

'F1-Lupus vs F1-Prediseased LSK cells' :

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
GO_ENZYME_ACTIVATOR_ACTIVITY	391	0.6710666	1.3832359	0	0.2588997
GO_REGULATION_OF_PROTEIN_SERI	403	0.6718564	1.3895319	0	0.2571424
GO_ENDOSOMAL_PART	344	0.67477906	1.3853567	0.003222342	0.25698587
GO_PURINE_NUCLEOBASE_METABOL	16	0.895425	1.3855412	0.0311042	0.25691342
GO_CALCIIUM_MEDIATED_SIGNALING	64	0.76634187	1.3858737	0.031047866	0.25687948
GO_SYMPORTER_ACTIVITY	100	0.7405091	1.3852551	0.017369727	0.2566772
GO_MODIFIED_AMINO_ACID_BINDIN	47	0.80190915	1.3895053	0.024489796	0.25646
GO_SPHINGOLIPID_BIOSYNTHETIC_P	60	0.76397103	1.3889934	0.051317614	0.25640625
GO_VIRUS_RECEPTOR_ACTIVITY	57	0.7745455	1.3858194	0.035278156	0.2563714
GO_CELLULAR_RESPONSE_TO_PROST	17	0.9142703	1.3894184	0.025931928	0.25610176
GO_POSITIVE_REGULATION_OF_NEU	20	0.88517135	1.3888983	0.028301887	0.2560527
GO_ACTIN_CYTOSKELETON_REORGAI	51	0.80187577	1.3847283	0.028328612	0.25604433
GO_REGULATION_OF_CYSTEINE_TYPI	21	0.8619443	1.3849261	0.06097561	0.25599495
GO_POSITIVE_REGULATION_OF_CELL	175	0.70958817	1.3852433	0.012865497	0.25598738
GO_PEPTIDE_CATABOLIC_PROCESS	18	0.892381	1.3888053	0.022913257	0.25570428
GO_REGULATION_OF_CARBOHYDRAI	66	0.76215506	1.3846388	0.030985916	0.25566703
GO_CLATHRIN_COATED_VESICLE	119	0.7207691	1.3903683	0.013365735	0.25563955
GO_ISOPRENOID_METABOLIC_PROCE	80	0.7512304	1.3883622	0.02890933	0.2555107
GO_RESPONSE_TO_PROGESTERONE	39	0.81662834	1.3852091	0.025714286	0.25537154
GO_REGULATION_OF_VASOCONSTRI	42	0.8065365	1.3894063	0.033045977	0.25536117
GO_POSITIVE_REGULATION_OF_ACTI	53	0.78891057	1.3841995	0.036568213	0.25535658
GO_REGULATION_OF_CELL_SUBSTRA	141	0.7141809	1.3863876	0.010600707	0.25529823
GO_GTP_RHO_BINDING	15	0.9141559	1.3906331	0.023696683	0.25520572
GO_MACROPHAGE_DIFFERENTIATIOI	18	0.8844071	1.3887557	0.0234375	0.25513396
GO_REGULATION_OF_CELLULAR_SEN	23	0.8681616	1.3924452	0.02603369	0.25513014
GO_RESPONSE_TO_X_RAY	28	0.8448824	1.384602	0.03937008	0.2551164
GO_APICAL_PLASMA_MEMBRANE	203	0.6902104	1.3901244	0.005636978	0.2551136
GO_POSITIVE_REGULATION_OF_PRO	91	0.7447436	1.3903242	0.025252525	0.25503594
GO_ORGANIC_ACID_TRANSPORT	181	0.69536173	1.3868183	0.011627907	0.25494775
GO_RESPONSE_TO_ISOQUINOLINE_A	21	0.87094766	1.3844733	0.03742515	0.25493532
GO_REGULATION_OF_CELL_AGING	28	0.8397684	1.3883345	0.04613095	0.2548654
GO_REGULATION_OF_LIPID_BIOSYNT	96	0.7423045	1.388008	0.015151516	0.25482544
GO_REGULATION_OF_COAGULATION	65	0.7698173	1.392335	0.030303031	0.2548201
GO_MONOCARBOXYLIC_ACID_TRANSC	86	0.7452284	1.3866922	0.031168832	0.25479576
GO_POSITIVE_REGULATION_OF_ADA	64	0.77578425	1.388661	0.032388665	0.25477678
GO_PHOTOTRANSDUCTION	27	0.8464539	1.3882073	0.0461997	0.25464937
GO_PROTEIN_KINASE_B_SIGNALING	30	0.8399604	1.3870646	0.029940119	0.25459576
GO_ALCOHOL_CATABOLIC_PROCESS	41	0.8091552	1.387936	0.038297873	0.25433785
GO_SPHINGOLIPID_METABOLIC_PRO	107	0.744251	1.3922809	0.011435832	0.25423843
GO_APICAL_PART_OF_CELL	251	0.6859719	1.3878832	0.006622517	0.25382328
GO_REGULATION_OF_FATTY_ACID_B	28	0.853016	1.3962702	0.028614458	0.25369343
GO_REGULATION_OF_STEM_CELL_PF	64	0.77603155	1.3922665	0.030831099	0.25347003
GO_HYDROLASE_ACTIVITY_ACTING_C	88	0.74731433	1.3878057	0.012936611	0.25337845
