REGULATION OF CATECHOLAMINE SECRETION	REGULATION OF CATECHOLAM	42	-0.4397539	-1.5073323	0.025171624	0.18156698	1	1315
HISTONE MRNA METABOLIC PROCESS	HISTONE MRNA METABOLIC PR	25	-0.5023693	-1.5062847	0.0247191	0.1821372	1	5633
REGULATION OF INFLAMMATORY RESPONSE	REGULATION OF INFLAMMATO	240	-0.33373713	-1.5062556	0.003533569	0.18148285	1	1359
PROTEIN TARGETING TO MITOCHONDRION	PROTEIN TARGETING TO MITO	44	-0.43842366	-1.5050302	0.025906736	0.18225285	1	6509
INTRINSIC COMPONENT OF MITOCHONDRIAL INNER MEMBRANE	INTRINSIC COMPONENT OF MIT	16	-0.5573384	-1.5046825	0.06508876	0.18203111	1	4339
CELLULAR RESPONSE TO KETONE	CELLULAR RESPONSE TO KETO	69	-0.4005081	-1.5040661	0.012953368	0.18211387	1	459
LIGASE ACTIVITY FORMING CARBON NITROGEN BONDS	LIGASE ACTIVITY FORMING CA	45	-0.4421545	-1.5025651	0.023316063	0.18338753	1	3552
REGULATION OF VASOCONSTRICTION	REGULATION OF VASOCONSTR	61	-0.41895628	-1.5004456	0.025773196	0.18529692	1	2883
CLATHRIN BINDING	CLATHRIN BINDING	52	-0.42702314	-1.5000782	0.029339854	0.18510163	1	1247
POSITIVE REGULATION OF HORMONE SECRETION	POSITIVE REGULATION OF HOR	107	-0.37145925	-1.498013	0.008902078	0.18706751	1	2412
OXIDOREDUCTASE ACTIVITY ACTING ON NAD P H QUINONE OR SIMILA	OXIDOREDUCTASE ACTIVITY A	46	-0.4393343	-1.4960595	0.042128604	0.18885854	1	7283
NCRNA 3 END PROCESSING	NCRNA 3 END PROCESSING	18	-0.5428576	-1.4953035	0.054545455	0.1891	1	5579
POSITIVE REGULATION OF ANION TRANSPORT	POSITIVE REGULATION OF ANIO	53	-0.41383368	-1.4939908	0.02238806	0.1901258	1	413
NEGATIVE REGULATION OF CYSTEINE TYPE ENDOPEPTIDASE ACTIVITY	NEGATIVE REGULATION OF CYS	76	-0.392046	-1.4939059	0.010752688	0.18951656	1	1310
THREONINE TYPE PEPTIDASE ACTIVITY	THREONINE TYPE PEPTIDASE A	18	-0.5419048	-1.492682	0.057815846	0.19043736	1	5887
REGULATION OF MACROPHAGE DIFFERENTIATION	REGULATION OF MACROPHAGE	19	-0.5425801	-1.4913406	0.051282052	0.1915715	1	621
LYMPHOCYTE ACTIVATION INVOLVED IN IMMUNE RESPONSE	LYMPHOCYTE ACTIVATION INV	70	-0.40071315	-1.4903527	0.013227513	0.1921314	1	1359
OVULATION	OVULATION	16	-0.5681397	-1.4900314	0.06431536	0.19183323	1	908
SALIVARY GLAND DEVELOPMENT	SALIVARY GLAND DEVELOPMEN	31	-0.4819838	-1.4893404	0.03803132	0.19208884	1	937
GAMMA TUBULIN COMPLEX	GAMMA TUBULIN COMPLEX	15	-0.57429147	-1.4893016	0.043392505	0.19148552	1	4428
CIRCULATORY SYSTEM PROCESS	CIRCULATORY SYSTEM PROCE	326	-0.32090357	-1.4887723	0	0.19147106	1	2338
RESPONSE TO INTERLEUKIN 4	RESPONSE TO INTERLEUKIN 4	28	-0.48238257	-1.4878048	0.049676027	0.1919718	1	465
