

Table S3. The significant biological processes, molecular functions and cellular components in Genetic group 1 and Genetic group 2 in the most efficient group.

The significant biological processes in Genetic group 1 in the most efficient group.					
Go term	Number of genes	LOR*	pvalue	padj	Biological process
GO:0140053	161	-0.981	6.07E-38	3.51E-33	mitochondrial gene expression
GO:0032543	134	-1.021	3.16E-35	6.08E-31	mitochondrial translation
GO:0070126	89	-1.104	1.77E-34	2.56E-30	mitochondrial translational termination
GO:0070125	88	-1.093	2.74E-33	3.17E-29	mitochondrial translational elongation
GO:0033108	87	-1.039	3.46E-28	1.82E-24	mitochondrial respiratory chain complex assembly
GO:0006415	102	-1.001	5.55E-28	2.67E-24	translational termination
GO:0034470	350	-0.534	1.08E-22	2.07E-19	ncRNA processing
GO:0010257	58	-1.082	2.04E-22	3.59E-19	NADH dehydrogenase complex assembly
GO:0032981	58	-1.082	2.04E-22	3.59E-19	mitochondrial respiratory chain complex I assembly
GO:0034660	436	-0.458	5.36E-21	6.59E-18	ncRNA metabolic process
GO:0006414	138	-0.763	2.59E-19	2.42E-16	translational elongation
GO:0008033	123	-0.763	3.69E-17	2.77E-14	tRNA processing
GO:0006399	176	-0.630	8.62E-17	6.15E-14	tRNA metabolic process
GO:0007005	498	-0.374	4.61E-16	2.99E-13	mitochondrion organization
GO:0006120	46	-1.000	1.40E-14	7.84E-12	mitochondrial electron transport, NADH to ubiquinone
GO:0009451	149	-0.625	1.72E-14	9.45E-12	RNA modification
GO:0042254	279	-0.460	2.74E-14	1.44E-11	ribosome biogenesis
GO:0022904	100	-0.772	8.85E-14	4.41E-11	respiratory electron transport chain
GO:0006400	82	-0.782	2.02E-13	9.74E-11	tRNA modification
GO:0006119	121	-0.679	3.37E-13	1.58E-10	oxidative phosphorylation
GO:0042773	81	-0.833	1.18E-12	5.07E-10	ATP synthesis coupled electron transport
GO:0022613	405	-0.354	2.14E-12	8.97E-10	ribonucleoprotein complex biogenesis
GO:0042775	80	-0.823	2.60E-12	1.07E-09	mitochondrial ATP synthesis coupled electron transport
GO:0022900	164	-0.537	2.26E-11	8.17E-09	electron transport chain
GO:0045333	177	-0.506	4.25E-11	1.45E-08	cellular respiration
GO:0016072	212	-0.453	4.92E-11	1.64E-08	rRNA metabolic process
GO:0006364	202	-0.462	6.00E-11	1.97E-08	rRNA processing
GO:0007007	41	-0.917	1.52E-10	4.67E-08	inner mitochondrial membrane organization
GO:0006520	343	-0.335	8.63E-10	2.19E-07	cellular amino acid metabolic process

GO:0015980	271	-0.377	1.02E-09	2.54E-07	energy derivation by oxidation of organic compounds
GO:1990542	89	-0.645	1.36E-09	3.27E-07	mitochondrial transmembrane transport
GO:0030150	18	-1.155	6.31E-09	1.36E-06	protein import into mitochondrial matrix
GO:0006839	242	-0.377	7.86E-09	1.64E-06	mitochondrial transport
GO:0006506	31	-0.955	1.71E-08	3.31E-06	GPI anchor biosynthetic process
GO:0006505	32	-0.937	1.72E-08	3.32E-06	GPI anchor metabolic process
GO:0006626	96	-0.557	7.76E-08	1.27E-05	protein targeting to mitochondrion
GO:0006744	16	-1.097	8.66E-08	1.39E-05	ubiquinone biosynthetic process
GO:1901663	16	-1.097	8.66E-08	1.39E-05	quinone biosynthetic process
GO:0044743	33	-0.851	2.52E-07	3.58E-05	protein transmembrane import into intracellular organelle
GO:0071806	58	-0.650	6.54E-07	8.42E-05	protein transmembrane transport
GO:0070131	16	-1.070	9.17E-07	1.16E-04	positive regulation of mitochondrial translation
GO:0065002	48	-0.700	1.45E-06	1.74E-04	intracellular protein transmembrane transport
GO:0043628	34	-0.770	1.48E-06	1.76E-04	ncRNA 3'-end processing
GO:0001522	17	-1.070	1.59E-06	1.88E-04	pseudouridine synthesis
GO:0015985	20	-0.962	1.96E-06	2.26E-04	energy coupled proton transport, down electrochemical gradient
GO:0015986	20	-0.962	1.96E-06	2.26E-04	ATP synthesis coupled proton transport
GO:1901605	197	-0.340	2.21E-06	2.49E-04	alpha-amino acid metabolic process
GO:0042158	93	-0.497	2.40E-06	2.66E-04	lipoprotein biosynthetic process
GO:0042407	29	-0.800	2.73E-06	2.96E-04	cristae formation
GO:0001510	76	-0.533	2.73E-06	2.96E-04	RNA methylation
GO:0009063	122	-0.423	3.18E-06	3.39E-04	cellular amino acid catabolic process
GO:0033617	18	-0.981	3.46E-06	3.64E-04	mitochondrial cytochrome c oxidase assembly
GO:0017004	30	-0.826	3.86E-06	3.98E-04	cytochrome complex assembly
GO:0016054	268	-0.285	3.90E-06	4.00E-04	organic acid catabolic process
GO:0046395	268	-0.285	3.90E-06	4.00E-04	carboxylic acid catabolic process
GO:0006497	88	-0.490	6.23E-06	5.99E-04	protein lipidation
GO:0000963	17	-1.034	6.50E-06	6.24E-04	mitochondrial RNA processing
GO:0042776	19	-0.938	6.99E-06	6.62E-04	mitochondrial ATP synthesis coupled proton transport
GO:0006457	209	-0.313	7.72E-06	7.28E-04	protein folding
GO:0000469	22	-0.877	8.19E-06	7.63E-04	cleavage involved in rRNA processing
GO:0016254	17	-0.983	8.23E-06	7.64E-04	preassembly of GPI anchor in ER membrane