GO_FLAVIN_ADENINE_DINUCLEOTIDI	64	0.7729831	1.3930515	0.028150134	0.2531531
KEGG_TOLL_LIKE_RECEPTOR_SIGNAL	85	0.7475892	1.392158	0.025735294	0.25310427
GO_INTERACTION_WITH_SYMBIONT	43	0.7952255	1.3877299	0.035460994	0.2530554
GO_REGULATION_OF_LIPID_METABC	212	0.693961	1.3962226	0.005580357	0.25297433
GO_L_AMINO_ACID_TRANSMEMBRA	40	0.8151692	1.3956802	0.03211679	0.25284326

KEGG_PATHOGENIC_ESCHERICHIA_C	51	0.79386634	1.3960974	0.024725275	0.25262114
GO_RETINA_LAYER_FORMATION	15	0.9045572	1.3920996	0.03169572	0.25258362
GO_CELL_CHEMOTAXIS	120	0.7163635	1.3876761	0.022031823	0.2525692
GO_DORSAL_VENTRAL_AXIS_SPECIFI	15	0.90469694	1.3969272	0.02866779	0.25246286
GO_DEFENSE_RESPONSE_TO_GRAM_	46	0.80984604	1.3955803	0.026098901	0.25240368
GO_REGULATION_OF_FAT_CELL_DIF	86	0.7496554	1.3919907	0.02022756	0.25224826
GO_NEGATIVE_REGULATION_OF_DEI	108	0.73994637	1.3938248	0.01726264	0.25219902
KEGG_FC_GAMMA_R_MEDIATED_PH	87	0.75941455	1.3960012	0.019206146	0.25211853
GO_CARBOHYDRATE_CATABOLIC_PR	84	0.7465197	1.3914713	0.032953106	0.25207448
GO_CELLULAR_GLUCOSE_HOMEOSTA	60	0.7761563	1.3968223	0.027586207	0.252062
GO_ORGANIC_ACID_SODIUM_SYMP	20	0.8893604	1.3917186	0.02878788	0.2518162
GO_NEGATIVE_REGULATION_OF_NEI	15	0.89928335	1.3919158	0.045528457	0.25176883
GO_REGULATION_OF_CELLULAR_EXT	21	0.8975049	1.3937553	0.014173228	0.251657
GO_REGULATION_OF_VESICLE_FUSIC	53	0.78650206	1.3935668	0.024793388	0.2516517
GO_POSITIVE_REGULATION_OF_G1_!	21	0.8876433	1.3941305	0.027522936	0.25161284
GO_RESPONSE_TO_INORGANIC_SUB:	376	0.6790438	1.3955692	0	0.25160706
GO_DEFENSE_RESPONSE_TO_FUNGU	20	0.87398446	1.3954576	0.03305785	0.25129992
GO_ORGANONITROGEN_COMPOUND	251	0.684584	1.3953285	0.003333333	0.25112608
GO_CALCIIUM_DEPENDENT_PROTEIN	46	0.79740155	1.3950715	0.040389974	0.2506281
GO_POSITIVE_REGULATION_OF_OXID	35	0.8176959	1.3945153	0.043041606	0.25059304
GO_PHOSPHOLIPASE_C_ACTIVITY	25	0.8530475	1.3953059	0.03748126	0.25037587
GO_CADHERIN_BINDING	21	0.8897422	1.3950344	0.027070064	0.2499143
GO_MITOCHONDRION_MORPHOGEN	18	0.9063884	1.3949457	0.0256	0.24953578
GO_NEGATIVE_REGULATION_OF_IMI	74	0.76031077	1.3987218	0.020860495	0.24648961
GO_RESPONSE_TO_PLATELET_DERIVI	17	0.9224143	1.4002033	0.009389672	0.24598709
GO_POSITIVE_REGULATION_OF_LIPI	98	0.74115235	1.3987151	0.020050125	0.24563035
GO_LATERAL_PLASMA_MEMBRANE	41	0.81446487	1.4001082	0.025677603	0.24545777
GO_UNSATURATED_FATTY_ACID_ME	65	0.77658457	1.3999009	0.020463847	0.24541892
GO_POSITIVE_REGULATION_OF_LIPI	16	0.9127667	1.4016418	0.018675722	0.24492411
GO_REGULATION_OF_FATTY_ACID_N	64	0.77811974	1.3986864	0.024423338	0.24489091
GO_PROTEIN_MATURATION	207	0.70158	1.3996778	0.005586592	0.24462365
GO_FATTY_ACID_DERIVATIVE_BIOSY	32	0.84789145	1.3998973	0.030701755	0.24455188
GO_AUTOPHAGY	315	0.6809226	1.4009458	0.003285871	0.24438773
GO_NEGATIVE_REGULATION_OF_ENI	30	0.84243774	1.4007846	0.038123168	0.24431887
GO_GASTRULATION_WITH_MOUTH_	19	0.8898029	1.3994286	0.027906977	0.24413678
GO_POSITIVE_REGULATION_OF_INTE	40	0.82889104	1.4016348	0.025641026	0.2440411
GO_NEGATIVE_REGULATION_OF_CYT	32	0.8426755	1.3996212	0.03976436	0.24398421
GO_POSITIVE_REGULATION_OF_INFL	81	0.75814503	1.4015944	0.02638191	0.2432796
GO_NEGATIVE_REGULATION_OF_PRC	78	0.7707205	1.4014115	0.02387268	0.24320309