REGULATION OF REACTIVE OXYGEN SPECIES METABOLIC PROCESS	REGULATION OF REACTIVE OX	132	-0.35306308	-1.4878005	0.016666668	0.19130246	1	1658
PALMITOYLTRANSFERASE ACTIVITY	PALMITOYLTRANSFERASE ACTI	28	-0.48619598	-1.487645	0.041942604	0.1908322	1	2869
SNARE BINDING	SNARE BINDING	110	-0.36425754	-1.4865952	0.018766755	0.19155277	1	2389
RESPONSE TO ATP	RESPONSE TO ATP	29	-0.47075677	-1.486306	0.039337475	0.19125162	1	716
U4 U6 X U5 TRI SNRNP COMPLEX	U4 U6 X U5 TRI SNRNP COMPLE	20	-0.5397503	-1.485856	0.059196617	0.19129172	1	5633
SYMPATHETIC NERVOUS SYSTEM DEVELOPMENT	SYMPATHETIC NERVOUS SYST	18	-0.55113745	-1.4858037	0.06198347	0.19068505	1	4342
LEUKOCYTE HOMEOSTASIS	LEUKOCYTE HOMEOSTASIS	52	-0.4181489	-1.4855887	0.030075189	0.19029953	1	2552
ALDITOL METABOLIC PROCESS	ALDITOL METABOLIC PROCESS	16	-0.5502645	-1.4855599	0.05788423	0.18970095	1	2980
OVULATION CYCLE	OVULATION CYCLE	99	-0.37328175	-1.4852479	0.0078125	0.18949583	1	1239
STRUCTURAL CONSTITUENT OF RIBOSOME	STRUCTURAL CONSTITUENT O	192	-0.34091878	-1.4844387	0	0.18993105	1	7457
REGULATION OF TRANSFORMING GROWTH FACTOR BETA PRODUCTI	REGULATION OF TRANSFORMI	21	-0.52256995	-1.482731	0.04112554	0.19133961	1	4265
TRANSCRIPTION FACTOR TFIID COMPLEX	TRANSCRIPTION FACTOR TFIID	19	-0.53149444	-1.4818634	0.047817048	0.19184008	1	3023
POSITIVE REGULATION OF IMMUNE EFFECTOR PROCESS	POSITIVE REGULATION OF IMMU	130	-0.3567113	-1.4795928	0.002976191	0.19405459	1	771
ENDOCRINE PROCESS	ENDOCRINE PROCESS	38	-0.44895583	-1.4793258	0.049411766	0.19377719	1	2174
REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE BY HORMON	REGULATION OF SYSTEMIC AR	30	-0.4736552	-1.47694	0.048034936	0.1962737	1	2174
DECIDUALIZATION	DECIDUALIZATION	20	-0.5194038	-1.4752	0.07594936	0.1978949	1	621

CARBOHYDRATE TRANSPORT	CARBOHYDRATE TRANSPORT	80	-0.37704593	-1.4748414	0.018324608	0.1976951	1	2681
NEUTRAL LIPID METABOLIC PROCESS	NEUTRAL LIPID METABOLIC PRO	76	-0.38658246	-1.4742677	0.015957447	0.19774294	1	2010
POSITIVE REGULATION OF SMOOTH MUSCLE CELL PROLIFERATION	POSITIVE REGULATION OF SMO	56	-0.41435722	-1.4736433	0.035885166	0.19787605	1	7
AMIDE TRANSPORT	AMIDE TRANSPORT	86	-0.37916154	-1.4723507	0.026954178	0.19893293	1	1753
POSITIVE REGULATION OF PRODUCTION OF MOLECULAR MEDIATOR O	POSITIVE REGULATION OF PRO	55	-0.4116909	-1.4718888	0.021791767	0.1988569	1	1444
POSITIVE REGULATION OF SYNAPTIC TRANSMISSION	POSITIVE REGULATION OF SYNA	101	-0.36916587	-1.4706763	0.008474576	0.19986254	1	1578
REGULATION OF SYSTEMIC ARTERIAL BLOOD PRESSURE MEDIATED BY	REGULATION OF SYSTEMIC ART	40	-0.44337496	-1.4702408	0.0647482	0.1998278	1	5670