GO:0000387	38	-0.705	8.85E-06	8.11E-04	spliceosomal snRNP assembly
GO:0016073	31	-0.734	9.04E-06	8.27E-04	snRNA metabolic process
GO:0030488	38	-0.687	9.08E-06	8.29E-04	tRNA methylation
GO:0008535	21	-0.895	9.39E-06	8.52E-04	respiratory chain complex IV assembly
GO:0097502	33	-0.851	1.02E-05	9.13E-04	mannosylation
GO:0062125	26	-0.927	1.03E-05	9.20E-04	regulation of mitochondrial gene expression
GO:0006743	17	-0.976	1.32E-05	1.15E-03	ubiquinone metabolic process
GO:0000154	33	-0.731	1.91E-05	1.57E-03	rRNA modification
GO:0042157	121	-0.390	2.07E-05	1.70E-03	lipoprotein metabolic process
GO:0070129	24	-0.942	2.39E-05	1.93E-03	regulation of mitochondrial translation
GO:0044282	424	-0.208	2.41E-05	1.94E-03	small molecule catabolic process
GO:0016180	25	-0.754	3.38E-05	2.58E-03	snRNA processing
GO:0042273	67	-0.496	3.63E-05	2.73E-03	ribosomal large subunit biogenesis
GO:0006264	12	-1.097	3.66E-05	2.74E-03	mitochondrial DNA replication
GO:0006122	12	-1.022	3.74E-05	2.78E-03	mitochondrial electron transport, ubiquinol to cytochrome c
GO:0030490	44	-0.602	3.75E-05	2.79E-03	maturation of SSU-rRNA
GO:0042274	63	-0.507	4.12E-05	3.01E-03	ribosomal small subunit biogenesis
GO:0090646	13	-1.018	4.83E-05	3.46E-03	mitochondrial tRNA processing
GO:0000959	43	-0.621	4.98E-05	3.54E-03	mitochondrial RNA metabolic process
GO:0090494	15	-0.950	5.67E-05	3.98E-03	dopamine uptake
GO:0033013	56	-0.529	7.54E-05	5.07E-03	tetrapyrrole metabolic process
GO:0009301	72	-0.462	7.64E-05	5.12E-03	snRNA transcription
GO:0042795	71	-0.465	7.78E-05	5.18E-03	snRNA transcription by RNA polymerase II
GO:0090305	282	-0.236	8.74E-05	5.74E-03	nucleic acid phosphodiester bond hydrolysis
GO:0034982	13	-1.059	8.77E-05	5.74E-03	mitochondrial protein processing
GO:0000466	22	-0.792	9.17E-05	5.96E-03	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO:1901606	103	-0.381	1.13E-04	7.15E-03	alpha-amino acid catabolic process
GO:0006851	25	-0.743	1.27E-04	7.90E-03	mitochondrial calcium ion transmembrane transport
GO:0090501	141	-0.325	1.35E-04	8.32E-03	RNA phosphodiester bond hydrolysis
GO:0006488	18	-0.928	1.42E-04	8.68E-03	dolichol-linked oligosaccharide biosynthetic process
GO:0098781	107	-0.366	1.50E-04	9.09E-03	ncRNA transcription
GO:0043624	211	-0.258	2.25E-04	1.29E-02	cellular protein complex disassembly