GO_TISSUE_HOMEOSTASIS	128	0.72124505	1.4022954	0.011042945	0.24261355
GO_CELL_ACTIVATION_INVOLVED_IN	110	0.7395869	1.4027643	0.013767209	0.24131495
GO_REGULATION_OF_MITOCHONDR	45	0.810969	1.4031951	0.030726258	0.24021506
GO_RETINA_HOMEOSTASIS	43	0.81230646	1.4042536	0.027220631	0.2398817
GO_REGULATION_OF_INTERLEUKIN_	52	0.79560167	1.4040978	0.021768708	0.23968789
GO_REGULATION_OF_TRANSCRIPTIO	19	0.89964163	1.4035283	0.022435898	0.2395883
GO_PHOSPHOLIPASE_C_ACTIVATING	47	0.8113322	1.4040194	0.024523161	0.23917368
GO_MEMBRANE_PROTEIN_INTRACEL	16	0.9005994	1.4047911	0.031613976	0.23907974
GO_EXTERNAL_SIDE_OF_PLASMA_M	177	0.70747316	1.4052079	0.009029346	0.23907533
GO_IRON_ION_TRANSPORT	40	0.82111394	1.4045955	0.027818449	0.23905763
GO_REGULATION_OF_PROTEIN_PHO	22	0.89291656	1.4050939	0.012480499	0.23865736

GO_REGULATION_OF_PROTEIN_ACTI	19	0.9123826	1.4055182	0.006153846	0.23857476
KEGG_ABC_TRANSPORTERS	34	0.8333482	1.4039854	0.019174041	0.23839362
GO_ERYTHROCYTE_HOMEOSTASIS	64	0.78990406	1.4059454	0.015789473	0.23832151
KEGG_ECM_RECEPTOR_INTERACTIO	72	0.77240944	1.4057931	0.020075282	0.23814954
GO_WATER_HOMEOSTASIS	40	0.8254635	1.4071773	0.018361581	0.23356207
KEGG_PATHWAYS_IN_CANCER	274	0.6929967	1.4074985	0.002166847	0.23308988
KEGG_BLADDER_CANCER	38	0.83237106	1.4085567	0.018597998	0.22911407
GO_APOPTOTIC_CELL_CLEARANCE	23	0.87142724	1.4095322	0.031201247	0.22837518
GO_REGULATION_OF_INTERLEUKIN_	82	0.7531842	1.4089277	0.015384615	0.22824395
GO_PHOSPHATIDYLSERINE_BINDING	23	0.87064373	1.4095271	0.03776435	0.22747135
GO_POSITIVE_REGULATION_OF_CELL	24	0.88423103	1.4093176	0.019578313	0.22747
GO_POSITIVE_REGULATION_OF_PRO	71	0.7736888	1.410172	0.014686248	0.2265447
GO_BASOLATERAL_PLASMA_MEMBR	160	0.7220456	1.4117787	0.004705882	0.22376351
GO_POSITIVE_REGULATION_OF_COA	19	0.89874214	1.4126902	0.01088647	0.22369197
GO_REGULATION_OF_CELL_JUNCTIO	56	0.7914457	1.411003	0.025956284	0.22356534
GO_LYTIC_VACUOLE	426	0.68913704	1.4129031	0	0.22354484
GO_EXOCYST	15	0.92146254	1.4131042	0.01540832	0.22349712
GO_HOMEOSTASIS_OF_NUMBER_OF	159	0.7206456	1.4138099	0.007211539	0.22337238
GO_FATTY_ACID_DERIVATIVE_METAI	55	0.80055207	1.4112563	0.018741634	0.22332233
GO_RESPONSE_TO_METAL_ION	256	0.6979849	1.4116756	0.006564552	0.22325225
GO_CELL_JUNCTION_ASSEMBLY	117	0.7392181	1.4126256	0.011111111	0.22298568
GO_PROTEIN_COMPLEX_INVOLVED_I	29	0.8528769	1.4137075	0.022189349	0.22286703
GO_MITOCHONDRION_ORGANIZATIO	493	0.6776178	1.4115672	0	0.22270937
GO_REGULATION_OF_PROTEIN_POLY	141	0.72315055	1.4124695	0.011990408	0.22266203
GO_PHAGOCYTOTIC_VESICLE	73	0.7709698	1.4135484	0.017173052	0.22248982
GO_RUFFLE	143	0.7281809	1.4142739	0.008284024	0.22220616
GO_REGULATION_OF_ANION_TRANS	22	0.8811512	1.4123667	0.021103896	0.22213253
GO_LIPOPOLYSACCHARIDE_MEDIATE	30	0.86571723	1.4146595	0.021341464	0.22145207
GO_REGULATION_OF_LIGASE_ACTIVI	116	0.7361986	1.415741	0.011070111	0.21722181
GO_ORGANIC_ANION_TRANSMEMBR	119	0.73568577	1.4173107	0.00373599	0.2121416
GO_RESPONSE_TO_ANTIANTIBIOTIC	41	0.82712984	1.4172411	0.024566473	0.21150811
GO_EMBRYONIC_HEMOPOIESIS	17	0.9145337	1.4185536	0.022544283	0.21056367
GO_ORGANIC_HYDROXY_COMPOUND	48	0.8134279	1.4183447	0.027247956	0.21045032
GO_REGULATION_OF_LIPID_STORAG	35	0.84602416	1.4181753	0.018080669	0.2101933