ENDONUCLEASE ACTIVITY	ENDONUCLEASE ACTIVITY	95	-0.37676018	-1.4698186	0.012658228	0.19981	1	4756
REGULATION OF CIRCADIAN RHYTHM	REGULATION OF CIRCADIAN RH	92	-0.37869564	-1.4671913	0.015625	0.20259586	1	1407
TETRAPYRROLE BINDING	TETRAPYRROLE BINDING	84	-0.3793695	-1.4671406	0.015228426	0.20200098	1	883
CYTOSOLIC PART	CYTOSOLIC PART	186	-0.33493024	-1.4666361	0	0.201992	1	7481
DNA DIRECTED RNA POLYMERASE III COMPLEX	DNA DIRECTED RNA POLYMERA	16	-0.5478966	-1.4656448	0.05567452	0.20272966	1	5690
RESPONSE TO TEMPERATURE STIMULUS	RESPONSE TO TEMPERATURE	128	-0.35419306	-1.4652139	0.016574586	0.20258796	1	1590
NEGATIVE REGULATION OF CARBOHYDRATE METABOLIC PROCESS	NEGATIVE REGULATION OF CAR	41	-0.4416111	-1.464601	0.03456221	0.20272787	1	1315
MULTICELLULAR ORGANISMAL RESPONSE TO STRESS	MULTICELLULAR ORGANISMAL	64	-0.39967018	-1.4625052	0.024509804	0.20488754	1	1215
INFLAMMATORY RESPONSE	INFLAMMATORY RESPONSE	339	-0.30894756	-1.462265	0	0.20454146	1	1084
REGULATION OF NEUROTRANSMITTER TRANSPORT	REGULATION OF NEUROTRANS	58	-0.39720213	-1.461888	0.02	0.2044358	1	2332
PROTEASOME ACCESSORY COMPLEX	PROTEASOME ACCESSORY CO	23	-0.49786693	-1.4602864	0.06696428	0.20589502	1	7613
ENDORIBONUCLEASE COMPLEX	ENDORIBONUCLEASE COMPLEX	17	-0.5443269	-1.4595349	0.057395145	0.2062938	1	3691
BLOOD COAGULATION FIBRIN CLOT FORMATION	BLOOD COAGULATION FIBRIN C	22	-0.5074394	-1.4568717	0.057522126	0.20938872	1	363
REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS	REGULATION OF CYTOKINE BIO	77	-0.38490415	-1.4566895	0.029333333	0.209007	1	215
REGULATION OF PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE	REGULATION OF PRODUCTION	85	-0.3711027	-1.4553424	0.009925558	0.2101326	1	1444
CYTOPLASMIC TRANSLATION	CYTOPLASMIC TRANSLATION	38	-0.4432526	-1.4531518	0.03837472	0.21257405	1	6994
RRNA MODIFICATION	RRNA MODIFICATION	22	-0.507285	-1.4518151	0.06521739	0.21370053	1	3881
REGULATION OF ADENYLATE CYCLASE ACTIVITY	REGULATION OF ADENYLATE CY	64	-0.3960506	-1.45106	0.029023746	0.21404397	1	1467
INTERMEDIATE FILAMENT ORGANIZATION	INTERMEDIATE FILAMENT ORGA	19	-0.52850926	-1.4508499	0.05882353	0.2136798	1	715
SNAP RECEPTOR ACTIVITY	SNAP RECEPTOR ACTIVITY	33	-0.45146918	-1.4497415	0.046838406	0.2145873	1	3297
CELLULAR RESPONSE TO HYDROGEN PEROXIDE	CELLULAR RESPONSE TO HYDR	55	-0.41078296	-1.4493854	0.04379562	0.2145949	1	216
RESPONSE TO BACTERIUM	RESPONSE TO BACTERIUM	370	-0.30817643	-1.4477462	0	0.21622553	1	1153
EXOCRINE SYSTEM DEVELOPMENT	EXOCRINE SYSTEM DEVELOPM	43	-0.41932932	-1.4467467	0.040302265	0.2168338	1	937