GO:0006490	19	-0.866	2.27E-04	1.30E-02	oligosaccharide-lipid intermediate biosynthetic process
GO:0036503	97	-0.381	2.40E-04	1.36E-02	ERAD pathway
GO:0033014	30	-0.686	2.52E-04	1.42E-02	tetrapyrrole biosynthetic process
GO:0072321	11	-0.980	2.61E-04	1.46E-02	chaperone-mediated protein transport
GO:0000462	34	-0.595	3.21E-04	1.74E-02	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)
GO:0042537	24	-0.735	3.43E-04	1.85E-02	benzene-containing compound metabolic process
GO:1901661	28	-0.646	3.52E-04	1.89E-02	quinone metabolic process
GO:0007006	125	-0.321	3.76E-04	1.99E-02	mitochondrial membrane organization
GO:0000460	27	-0.670	3.93E-04	2.07E-02	maturation of 5.8S rRNA
GO:0035269	18	-0.964	4.43E-04	2.29E-02	protein O-linked mannosylation
GO:0006888	203	-0.240	6.80E-04	3.32E-02	endoplasmic reticulum to Golgi vesicle-mediated transport
GO:0090502	70	-0.411	6.83E-04	3.33E-02	RNA phosphodiester bond hydrolysis, endonucleolytic
GO:0016074	13	-0.849	7.86E-04	3.75E-02	snoRNA metabolic process
GO:0070585	139	-0.287	8.13E-04	3.86E-02	protein localization to mitochondrion
GO:0046034	270	-0.205	8.46E-04	4.00E-02	ATP metabolic process
GO:0035437	12	-0.879	1.01E-03	4.66E-02	maintenance of protein localization in endoplasmic reticulum
GO:0042255	57	-0.431	1.03E-03	4.72E-02	ribosome assembly
GO:0034976	274	-0.200	1.07E-03	4.87E-02	response to endoplasmic reticulum stress
GO:0015697	12	-0.956	1.09E-03	4.96E-02	quaternary ammonium group transport
GO:0042110	431	0.628	6.49E-36	1.87E-31	T cell activation
GO:0002694	476	0.557	1.55E-31	1.49E-27	regulation of leukocyte activation
GO:0001525	481	0.540	4.36E-31	3.60E-27	angiogenesis
GO:0050900	400	0.583	1.83E-29	1.32E-25	leukocyte migration
GO:0006909	256	0.736	7.84E-29	5.03E-25	phagocytosis
GO:0051249	395	0.579	1.65E-28	9.54E-25	regulation of lymphocyte activation
GO:0045785	386	0.568	1.93E-27	8.58E-24	positive regulation of cell adhesion
GO:2000147	500	0.499	3.92E-27	1.62E-23	positive regulation of cell motility
GO:0030335	479	0.503	1.89E-26	7.26E-23	positive regulation of cell migration
GO:0002521	488	0.496	3.23E-26	1.17E-22	leukocyte differentiation
GO:0042060	462	0.502	5.27E-26	1.79E-22	wound healing
GO:0002764	353	0.569	8.01E-25	2.57E-21	immune response-regulating signaling pathway

GO:0002768	351	0.570	8.64E-25	2.63E-21	immune response-regulating cell surface receptor signaling pathway
GO:0007159	313	0.605	1.13E-24	3.27E-21	leukocyte cell-cell adhesion
GO:0043299	493	0.478	1.34E-24	3.69E-21	leukocyte degranulation
GO:0050863	296	0.610	2.35E-24	6.18E-21	regulation of T cell activation
GO:0050867	306	0.597	6.12E-24	1.54E-20	positive regulation of cell activation
GO:0031589	338	0.551	2.24E-23	5.40E-20	cell-substrate adhesion
GO:0002250	352	0.547	2.77E-23	6.15E-20	adaptive immune response
GO:0002696	297	0.597	2.73E-23	6.15E-20	positive regulation of leukocyte activation
GO:0070661	271	0.619	3.17E-23	6.78E-20	leukocyte proliferation
GO:0038094	82	1.056	5.35E-23	1.10E-19	Fc-gamma receptor signaling pathway
GO:1903037	280	0.611	6.09E-23	1.21E-19	regulation of leukocyte cell-cell adhesion
GO:0022407	375	0.517	2.15E-22	3.59E-19	regulation of cell-cell adhesion
GO:0001819	356	0.534	2.07E-22	3.59E-19	positive regulation of cytokine production
GO:0002429	323	0.563	2.24E-22	3.59E-19	immune response-activating cell surface receptor signaling pathway
GO:0002757	323	0.563	2.24E-22	3.59E-19	immune response-activating signal transduction
GO:0043087	436	0.476	3.81E-22	5.95E-19	regulation of GTPase activity
GO:0002431	84	1.039	4.55E-22	6.91E-19	Fc receptor mediated stimulatory signaling pathway
GO:0030098	332	0.540	7.20E-22	1.07E-18	lymphocyte differentiation
GO:1901342	310	0.558	7.81E-22	1.13E-18	regulation of vasculature development
GO:0002433	78	1.059	8.46E-22	1.16E-18	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
GO:0038096	78	1.059	8.46E-22	1.16E-18	Fc-gamma receptor signaling pathway involved in phagocytosis
GO:0051251	254	0.622	1.10E-21	1.48E-18	positive regulation of lymphocyte activation
GO:0032943	250	0.620	1.57E-21	2.06E-18	mononuclear cell proliferation
GO:0042119	458	0.460	1.64E-21	2.10E-18	neutrophil activation
GO:0043547	364	0.510	3.07E-21	3.86E-18	positive regulation of GTPase activity
GO:0036230	464	0.449	6.56E-21	7.90E-18	granulocyte activation
GO:1903039	205	0.678	6.95E-21	8.20E-18	positive regulation of leukocyte cell-cell adhesion
GO:0046651	248	0.610	8.00E-21	9.25E-18	lymphocyte proliferation
GO:0043312	447	0.456	9.09E-21	1.03E-17	neutrophil degranulation
GO:0002283	449	0.454	1.16E-20	1.28E-17	neutrophil activation involved in immune response