GO_POSITIVE_REGULATION_OF_CAR	57	0.7959189	1.418883	0.017615177	0.21011487
GO_POSITIVE_REGULATION_OF_LEUC	64	0.7924632	1.4181387	0.015006822	0.2094152
GO_ACID_SECRETION	38	0.82966375	1.4198306	0.022857143	0.20877442
GO_RESPONSE_TO_IONIZING_RADIA	127	0.74133456	1.4196442	0.005966587	0.20859575
GO_ENDODERM_DEVELOPMENT	56	0.8041762	1.4195125	0.011065007	0.2082969
GO_NEGATIVE_REGULATION_OF_CEL	19	0.9261853	1.4213054	0.009419153	0.2077998
GO_MRNA_PROCESSING	358	0.6943593	1.4215595	0	0.20759606
GO_ORGANIC_HYDROXY_COMPOUND	105	0.76272804	1.4203508	0.008728179	0.20720166
KEGG_HEMATOPOIETIC_CELL_LINEA	71	0.77633274	1.4212623	0.022727273	0.20694152
GO_RUFFLE_MEMBRANE	70	0.7734134	1.4211653	0.01953125	0.20635144
GO_REGULATION_OF_HUMORAL_IM	27	0.86211973	1.4207537	0.02503682	0.20629472
GO_RESPONSE_TO_KETONE	138	0.7354733	1.4210359	0.005882353	0.2060156
GO_NEGATIVE_REGULATION_OF_FIB	23	0.8949708	1.4231192	0.013353116	0.20441607
GO_COATED_VESICLE	181	0.7208656	1.4227694	0.008139535	0.20404051
GO_CELLULAR_RESPONSE_TO_CARBO	60	0.8023996	1.4230093	0.008368201	0.20386334
GO_PROTEOGLYCAN_BIOSYNTHETIC_	44	0.80811137	1.4226776	0.023054754	0.20346358

GO_PROTEIN_N_TERMINUS_BINDING	93	0.7610034	1.4239099	0.015306123	0.20183426
GO_REGULATION_OF_GLYCOPROTEIN	34	0.8359414	1.4255521	0.02111614	0.19971035
GO_RESPONSE_TO_FUNGUS	30	0.8584242	1.4246293	0.017001545	0.19967473
GO_CELL_JUNCTION_ORGANIZATION	150	0.726061	1.4262102	0.004784689	0.19876848
GO_AMINO_ACID_TRANSMEMBRANE	57	0.806271	1.4255478	0.013386881	0.1987183
KEGG_ARACHIDONIC_ACID_METABO	34	0.839859	1.4253765	0.025824964	0.19835036
GO_REGULATION_OF_PEPTIDASE_AC	256	0.70682245	1.4260821	0.002207506	0.19822766
GO_NEURAL_RETINA_DEVELOPMENT	35	0.83786446	1.4253616	0.02238806	0.19741297
GO_REGULATION_OF_ADHERENS_JU	43	0.82717437	1.4273908	0.017069701	0.19570443
GO_SOLUTE_SODIUM_SYMPORTER_A	32	0.8525916	1.4272536	0.020895522	0.19526431
GO_ERYTHROCYTE_DEVELOPMENT	20	0.89451516	1.4280015	0.015748031	0.19393834
GO_PLASMA_MEMBRANE_RAFT	66	0.7840056	1.4286711	0.015957447	0.19307324
GO_EXTRACELLULAR_MATRIX	285	0.7026269	1.4290985	0.00326087	0.1921883
GO_MOTILE_CILIUM	67	0.78990436	1.4286613	0.014379085	0.19210237
GO_REGULATION_OF_NEUTROPHIL_I	24	0.8941772	1.4305212	0.013595167	0.18905438
GO_ACTIVE_TRANSMEMBRANE_TRAI	250	0.7061822	1.4312853	0.001106195	0.18890196
GO_REGULATION_OF_NECROTIC_CEL	20	0.90380687	1.4303837	0.00619195	0.18859313
GO_SYNAPSIS	19	0.9107394	1.4312111	0.020092735	0.1882253
GO_LIPID_PARTICLE	49	0.80733633	1.4302732	0.012379643	0.18817669
GO_HYDROLASE_ACTIVITY_ACTING_C	117	0.7464428	1.4320216	0.011138614	0.18777367
GO_REGULATION_OF_LEUKOCYTE_M	119	0.7432381	1.4310766	0.009937888	0.18768051
GO_CELLULAR_RESPONSE_TO_PROST	19	0.91166484	1.4318765	0.011570248	0.18739672
GO_UDP_GLYCOSYLTRANSFERASE_AC	88	0.7656266	1.4326239	0.011292347	0.18634646
GO_REGULATION_OF_REACTIVE_OXY	127	0.74288654	1.4333649	0.008599509	0.1841296
GO_POSITIVE_REGULATION_OF_INTE	53	0.8149337	1.4337317	0.010973937	0.18355076
KEGG_FOCAL_ADHESION	173	0.7204518	1.4356046	0.004667445	0.18245937
GO_P53_BINDING	57	0.8147499	1.4348276	0.018156424	0.18184312
GO_POSITIVE_REGULATION_OF_EXTF	45	0.81983155	1.4346428	0.013812155	0.18160927