RESPONSE TO PROTOZOAN	RESPONSE TO PROTOZOAN	18	-0.5235125	-1.446707	0.07392197	0.21622217	1	140
AMINO ACID BETAINE METABOLIC PROCESS	AMINO ACID BETAINE METABOL	18	-0.54725134	-1.4463378	0.07949791	0.21608591	1	3055
MYELOID LEUKOCYTE MIGRATION	MYELOID LEUKOCYTE MIGRATIO	73	-0.38488442	-1.4457092	0.02917772	0.21628095	1	1194
RESPONSE TO EXTRACELLULAR STIMULUS	RESPONSE TO EXTRACELLULAR	410	-0.30303368	-1.442221	0	0.22055115	1	1712
REGULATION OF NECROTIC CELL DEATH	REGULATION OF NECROTIC CE	23	-0.49624252	-1.4419107	0.07522124	0.22035748	1	1468
REGULATION OF ENDOCRINE PROCESS	REGULATION OF ENDOCRINE P	44	-0.42229626	-1.4413791	0.02739726	0.22047465	1	1038
POSITIVE REGULATION OF SECRETION	POSITIVE REGULATION OF SECR	316	-0.310219	-1.441378	0	0.21982126	1	2412
RNA CAPPING	RNA CAPPING	34	-0.44613087	-1.4404988	0.058252428	0.22034411	1	5723
REGULATION OF LYASE ACTIVITY	REGULATION OF LYASE ACTIVIT	78	-0.3792947	-1.4400505	0.031088082	0.22040416	1	922
MULTI MULTICELLULAR ORGANISM PROCESS	MULTI MULTICELLULAR ORGAN	178	-0.3349211	-1.4370419	0.006230529	0.22397721	1	1639
NEGATIVE REGULATION OF CYTOKINE SECRETION	NEGATIVE REGULATION OF CYT	31	-0.45390552	-1.4363214	0.058441557	0.22433162	1	1359
CELLULAR RESPONSE TO GLUCOSE STARVATION	CELLULAR RESPONSE TO GLUC	30	-0.45526192	-1.4361544	0.05491991	0.22391376	1	3972
OXIDOREDUCTASE ACTIVITY ACTING ON PEROXIDE AS ACCEPTOR	OXIDOREDUCTASE ACTIVITY AC	35	-0.4403891	-1.43615	0.049763035	0.2232646	1	40

POSITIVE REGULATION OF NF KAPPAB TRANSCRIPTION FACTOR ACTIV	POSITIVE REGULATION OF NF K		112	-0.354142	-1.435459	0.016	0.22362961	1	1468
POSITIVE REGULATION OF ALPHA BETA T CELL DIFFERENTIATION	POSITIVE REGULATION OF ALPH		31	-0.45109162	-1.4343241	0.058956917	0.22453584	1	2
NEGATIVE REGULATION OF PROTEOLYSIS	NEGATIVE REGULATION OF PRO		253	-0.3157989	-1.4331231	0	0.22563861	1	1310
REGULATION OF ALPHA BETA T CELL DIFFERENTIATION	REGULATION OF ALPHA BETA T		37	-0.43442369	-1.4322191	0.057208236	0.22635579	1	2
POSITIVE REGULATION OF PEPTIDE SECRETION	POSITIVE REGULATION OF PEPT		82	-0.36715126	-1.4312605	0.021447722	0.22703332	1	2412
REGULATION OF DOPAMINE SECRETION	REGULATION OF DOPAMINE SE		22	-0.49248195	-1.430936	0.06048387	0.22685581	1	867
OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCOR	OXIDOREDUCTASE ACTIVITY AC		26	-0.47041622	-1.4301897	0.06593407	0.22718418	1	1206
MULTI ORGANISM METABOLIC PROCESS	MULTI ORGANISM METABOLIC P		128	-0.34645948	-1.4299927	0.009345794	0.22683115	1	7455