GO:0002446	460	0.444	2.96E-20	3.23E-17	neutrophil mediated immunity
GO:0045765	280	0.561	3.50E-20	3.75E-17	regulation of angiogenesis
GO:0022604	477	0.430	4.68E-20	4.91E-17	regulation of cell morphogenesis
GO:0022409	241	0.604	7.01E-20	7.23E-17	positive regulation of cell-cell adhesion
GO:0002253	402	0.471	7.64E-20	7.75E-17	activation of immune response
GO:0032970	360	0.493	1.07E-19	1.07E-16	regulation of actin filament-based process
GO:0070663	207	0.656	1.13E-19	1.11E-16	regulation of leukocyte proliferation
GO:0051056	333	0.508	1.78E-19	1.71E-16	regulation of small GTPase mediated signal transduction
GO:0007265	433	0.446	2.04E-19	1.93E-16	Ras protein signal transduction
GO:0030198	354	0.488	2.73E-19	2.51E-16	extracellular matrix organization
GO:0043062	355	0.486	3.23E-19	2.91E-16	extracellular structure organization
GO:0032103	469	0.423	4.60E-19	4.09E-16	positive regulation of response to external stimulus
GO:0007162	255	0.568	5.16E-19	4.52E-16	negative regulation of cell adhesion
GO:0007015	378	0.468	9.14E-19	7.88E-16	actin filament organization
GO:0032956	317	0.509	1.17E-18	9.98E-16	regulation of actin cytoskeleton organization
GO:0032944	197	0.648	2.19E-18	1.83E-15	regulation of mononuclear cell proliferation
GO:0001667	381	0.456	2.51E-18	2.07E-15	ameboidal-type cell migration
GO:0007160	216	0.593	3.77E-18	3.06E-15	cell-matrix adhesion
GO:0050870	191	0.648	4.05E-18	3.25E-15	positive regulation of T cell activation
GO:0050878	463	0.411	5.44E-18	4.31E-15	regulation of body fluid levels
GO:0050670	196	0.641	5.62E-18	4.39E-15	regulation of lymphocyte proliferation
GO:0002683	376	0.445	3.13E-17	2.41E-14	negative regulation of immune system process
GO:0008360	148	0.705	3.47E-17	2.64E-14	regulation of cell shape
GO:0050817	310	0.486	4.60E-17	3.41E-14	coagulation
GO:0090066	479	0.392	5.11E-17	3.74E-14	regulation of anatomical structure size
GO:0002697	351	0.460	7.35E-17	5.31E-14	regulation of immune effector process
GO:0007599	311	0.480	9.46E-17	6.66E-14	hemostasis
GO:0010631	274	0.508	1.37E-16	9.56E-14	epithelial cell migration
GO:0090130	283	0.498	1.67E-16	1.15E-13	tissue migration
GO:0030099	383	0.433	1.98E-16	1.35E-13	myeloid cell differentiation
GO:0030217	231	0.552	2.10E-16	1.41E-13	T cell differentiation
GO:0007596	306	0.477	2.48E-16	1.65E-13	blood coagulation
GO:0090132	277	0.501	2.51E-16	1.65E-13	epithelium migration