GO_CYTOKINE_PRODUCTION	101	0.76711917	1.4355952	0.008652657	0.18143667
GO_POSITIVE_REGULATION_OF_INTE	54	0.8075491	1.4344373	0.02097902	0.18139057
GO_POSITIVE_REGULATION_OF_WOI	37	0.86142504	1.4354668	0.004451039	0.18098699
GO_POSITIVE_REGULATION_OF_CYT	311	0.70002127	1.4353383	0	0.18059261
GO_NEGATIVE_REGULATION_OF_SEC	136	0.73868227	1.4368517	0.006097561	0.1801364
GO_MRNA_3_END_PROCESSING	67	0.79177445	1.4363801	0.02549575	0.17991702
GO_CELL_SUBSTRATE_JUNCTION_AS	38	0.8342993	1.4367082	0.023529412	0.17966396
GO_CARBOHYDRATE_BIOSYNTHETIC	98	0.75872743	1.4379474	0.014066496	0.17758326
GO_POSITIVE_REGULATION_OF_FAT	40	0.8397142	1.4377327	0.020028612	0.17736356
GO_CELLULAR_TRANSITION_METAL	60	0.79767174	1.4390132	0.015027323	0.17512368
GO_REGULATION_OF_WOUND_HEAL	95	0.7628251	1.4393822	0.006321113	0.17460372
GO_PEPTIDE_CROSS_LINKING	18	0.92375034	1.4389344	0.014018691	0.17434041
GO_POSITIVE_REGULATION_OF_ERYT	21	0.9266866	1.4405563	0.003139718	0.17370944
GO_NEGATIVE_REGULATION_OF_CYT	173	0.73181534	1.4404272	0.003464203	0.17315589
GO_RESPONSE_TO_PROSTAGLANDIN	20	0.9099377	1.4402688	0.019431988	0.17280611
KEGG_ALZHEIMERS_DISEASE	138	0.74394655	1.4400414	0.004830918	0.1726903
GO_PROTEIN_IMPORT	130	0.7423372	1.4430523	0.003640777	0.16567287
GO_REGULATION_OF_ERYTHROCYTE	34	0.8623919	1.444616	0.005813954	0.16540305
GO_REGULATION_OF_EXTRINSIC_API	127	0.7498144	1.4439099	0.007425743	0.16500248
GO_MITOGEN_ACTIVATED_PROTEIN	22	0.8944767	1.4444305	0.01104101	0.16499029
GO_NUCLEOBASE_METABOLIC_PROC	32	0.8675055	1.443037	0.011730205	0.16468658
GO_AMINO_ACID_TRANSMEMBRANE	50	0.81056166	1.4437698	0.014986376	0.16452987

GO_ORGANIC_ACID_TRANSMEMBRA	79	0.77928954	1.443636	0.009090909	0.16406223
GO_POSITIVE_REGULATION_OF_REAI	73	0.7972111	1.444391	0.007884363	0.16401884
GO_TRANSITION_METAL_ION_HOME	84	0.776557	1.4455775	0.010126582	0.16384181
GO_DOUBLE_STRANDED_RNA_BINDI	53	0.8113217	1.4453584	0.012569833	0.16368213
KEGG_LEISHMANIA_INFECTION	63	0.79842716	1.4482554	0.01462766	0.16279654
GO_HOMOLOGOUS_CHROMOSOME_	26	0.89796317	1.4481735	0.01065449	0.16189021
GO_VESICLE_LUMEN	73	0.79024005	1.4513929	0.005089059	0.16143888
GO_POSITIVE_REGULATION_OF_CELL	58	0.806507	1.4480668	0.012622721	0.1611654
GO_POSITIVE_REGULATION_OF_CYTC	75	0.78179157	1.4517814	0.014084507	0.16102274
GO_REGULATION_OF_RESPONSE_TO	181	0.7197969	1.4471078	0.002325581	0.16068457
GO_REGULATION_OF_TUMOR_NECR	87	0.77564013	1.446595	0.002607562	0.16067524
GO_REGULATION_OF_LEUKOCYTE_CI	76	0.7871527	1.4510202	0.002656043	0.1605468
GO_REGULATION_OF_OXIDOREDUCT	67	0.79665345	1.4513175	0.005563282	0.16050555
GO_ATPASE_ACTIVITY_COUPLED	272	0.71061164	1.4468844	0	0.16043122
GO_ENDOCYTOSIS	412	0.6993187	1.4474756	0	0.16023207
GO_NEGATIVE_REGULATION_OF_IMI	286	0.7152714	1.4480436	0.002173913	0.16014531
GO_MYELOID_CELL_HOMEOSTASIS	78	0.78517073	1.4508524	0.005270092	0.16011924
GO_MONOSACCHARIDE_BINDING	53	0.8220276	1.4503675	0.009589041	0.15969568
GO_REGULATION_OF_FIBROBLAST_P	66	0.8062344	1.4495573	0.00795756	0.15958562
GO_ATPASE_ACTIVITY_COUPLED_TO	96	0.76740044	1.4494047	0.010012516	0.1592069
GO_PROTEIN_SERINE_THREONINE_K	16	0.95387214	1.4502172	0.001579779	0.15913166
GO_SINGLE_STRANDED_DNA_BINDIN	73	0.8107194	1.4480263	0.006578947	0.15909414
GO_ACUTE_PHASE_RESPONSE	28	0.89372176	1.4508358	0.004444445	0.15898944