CELLULAR METABOLIC COMPOUND SALVAGE	CELLULAR METABOLIC COMPOU		31	-0.46260047	-1.4293532	0.06418219	0.22725613	1	6576
DIGESTION	DIGESTION		100	-0.35716358	-1.4273509	0.021917809	0.22956927	1	1486
NUCLEOBASE BIOSYNTHETIC PROCESS	NUCLEOBASE BIOSYNTHETIC PI		17	-0.5214006	-1.424214	0.07805907	0.23370193	1	3055
REGULATION OF LIGASE ACTIVITY	REGULATION OF LIGASE ACTIVIT		119	-0.3451833	-1.4221232	0.012618297	0.23615907	1	5893
NEGATIVE REGULATION OF CALCIUM ION TRANSPORT	NEGATIVE REGULATION OF CAL		44	-0.421213	-1.421	0.035799522	0.23723716	1	400
INTERMEDIATE FILAMENT BASED PROCESS	INTERMEDIATE FILAMENT BASE		37	-0.42383933	-1.4203533	0.049881235	0.2375629	1	2001
NEGATIVE REGULATION OF BLOOD PRESSURE	NEGATIVE REGULATION OF BLO		41	-0.41764176	-1.4201684	0.055309735	0.23712546	1	3922
REGULATION OF RESPONSE TO WOUNDING	REGULATION OF RESPONSE TO		344	-0.30643508	-1.4168161	0	0.24156949	1	1311
ENDORIBONUCLEASE ACTIVITY PRODUCING 5 PHOSPHOMONOESTERS	ENDORIBONUCLEASE ACTIVITY		25	-0.47995478	-1.4150153	0.0787037	0.24379633	1	4909
RESPONSE TO TRANSITION METAL NANOPARTICLE	RESPONSE TO TRANSITION ME		130	-0.33859673	-1.4145788	0.009118541	0.2437639	1	1277
NUCLEIC ACID PHOSPHODIESTER BOND HYDROLYSIS	NUCLEIC ACID PHOSPHODIESTI		208	-0.32388794	-1.4141859	0	0.24365608	1	5057
EXCRETION	EXCRETION		42	-0.41379026	-1.4121912	0.0520362	0.24602704	1	1706
POSITIVE REGULATION OF DNA REPLICATION	POSITIVE REGULATION OF DNA		78	-0.3629849	-1.4110427	0.025252525	0.24713914	1	229
FOLIC ACID METABOLIC PROCESS	FOLIC ACID METABOLIC PROCE		17	-0.51644874	-1.4109027	0.08898305	0.24661696	1	5705
GLYCOSYL COMPOUND CATABOLIC PROCESS	GLYCOSYL COMPOUND CATABO		31	-0.45353988	-1.4098713	0.073068894	0.24746238	1	3179
LEUKOCYTE CHEMOTAXIS	LEUKOCYTE CHEMOTAXIS		91	-0.35307142	-1.4085457	0.02406417	0.24878691	1	1201
PIGMENT METABOLIC PROCESS	PIGMENT METABOLIC PROCESS		52	-0.4023851	-1.4080186	0.06367925	0.24888144	1	3591
PROTEIN LOCALIZATION TO MITOCHONDRION	PROTEIN LOCALIZATION TO MIT		59	-0.38216123	-1.4079753	0.035545025	0.2482795	1	7082
METAL CLUSTER BINDING	METAL CLUSTER BINDING		55	-0.39306262	-1.4076259	0.066831686	0.2480896	1	7443
POSITIVE REGULATION OF CHEMOKINE PRODUCTION	POSITIVE REGULATION OF CHE		40	-0.42287114	-1.4073389	0.061926607	0.2478202	1	319
POSITIVE REGULATION OF INSULIN SECRETION INVOLVED IN CELLULAR	POSITIVE REGULATION OF INSU		23	-0.488199	-1.4059256	0.09684685	0.24928598	1	4886

Down Regulated in APC^Pirc/++OX in relation to wild-type									
NAME	GS follow li	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX
EXTRACELLULAR MATRIX COMPONENT	EXTRACELLUL	Details ...	111	0.6992233	2.5978312	0	0	0	2354
ENSHEATHMENT OF NEURONS	ENSHEATHME	Details ...	83	0.6816524	2.414752	0	0	0	1680
PROTEINACEOUS EXTRACELLULAR MATRIX	PROTEINACEO	Details ...	292	0.5758632	2.3865523	0	0	0	1716
EXTRACELLULAR MATRIX BINDING	EXTRACELLUL	Details ...	41	0.739514	2.3541222	0	0	0	1697
EXTRACELLULAR MATRIX	EXTRACELLUL	Details ...	351	0.55319816	2.3176136	0	0	0	2452
COLLAGEN BINDING	COLLAGEN BIN	Details ...	50	0.708326	2.3174088	0	0	0	1620
REGULATION OF CARTILAGE DEVELOPMENT	REGULATION O	Details ...	51	0.70255125	2.3109586	0	0	0	2601
COLLAGEN TRIMER	COLLAGEN TR	Details ...	67	0.66677797	2.3083568	0	0	0	1679
REGULATION OF CHONDROCYTE DIFFERENTIATION	REGULATION O	Details ...	37	0.76406735	2.3068252	0	0	0	2601
BASEMENT MEMBRANE	BASEMENT ME	Details ...	81	0.6520201	2.280848	0	0	0	2354
COMPLEX OF COLLAGEN TRIMERS	COMPLEX OF C	Details ...	22	0.83910173	2.278998	0	0	0	1679

BONE DEVELOPMENT	BONE DEVELO	Details ...	141	0.5865296	2.270413	0	0	0	2185
CELL MATRIX ADHESION	CELL MATRIX	Details ...	103	0.61496246	2.2502763	0	0	0	2437
EXTRACELLULAR STRUCTURE ORGANIZATION	EXTRACELLUL	Details ...	260	0.5402207	2.222778	0	1.49E-04	0.002	2473
CELL SUBSTRATE ADHESION	CELL SUBSTR	Details ...	144	0.5697678	2.1820848	0	3.47E-04	0.005	2437
CHONDROCYTE DIFFERENTIATION	CHONDROCY	Details ...	53	0.66284615	2.1816912	0	3.25E-04	0.005	2139
NEGATIVE REGULATION OF TRANSFORMING GROWTH FACTOR BETA	NEGATIVE RE	Details ...	59	0.6378764	2.155715	0	4.90E-04	0.008	1105
SCHWANN CELL DIFFERENTIATION	SCHWANN CE	Details ...	30	0.73784286	2.151092	0	5.81E-04	0.01	2575
CANONICAL WNT SIGNALING PATHWAY	CANONICAL W	Details ...	75	0.6160004	2.1480687	0	6.04E-04	0.011	1589
SKELETAL SYSTEM DEVELOPMENT	SKELETAL SYS	Details ...	396	0.49951655	2.126146	0	0.001146836	0.021	2185
ENDOCHONDRAL BONE MORPHOGENESIS	ENDOCHOND	Details ...	41	0.6743561	2.1220813	0	0.001192407	0.023	2161
BONE MORPHOGENESIS	BONE MORPH	Details ...	69	0.61362857	2.1189167	0	0.001327559	0.027	2161
CONNECTIVE TISSUE DEVELOPMENT	CONNECTIVE	Details ...	166	0.5346225	2.1020133	0	0.001723111	0.036	2185
CARTILAGE DEVELOPMENT	CARTILAGE DE	Details ...	128	0.55716497	2.1002471	0	0.001651315	0.036	2185
POSITIVE REGULATION OF STEM CELL DIFFERENTIATION	POSITIVE REG	Details ...	43	0.65838027	2.0897753	0	0.001878162	0.043	1063
REGULATION OF STEM CELL DIFFERENTIATION	REGULATION	Details ...	95	0.5726009	2.0874763	0	0.001886995	0.045	1221
REGULATION OF CELLULAR RESPONSE TO TRANSFORMING GROWTH	REGULATION	Details ...	87	0.5764726	2.0872536	0	0.001817106	0.045	1105