GO:0071346	146	0.690	6.70E-16	4.30E-13	cellular response to interferon-gamma
GO:0034341	163	0.653	7.25E-16	4.60E-13	response to interferon-gamma
GO:0009615	282	0.488	1.10E-15	6.89E-13	response to virus
GO:0032535	354	0.434	1.31E-15	8.11E-13	regulation of cellular component size
GO:0071900	492	0.369	1.57E-15	9.67E-13	regulation of protein serine/threonine kinase activity
GO:0060326	268	0.492	2.18E-15	1.33E-12	cell chemotaxis
GO:0050673	379	0.412	2.24E-15	1.35E-12	epithelial cell proliferation
GO:0042098	173	0.615	2.29E-15	1.36E-12	T cell proliferation
GO:0010810	204	0.556	2.89E-15	1.70E-12	regulation of cell-substrate adhesion
GO:0038093	179	0.605	4.72E-15	2.75E-12	Fc receptor signaling pathway
GO:0071902	327	0.442	4.99E-15	2.88E-12	positive regulation of protein serine/threonine kinase activity
GO:0018212	351	0.424	5.52E-15	3.16E-12	peptidyl-tyrosine modification
GO:0018108	348	0.421	1.13E-14	6.38E-12	peptidyl-tyrosine phosphorylation
GO:0043406	254	0.489	1.60E-14	8.90E-12	positive regulation of MAP kinase activity
GO:0002831	354	0.418	1.86E-14	1.01E-11	regulation of response to biotic stimulus
GO:1902903	323	0.436	2.04E-14	1.10E-11	regulation of supramolecular fiber organization
GO:0030168	149	0.639	2.07E-14	1.11E-11	platelet activation
GO:0002221	185	0.586	2.47E-14	1.31E-11	pattern recognition receptor signaling pathway
GO:0051271	295	0.445	3.69E-14	1.92E-11	negative regulation of cellular component movement
GO:0034329	395	0.387	3.87E-14	2.00E-11	cell junction assembly
GO:0070665	132	0.693	4.52E-14	2.31E-11	positive regulation of leukocyte proliferation
GO:0031349	338	0.420	4.57E-14	2.32E-11	positive regulation of defense response
GO:0110053	240	0.496	7.23E-14	3.64E-11	regulation of actin filament organization
GO:0051607	202	0.537	9.10E-14	4.49E-11	defense response to virus
GO:0040013	293	0.438	9.57E-14	4.69E-11	negative regulation of locomotion
GO:0007409	462	0.351	1.31E-13	6.36E-11	axonogenesis
GO:0043405	329	0.412	2.33E-13	1.11E-10	regulation of MAP kinase activity
GO:0010632	216	0.504	2.50E-13	1.18E-10	regulation of epithelial cell migration
GO:0042129	145	0.620	3.96E-13	1.85E-10	regulation of T cell proliferation
GO:0042113	224	0.496	4.36E-13	1.99E-10	B cell activation
GO:0046631	134	0.626	4.35E-13	1.99E-10	alpha-beta T cell activation
GO:0032946	127	0.678	4.31E-13	1.99E-10	positive regulation of mononuclear cell proliferation

GO:0046777	236	0.474	4.55E-13	2.05E-10	protein autophosphorylation
GO:1903706	438	0.352	5.09E-13	2.26E-10	regulation of hemopoiesis
GO:0050853	56	0.976	5.06E-13	2.26E-10	B cell receptor signaling pathway
GO:1904018	180	0.541	9.91E-13	4.37E-10	positive regulation of vasculature development
GO:0002703	180	0.542	1.07E-12	4.68E-10	regulation of leukocyte mediated immunity
GO:0050671	126	0.667	1.08E-12	4.68E-10	positive regulation of lymphocyte proliferation
GO:0099024	58	0.908	1.16E-12	4.98E-10	plasma membrane invagination
GO:0050678	324	0.399	1.21E-12	5.14E-10	regulation of epithelial cell proliferation
GO:0008154	192	0.521	2.10E-12	8.85E-10	actin polymerization or depolymerization
GO:0045766	161	0.563	2.16E-12	8.99E-10	positive regulation of angiogenesis
GO:0048017	176	0.532	2.84E-12	1.16E-09	inositol lipid-mediated signaling
GO:0001952	113	0.651	2.87E-12	1.17E-09	regulation of cell-matrix adhesion
GO:1902105	260	0.439	4.16E-12	1.68E-09	regulation of leukocyte differentiation
GO:2000146	262	0.429	5.01E-12	2.01E-09	negative regulation of cell motility
GO:0030595	196	0.497	5.63E-12	2.24E-09	leukocyte chemotaxis
GO:0050866	181	0.524	5.91E-12	2.34E-09	negative regulation of cell activation
GO:0002460	235	0.461	5.97E-12	2.35E-09	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0043542	197	0.497	6.07E-12	2.37E-09	endothelial cell migration
GO:0032147	324	0.387	6.79E-12	2.62E-09	activation of protein kinase activity
GO:0048015	173	0.527	6.79E-12	2.62E-09	phosphatidylinositol-mediated signaling
GO:1901653	369	0.362	8.20E-12	3.14E-09	cellular response to peptide
GO:1901343	114	0.634	8.89E-12	3.38E-09	negative regulation of vasculature development
GO:0031341	80	0.748	1.07E-11	4.03E-09	regulation of cell killing
GO:0030336	251	0.430	1.15E-11	4.31E-09	negative regulation of cell migration
GO:0010634	139	0.576	1.55E-11	5.77E-09	positive regulation of epithelial cell migration
GO:0045088	270	0.420	1.69E-11	6.25E-09	regulation of innate immune response
GO:0043254	404	0.341	2.06E-11	7.54E-09	regulation of protein-containing complex assembly
GO:0002224	138	0.598	2.06E-11	7.54E-09	toll-like receptor signaling pathway