GO_DEFENSE_RESPONSE_TO_GRAM_	33	0.8583844	1.4499991	0.012931035	0.1588785
GO_MULTICELLULAR_ORGANISMAL_	194	0.7321961	1.4529561	0.001150748	0.15746321
GO_MONOCARBOXYLIC_ACID_BINDII	34	0.8646592	1.4539578	0.010248902	0.15444118
GO_HEPARIN_BINDING	100	0.7757374	1.4545935	0.003740648	0.15325008
GO_REGULATION_OF_TOLL_LIKE_REC	43	0.8359863	1.4551413	0.012640449	0.15198639
GO_SECRETORY_GRANULE_LUMEN	54	0.8195987	1.4561164	0.006887052	0.15189089
GO_REGULATION_OF_CYTOKINE_PRC	458	0.6978737	1.4557939	0	0.15071778
GO_RESPONSE_TO_ISCHEMIA	24	0.8977256	1.4561133	0.006097561	0.150656
KEGG_REGULATION_OF_ACTIN_CYTC	181	0.7418393	1.457022	0.003401361	0.14950073
GO_ANTIGEN_PROCESSING_AND_PR	54	0.8260309	1.4581767	0.00698324	0.14862838
GO_NEGATIVE_REGULATION_OF_EST	165	0.73832494	1.4599246	0.007058824	0.14838174
GO_MONOCARBOXYLIC_ACID_TRAN	28	0.8866444	1.4579076	0.004531722	0.14835224
GO_ORGANELLE_DISASSEMBLY	151	0.7416605	1.4603972	0.004756243	0.14782538
GO_RESPONSE_TO_MOLECULE_OF_B	273	0.71828264	1.459859	0.001091703	0.14735715
GO_POSITIVE_REGULATION_OF_CYTC	52	0.8072244	1.4578605	0.016830295	0.14730717
GO_POSITIVE_REGULATION_OF_CELL	82	0.78628623	1.4597732	0.009079118	0.14633228
GO_POSITIVE_REGULATION_OF_PRO	158	0.7366934	1.4596721	0.002386635	0.14547575
GO_RESPONSE_TO_PROSTAGLANDIN	23	0.9055794	1.4593921	0.009803922	0.1452219
GO_REGULATION_OF_PROTEIN_SECF	291	0.7138022	1.4618478	0	0.14317374
GO_EXTRACELLULAR_MATRIX_DISAS:	53	0.8175001	1.462769	0.015172414	0.14112766
GO_CYTOPLASMIC_VESICLE_PART	443	0.7079127	1.4632969	0	0.14023858
GO_GLYCOSAMINOGLYCAN_BINDING	129	0.7572946	1.4644489	0.004889976	0.1369867
GO_REGULATION_OF_VESICLE_MEDI	367	0.7081478	1.465346	0	0.13461503
KEGG_PRION_DISEASES	30	0.88214034	1.4686072	0.004545454	0.12701444
GO_NEGATIVE_REGULATION_OF_TRA	332	0.7126796	1.4676592	0	0.12691948
KEGG_SMALL_CELL_LUNG_CANCER	78	0.7967757	1.4685948	0.005270092	0.12584586
GO_GRANULOCYTE_MIGRATION	50	0.83925575	1.4684283	0.002816901	0.1253224

GO_PHAGOCYTOSIS	157	0.7511608	1.469462	0	0.12508976
GO_CELLULAR_CARBOHYDRATE_MET	112	0.7655532	1.4706421	0.006119951	0.12335611
GO_REGULATION_OF_GRANULOCYTE	29	0.8930961	1.470251	0.004538578	0.123291835
GO_CYTOPLASMIC_STRESS_GRANULE	29	0.89516973	1.4722273	0.008759124	0.119665116
KEGG_NOD_LIKE_RECEPTOR_SIGNAL	50	0.8302313	1.4719626	0.004087193	0.11930569
GO_SUBSTRATE_ADHESION_DEPEND	36	0.87596	1.4756073	0.004341534	0.113049276
GO_HEMATOPOIETIC_PROGENITOR_I	83	0.79087776	1.475327	0.005063291	0.11303178
GO_LEUKOCYTE_MIGRATION	208	0.737655	1.4750528	0	0.11272944
GO_RESPONSE_TO_WOUNDING	421	0.7160938	1.4761423	0	0.112434395
GO_HIPPO_SIGNALING	25	0.89429826	1.4748809	0.009375	0.1120521
GO_RECEPTOR_SIGNALING_PROTEIN	81	0.8024431	1.4767913	0.002628121	0.11142659
GO_POSITIVE_REGULATION_OF_PHA	38	0.8703028	1.4777876	0.008658009	0.11072228
KEGG_RETINOL_METABOLISM	19	0.9272097	1.4774547	0.007861636	0.11044218
GO_REGULATION_OF_RNA_SPLICING	81	0.79849863	1.4783403	0.005263158	0.110175535
GO_IMMUNE_EFFECTOR_PROCESS	363	0.7215748	1.4796824	0	0.108202316
GO_RNA_POLYMERASE_II_CORE_PRC	47	0.84762424	1.4796174	0.004231312	0.10718369
GO_REGULATION_OF_PHOSPHOPRO	51	0.8282527	1.4823349	0.00672043	0.104748234
GO_ANTIGEN_PROCESSING_AND_PR	166	0.75348854	1.481119	0.001162791	0.104571655