SKELETAL SYSTEM MORPHOGENESIS	SKELETAL SYS	Details ...	166	0.5279275	2.0839016	0	0.001939769	0.05	2161
PERIPHERAL NERVOUS SYSTEM AXON ENSHEATHMENT	PERIPHERAL N	Details ...	21	0.7728995	2.0830863	0	0.001979958	0.053	1182
COLLAGEN FIBRIL ORGANIZATION	COLLAGEN FIB	Details ...	34	0.6993348	2.0652502	0	0.002575385	0.071	2608
MEMBRANE PROTEIN PROTEOLYSIS	MEMBRANE P	Details ...	33	0.69261014	2.0591502	0	0.002794588	0.078	1947
SCHWANN CELL DEVELOPMENT	SCHWANN CE	Details ...	25	0.73166883	2.0539007	0	0.003031134	0.087	1867
REGULATION OF CELLULAR RESPONSE TO GROWTH FACTOR STIMULU	REGULATION	Details ...	197	0.5097253	2.051497	0	0.003001672	0.089	1206
SMAD BINDING	SMAD BINDIN	Details ...	62	0.6049491	2.0484452	0	0.002975029	0.09	2476
BETA CATENIN BINDING	BETA CATENIN	Details ...	73	0.5839476	2.0358965	0	0.003485941	0.109	1734
EXTRACELLULAR MATRIX STRUCTURAL CONSTITUENT	EXTRACELLUL	Details ...	63	0.59945196	2.0261571	0	0.003822845	0.123	1679
APPENDAGE DEVELOPMENT	APPENDAGE D	Details ...	133	0.5279114	2.0248644	0	0.003775477	0.125	2802
REGULATION OF SMALL GTPASE MEDIATED SIGNAL TRANSDUCTION	REGULATION	Details ...	248	0.49366313	2.024741	0	0.003676122	0.125	2584
GLIAL CELL DIFFERENTIATION	GLIAL CELL DI	Details ...	123	0.535029	2.015629	0	0.004114042	0.138	1989
REGULATION OF LAMELLIPODIUM ORGANIZATION	REGULATION	Details ...	32	0.68065745	2.0149183	0	0.004011191	0.138	2160
EMBRYONIC EYE MORPHOGENESIS	EMBRYONIC E	Details ...	31	0.677109	2.01426	0.001795332	0.003913357	0.138	1025
ENDODERM DEVELOPMENT	ENDODERM D	Details ...	60	0.5972082	2.0071712	0	0.004468182	0.159	1366
REGULATION OF EPITHELIAL TO MESENCHYMAL TRANSITION	REGULATION	Details ...	58	0.6034728	2.0067313	0	0.004364271	0.159	1221
SENSORY ORGAN MORPHOGENESIS	SENSORY OR	Details ...	206	0.49415582	2.0053625	0	0.004525335	0.17	2409
LAMELLIPODIUM MEMBRANE	LAMELLIPODIU	Details ...	19	0.7451145	2.0038557	0	0.004563333	0.175	1858
NEGATIVE REGULATION OF CELL JUNCTION ASSEMBLY	NEGATIVE RE	Details ...	18	0.76398754	2.0000577	0	0.004893971	0.193	2160
MUSCLE ORGAN DEVELOPMENT	MUSCLE ORG	Details ...	230	0.49222553	1.9988596	0	0.0049667	0.201	1537
EAR DEVELOPMENT	EAR DEVELOP	Details ...	159	0.5118388	1.9982015	0	0.004905887	0.202	2049
TRABECULA FORMATION	TRABECULA F	Details ...	20	0.7541097	1.9968579	0	0.004869513	0.205	1946
POSITIVE REGULATION OF CARTILAGE DEVELOPMENT	POSITIVE REG	Details ...	21	0.7382876	1.9934283	0	0.005042414	0.216	2846
NEGATIVE REGULATION OF CELLULAR RESPONSE TO GROWTH FACTO	NEGATIVE RE	Details ...	104	0.53408754	1.9905947	0	0.005230209	0.226	1206