GO:0032612	43	0.953	2.26E-11	8.17E-09	interleukin-1 production
GO:0002237	318	0.383	2.41E-11	8.65E-09	response to molecule of bacterial origin
GO:0002685	185	0.499	2.58E-11	9.21E-09	regulation of leukocyte migration
GO:0048010	92	0.705	2.65E-11	9.39E-09	vascular endothelial growth factor receptor signaling pathway
GO:0031295	55	0.861	2.80E-11	9.87E-09	T cell costimulation
GO:0002695	160	0.536	3.10E-11	1.09E-08	negative regulation of leukocyte activation
GO:0019932	416	0.330	3.15E-11	1.09E-08	second-messenger-mediated signaling
GO:0097529	184	0.494	3.29E-11	1.14E-08	myeloid leukocyte migration
GO:0050769	464	0.312	3.61E-11	1.24E-08	positive regulation of neurogenesis
GO:0031334	234	0.440	4.03E-11	1.38E-08	positive regulation of protein-containing complex assembly
GO:0046578	234	0.438	4.47E-11	1.51E-08	regulation of Ras protein signal transduction
GO:0006911	49	0.915	4.48E-11	1.51E-08	phagocytosis, engulfment
GO:0050920	202	0.466	5.42E-11	1.79E-08	regulation of chemotaxis
GO:0007229	106	0.662	5.43E-11	1.79E-08	integrin-mediated signaling pathway
GO:0050729	135	0.565	7.44E-11	2.43E-08	positive regulation of inflammatory response
GO:0046634	89	0.681	8.70E-11	2.82E-08	regulation of alpha-beta T cell activation
GO:0050854	60	0.819	8.76E-11	2.83E-08	regulation of antigen receptor-mediated signaling pathway
GO:0032496	307	0.378	9.26E-11	2.97E-08	response to lipopolysaccharide
GO:0001776	84	0.734	1.03E-10	3.28E-08	leukocyte homeostasis
GO:0002285	161	0.519	1.12E-10	3.54E-08	lymphocyte activation involved in immune response
GO:0002699	188	0.485	1.13E-10	3.56E-08	positive regulation of immune effector process
GO:2000181	103	0.628	1.13E-10	3.56E-08	negative regulation of blood vessel morphogenesis
GO:0010975	487	0.297	1.24E-10	3.88E-08	regulation of neuron projection development
GO:0031294	56	0.831	1.33E-10	4.14E-08	lymphocyte costimulation
GO:0008064	163	0.515	1.49E-10	4.61E-08	regulation of actin polymerization or depolymerization
GO:0050727	317	0.366	1.56E-10	4.77E-08	regulation of inflammatory response
GO:0002573	197	0.465	1.58E-10	4.82E-08	myeloid leukocyte differentiation
GO:0046632	100	0.637	1.60E-10	4.86E-08	alpha-beta T cell differentiation
GO:0007266	198	0.460	1.69E-10	5.10E-08	Rho protein signal transduction
GO:0051983	98	0.667	1.81E-10	5.42E-08	regulation of chromosome segregation

GO:0031098	302	0.372	1.96E-10	5.83E-08	stress-activated protein kinase signaling cascade
GO:0030832	164	0.510	1.98E-10	5.87E-08	regulation of actin filament length
GO:2000106	78	0.755	2.03E-10	6.00E-08	regulation of leukocyte apoptotic process
GO:0002449	223	0.433	2.12E-10	6.20E-08	lymphocyte mediated immunity
GO:0001935	140	0.536	2.12E-10	6.20E-08	endothelial cell proliferation
GO:0007163	210	0.444	2.44E-10	7.09E-08	establishment or maintenance of cell polarity
GO:0097305	233	0.420	2.50E-10	7.23E-08	response to alcohol
GO:0007249	253	0.405	2.54E-10	7.31E-08	I-kappaB kinase/NF-kappaB signaling
GO:0030900	381	0.328	2.57E-10	7.35E-08	forebrain development
GO:0045123	61	0.789	2.91E-10	8.28E-08	cellular extravasation
GO:0030041	165	0.502	2.96E-10	8.40E-08	actin filament polymerization
GO:0051480	345	0.343	3.05E-10	8.60E-08	regulation of cytosolic calcium ion concentration
GO:0050679	185	0.466	3.08E-10	8.63E-08	positive regulation of epithelial cell proliferation
GO:0140014	264	0.395	3.10E-10	8.65E-08	mitotic nuclear division
GO:0010324	66	0.770	3.14E-10	8.72E-08	membrane invagination
GO:0050851	218	0.436	3.30E-10	9.14E-08	antigen receptor-mediated signaling pathway
GO:0016525	101	0.618	3.33E-10	9.18E-08	negative regulation of angiogenesis
GO:0000082	240	0.412	3.54E-10	9.69E-08	G1/S transition of mitotic cell cycle
GO:0071496	300	0.368	3.85E-10	1.05E-07	cellular response to external stimulus
GO:0001906	128	0.559	4.16E-10	1.13E-07	cell killing
GO:0070371	284	0.378	4.18E-10	1.13E-07	ERK1 and ERK2 cascade
GO:0032271	198	0.454	4.68E-10	1.26E-07	regulation of protein polymerization
GO:0050730	240	0.407	5.19E-10	1.39E-07	regulation of peptidyl-tyrosine phosphorylation
GO:0048872	245	0.404	5.39E-10	1.43E-07	homeostasis of number of cells
GO:0032611	35	0.961	5.47E-10	1.45E-07	interleukin-1 beta production
GO:0007204	308	0.357	6.30E-10	1.66E-07	positive regulation of cytosolic calcium ion concentration
GO:0033002	187	0.461	6.51E-10	1.71E-07	muscle cell proliferation
GO:0030833	146	0.526	6.75E-10	1.77E-07	regulation of actin filament polymerization
GO:0032652	39	0.933	6.86E-10	1.79E-07	regulation of interleukin-1 production
GO:0000910	160	0.500	7.05E-10	1.83E-07	cytokinesis
GO:0071559	236	0.405	7.32E-10	1.89E-07	response to transforming growth factor beta