GO_GLYCOPROTEIN_BINDING	79	0.8019282	1.4819627	0.003851091	0.10450269
GO_POSITIVE_REGULATION_OF_RESF	228	0.74435055	1.4815714	0	0.10437657
GO_SULFUR_COMPOUND_BINDING	169	0.74916065	1.4844435	0.001150748	0.09908825
GO_ACUTE_INFLAMMATORY_RESPOI	54	0.84952265	1.4850565	0.005479452	0.098490976
GO_HOMEOSTASIS_OF_NUMBER_OF	29	0.9099589	1.4860469	0.001457726	0.09768125
GO_TRANSLATION_INITIATION_FACT	24	0.92101806	1.4857361	0.003053435	0.0974839
GO_CHROMOSOME_ORGANIZATION	29	0.9012918	1.4870684	0.004518072	0.09579823
GO_REGULATION_OF_DEFENSE_RESF	149	0.7565605	1.4890727	0	0.09455375
GO_POSITIVE_REGULATION_OF_END	91	0.7951661	1.488419	0.001237624	0.09422239
GO_TOLL_LIKE_RECEPTOR_SIGNALIN	80	0.8060479	1.4888322	0.002590674	0.09407946
GO_DEFENSE_RESPONSE_TO_BACTEF	128	0.7727464	1.4880652	0.001183432	0.09404926
GO_MEIOTIC_CHROMOSOME_SEGRE	38	0.877483	1.490248	0.005763689	0.09361639
GO_OVULATION_CYCLE	81	0.80149305	1.4899879	0	0.09326086
GO_MEMBRANE_PROTEIN_PROTEOL	34	0.9025521	1.4911565	0.001432665	0.09209069
GO_RESPONSE_TO_ACID_CHEMICAL	230	0.7342309	1.4927473	0.001112347	0.09030842
GO_LIPID_LOCALIZATION	190	0.75254935	1.4923247	0.001165501	0.09022089
GO_RESPONSE_TO_BACTERIUM	368	0.7294989	1.4964268	0	0.088883534
GO_REGULATION_OF_VASCULATURE	180	0.76137865	1.496369	0.001129944	0.08766282
GO_POSITIVE_REGULATION_OF_SUB	22	0.9367504	1.4960338	0.001577287	0.08748766
GO_CELLULAR_RESPONSE_TO_INTER	61	0.82962984	1.4981248	0.008010681	0.086862646
GO_RESPONSE_TO_TRANSITION_ME	110	0.79168004	1.497718	0	0.08661924
GO_ANTIGEN_PROCESSING_AND_PR	143	0.77386403	1.4959646	0	0.08639467
GO_TRANSCRIPTION_FROM_RNA_PC	34	0.9002312	1.5015423	0.004310345	0.086360805
GO_MACROMITOPHAGY	106	0.78936166	1.4957722	0.002466091	0.085730426
GO_POSITIVE_REGULATION_OF_RESF	120	0.7872903	1.5023636	0	0.085579805
GO_CELLULAR_DEFENSE_RESPONSE	44	0.87303346	1.5015122	0.002824859	0.08484973
GO_PHOSPHOLIPASE_ACTIVITY	69	0.8201713	1.4956818	0.002617801	0.08476026
GO_WOUND_HEALING	351	0.72584337	1.5004772	0	0.08463192
GO_REGULATION_OF_DEFENSE_RESF	99	0.8055985	1.4995626	0.002506266	0.08435408
GO_POSITIVE_REGULATION_OF_CELL	89	0.81436986	1.5012543	0.002607562	0.08401685
GO_MEMBRANE_PROTEIN_ECTODOM	21	0.9376861	1.495616	0.001512859	0.08367389
GO_POSITIVE_REGULATION_OF_TUM	52	0.8504013	1.5004181	0.001404494	0.08334222

GO_CYTOSOLIC_RIBOSOME	76	-0.8031924	-1.7584364	0	0.08065487
GO_LIPASE_ACTIVITY	81	0.8101671	1.5047761	0.002518892	0.08012572
GO_PLATELET_ALPHA_GRANULE_LU	40	0.87253755	1.5059084	0.002781641	0.07899851
GO_PLATELET_ACTIVATION	125	0.7794091	1.5086349	0.001215067	0.07471719
GO_HEMOSTASIS	238	0.7461289	1.5106449	0	0.074015945
GO_XENOPHAGY	77	0.8315904	1.5083662	0	0.07376768
GO_PEPTIDASE_ACTIVATOR_ACTIVIT	31	0.9078097	1.5104078	0.001428571	0.073044606
GO_ACTIVATION_OF_IMMUNE_RESP	357	0.731661	1.5099161	0	0.07277365
GO_POSITIVE_REGULATION_OF_PRO	313	0.74112564	1.5139741	0	0.0664844
GO_SECRETORY_GRANULE_MEMBRA	58	0.8391292	1.5215753	0	0.06589024
GO_POSITIVE_REGULATION_OF_CHE	96	0.8127813	1.522801	0.001272265	0.06481004
GO_POSITIVE_REGULATION_OF_IMM	461	0.7249544	1.515187	0	0.06466402
GO_REGULATION_OF_BODY_FLUID_I	373	0.73540103	1.5214955	0	0.06419454
GO_COLLAGEN_BINDING	51	0.8554349	1.5160356	0.002754821	0.06398163