GO:0071260	75	0.729	7.69E-10	1.98E-07	cellular response to mechanical stimulus
GO:0007059	301	0.362	7.85E-10	2.01E-07	chromosome segregation
GO:0071887	99	0.638	8.09E-10	2.06E-07	leukocyte apoptotic process
GO:0051051	421	0.304	8.99E-10	2.27E-07	negative regulation of transport
GO:0042102	90	0.672	9.13E-10	2.30E-07	positive regulation of T cell proliferation
GO:0001910	61	0.763	1.09E-09	2.71E-07	regulation of leukocyte mediated cytotoxicity
GO:0045619	160	0.491	1.10E-09	2.74E-07	regulation of lymphocyte differentiation
GO:0010594	155	0.494	1.11E-09	2.74E-07	regulation of endothelial cell migration
GO:0070302	226	0.412	1.18E-09	2.90E-07	regulation of stress-activated protein kinase signaling cascade
GO:0019882	195	0.445	1.23E-09	3.02E-07	antigen processing and presentation
GO:0043122	222	0.413	1.27E-09	3.10E-07	regulation of I-kappaB kinase/NF-kappaB signaling
GO:0060348	215	0.418	1.31E-09	3.17E-07	bone development
GO:0071375	312	0.348	1.31E-09	3.18E-07	cellular response to peptide hormone stimulus
GO:0051235	298	0.356	1.52E-09	3.65E-07	maintenance of location
GO:0031343	54	0.817	1.78E-09	4.24E-07	positive regulation of cell killing
GO:0072678	60	0.803	1.80E-09	4.29E-07	T cell migration
GO:0007044	98	0.604	1.88E-09	4.44E-07	cell-substrate junction assembly
GO:0150115	98	0.604	1.88E-09	4.44E-07	cell-substrate junction organization
GO:0010769	299	0.349	2.47E-09	5.81E-07	regulation of cell morphogenesis involved in differentiation
GO:0032273	125	0.541	2.51E-09	5.86E-07	positive regulation of protein polymerization
GO:0019058	299	0.349	2.78E-09	6.47E-07	viral life cycle
GO:0045637	221	0.407	2.95E-09	6.84E-07	regulation of myeloid cell differentiation
GO:0022408	161	0.472	3.31E-09	7.66E-07	negative regulation of cell-cell adhesion
GO:0044843	254	0.377	3.40E-09	7.82E-07	cell cycle G1/S phase transition
GO:0150076	63	0.745	3.41E-09	7.82E-07	neuroinflammatory response
GO:0009612	209	0.417	3.45E-09	7.89E-07	response to mechanical stimulus
GO:0060560	231	0.393	3.48E-09	7.93E-07	developmental growth involved in morphogenesis
GO:0051250	132	0.524	3.89E-09	8.82E-07	negative regulation of lymphocyte activation
GO:0043434	426	0.290	3.94E-09	8.89E-07	response to peptide hormone
GO:0032872	224	0.399	4.03E-09	9.05E-07	regulation of stress-activated MAPK cascade
GO:0006874	440	0.285	4.19E-09	9.37E-07	cellular calcium ion homeostasis