GO_SECRETION_BY_CELL	363	0.7401548	1.5201163	0	0.06358665
GO_POSITIVE_REGULATION_OF_VASI	105	0.79582894	1.5212007	0.001282051	0.06307846
GO_DNA_GEOMETRIC_CHANGE	74	0.83481187	1.5185463	0.002607562	0.062228188
GO_RESPONSE_TO_INTERLEUKIN_1	83	0.82848465	1.5200843	0	0.062056404
GO_SECRETORY_VESICLE	314	0.7399024	1.5181774	0	0.061589736
GO_REGULATION_OF_IMMUNE_EFFE	330	0.7411994	1.5197958	0	0.06099513
GO_POSITIVE_REGULATION_OF_PEP1	125	0.7995411	1.525151	0	0.060800787
GO_CELLULAR_RESPONSE_TO_FATTY	40	0.8886359	1.5179287	0.001440922	0.060799588
GO_ANTIGEN_PROCESSING_AND_PR	76	0.8364477	1.527763	0.001310616	0.05656041
GO_RNA_POLYADENYLATION	26	0.94144505	1.5285422	0.001531394	0.056478802
GO_SECRETORY_GRANULE	234	0.7530487	1.5319781	0.001119821	0.051010247
GO_REGULATION_OF_RESPONSE_TO	310	0.7462963	1.5338279	0	0.04924262
GO_CELLULAR_COMPONENT_DISASS	428	0.7440152	1.535969	0	0.047773257
GO_REGULATION_OF_INFLAMMATOI	218	0.7594258	1.5356077	0	0.046895087
GO_CARBOHYDRATE_BINDING	179	0.77723575	1.5397164	0	0.046363447
GO_ORGANIC_ACID_BINDING	131	0.79162437	1.5377107	0.002430134	0.04606568
GO_ENDOPLASMIC_RETICULUM_GOI	85	0.8319035	1.5395662	0	0.04456881
GO_RESPONSE_TO_FATTY_ACID	63	0.8668897	1.5456575	0	0.0438962
GO_DEFENSE_RESPONSE_TO_OTHER	319	0.76249194	1.5455157	0	0.041701388
GO_REGULATION_OF_CYTOKINE_SEC	112	0.8081981	1.5443952	0	0.04116714
GO_REGULATED_EXOCYTOSIS	166	0.78794616	1.5438621	0	0.040139727
GO_EXOCYTOSIS	241	0.7681065	1.5503888	0	0.036388054
GO_SECRETION	428	0.7465624	1.5535684	0	0.03333256
GO_PLATELET_ALPHA_GRANULE	58	0.8783453	1.5574318	0	0.028932326
GO_PATTERN_RECOGNITION_RECEP1	98	0.82542396	1.5624008	0.0025	0.024746414
GO_DNA_DEPENDENT_ATPASE_ACTI'	76	0.8523078	1.5672786	0	0.023519581
GO_REGULATION_OF_ENDOCYTOSIS	161	0.8035341	1.5685447	0	0.02347467
GO_REGULATION_OF_PHAGOCYTOSI	55	0.883744	1.570391	0	0.023121553
GO_INFLAMMATORY_RESPONSE	343	0.76378745	1.5732214	0	0.022054566
GO_DRUG_BINDING	81	0.84068173	1.5669509	0	0.021997213
GO_POSITIVE_REGULATION_OF_DEFI	298	0.7768296	1.5867442	0	0.014053755
GO_INNATE_IMMUNE_RESPONSE_AC	97	0.85359335	1.5863489	0	0.012736243
GO_PLATELET_DEGRANULATION	82	0.8596599	1.5960006	0	0.009980717
GO_REGULATION_OF_INNATE_IMML	296	0.7923152	1.6120188	0	0.003089506
GO_INNATE_IMMUNE_RESPONSE	389	0.79644066	1.6373044	0	0.002180886
GO_ACTIVATION_OF_INNATE_IMMU	184	0.82784843	1.6238768	0	0.001904827

GO_RNA_3_END_PROCESSING	88	0.87905	1.6215707	0	0.001523862
GO_POSITIVE_REGULATION_OF_INN/	217	0.81513965	1.6310583	0	0.001453924
GO_REGULATION_OF_CELL_SHAPE	119	0.868641	1.6661687	0	0.001088274

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0.99	2035
0.984	1509
0.985	863
0.991	1443
0.987	1627
0.988	1489
0.986	773
0.991	32
0.987	1371

0.1	798
0.977	1443
0.973	565
0.96	1611
0.951	1627
0.964	1489
0.951	1009
0.953	1371
0.924	1116
0.86	1265
0.85	1703
0.916	1727
0.86	1639
0.911	683
0.871	1936
0.861	1892
0.884	31
0.872	1074
0.892	1680
0.874	1700
0.828	1116
0.893	1034
0.802	1580
0.792	195
0.747	1265
0.723	1687
0.674	2035
0.686	1687
0.622	1391
0.654	1500
0.624	171
0.527	1357
0.527	1402
0.54	879
0.547	1998
0.44	1998
0.401	1936
0.344	964
0.292	991
0.249	802
0.23	1479
0.207	1371
0.184	1687
0.25	1395
0.095	1577
0.097	596
0.06	658
0.017	1577
0.004	1406
0.007	991

0.007	195
0.004	1577
0.001	816