GO:0001936	124	0.526	4.20E-09	9.37E-07	regulation of endothelial cell proliferation
GO:0002706	128	0.528	4.23E-09	9.40E-07	regulation of lymphocyte mediated immunity
GO:0008361	177	0.444	4.41E-09	9.76E-07	regulation of cell size
GO:0050764	91	0.639	4.54E-09	1.00E-06	regulation of phagocytosis
GO:0070372	268	0.364	4.74E-09	1.04E-06	regulation of ERK1 and ERK2 cascade
GO:0006898	243	0.378	4.92E-09	1.08E-06	receptor-mediated endocytosis
GO:0030888	61	0.790	5.09E-09	1.11E-06	regulation of B cell proliferation
GO:0002819	144	0.498	5.13E-09	1.12E-06	regulation of adaptive immune response
GO:0060485	263	0.362	6.13E-09	1.33E-06	mesenchyme development
GO:0043123	176	0.444	6.73E-09	1.45E-06	positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0014065	142	0.490	6.82E-09	1.46E-06	phosphatidylinositol 3-kinase signaling
GO:0072676	94	0.616	6.96E-09	1.49E-06	lymphocyte migration
GO:0000819	176	0.446	7.03E-09	1.49E-06	sister chromatid segregation
GO:0061572	150	0.478	7.12E-09	1.50E-06	actin filament bundle organization
GO:0042100	82	0.653	7.11E-09	1.50E-06	B cell proliferation
GO:0055074	452	0.277	7.20E-09	1.51E-06	calcium ion homeostasis
GO:0071560	230	0.385	7.31E-09	1.53E-06	cellular response to transforming growth factor beta stimulus
GO:0097530	125	0.520	8.26E-09	1.72E-06	granulocyte migration
GO:0051403	274	0.353	8.44E-09	1.75E-06	stress-activated MAPK cascade
GO:0048608	425	0.283	8.76E-09	1.81E-06	reproductive structure development
GO:0003012	432	0.281	8.88E-09	1.83E-06	muscle system process
GO:0060333	65	0.720	9.39E-09	1.92E-06	interferon-gamma-mediated signaling pathway
GO:0050868	101	0.577	1.02E-08	2.09E-06	negative regulation of T cell activation
GO:0031532	99	0.578	1.03E-08	2.10E-06	actin cytoskeleton reorganization
GO:0045580	131	0.506	1.11E-08	2.26E-06	regulation of T cell differentiation
GO:0048771	161	0.455	1.12E-08	2.26E-06	tissue remodeling
GO:0045931	149	0.477	1.14E-08	2.29E-06	positive regulation of mitotic cell cycle
GO:0002228	51	0.761	1.16E-08	2.34E-06	natural killer cell mediated immunity
GO:0031346	373	0.298	1.27E-08	2.54E-06	positive regulation of cell projection organization
GO:0043491	239	0.374	1.37E-08	2.72E-06	protein kinase B signaling
GO:0042116	88	0.602	1.39E-08	2.75E-06	macrophage activation
GO:0048041	82	0.619	1.45E-08	2.88E-06	focal adhesion assembly

GO:1901888	191	0.413	1.48E-08	2.92E-06	regulation of cell junction assembly
GO:0034765	462	0.267	1.53E-08	3.00E-06	regulation of ion transmembrane transport
GO:0038083	37	0.844	1.55E-08	3.03E-06	peptidyl-tyrosine autophosphorylation
GO:0051090	405	0.285	1.68E-08	3.28E-06	regulation of DNA-binding transcription factor activity
GO:0048638	327	0.316	1.70E-08	3.31E-06	regulation of developmental growth
GO:0001818	209	0.396	1.71E-08	3.31E-06	negative regulation of cytokine production
GO:0032651	31	0.938	1.90E-08	3.66E-06	regulation of interleukin-1 beta production
GO:0002833	221	0.385	1.96E-08	3.74E-06	positive regulation of response to biotic stimulus
GO:0002286	89	0.599	2.05E-08	3.91E-06	T cell activation involved in immune response
GO:0050864	113	0.549	2.12E-08	4.03E-06	regulation of B cell activation
GO:1902905	193	0.408	2.14E-08	4.06E-06	positive regulation of supramolecular fiber organization
GO:0042267	48	0.773	2.17E-08	4.09E-06	natural killer cell mediated cytotoxicity
GO:0043534	112	0.537	2.24E-08	4.22E-06	blood vessel endothelial cell migration
GO:1903829	321	0.317	2.26E-08	4.24E-06	positive regulation of cellular protein localization
GO:0061458	428	0.274	2.29E-08	4.28E-06	reproductive system development
GO:0050808	393	0.285	2.45E-08	4.57E-06	synapse organization
GO:0046822	107	0.547	2.48E-08	4.62E-06	regulation of nucleocytoplasmic transport
GO:0014066	118	0.517	2.66E-08	4.93E-06	regulation of phosphatidylinositol 3-kinase signaling
GO:0034109	80	0.616	3.04E-08	5.62E-06	homotypic cell-cell adhesion
GO:0048660	132	0.489	3.21E-08	5.91E-06	regulation of smooth muscle cell proliferation
GO:0050731	177	0.419	3.34E-08	6.12E-06	positive regulation of peptidyl-tyrosine phosphorylation
GO:0010959	369	0.291	3.40E-08	6.22E-06	regulation of metal ion transport
GO:0072503	467	0.259	3.51E-08	6.40E-06	cellular divalent inorganic cation homeostasis
GO:0051017	148	0.457	3.55E-08	6.44E-06	actin filament bundle assembly
GO:0001909	88	0.599	3.55E-08	6.44E-06	leukocyte mediated cytotoxicity
GO:0003158	119	0.508	3.63E-08	6.56E-06	endothelium development
GO:0071216	211	0.388	3.64E-08	6.56E-06	cellular response to biotic stimulus

GO:0010721	326	0.308	3.73E-08	6.69E-06	negative regulation of cell development
GO:0048588	219	0.375	3.84E-08	6.87E-06	developmental cell growth
GO:0048659	133	0.483	4.07E-08	7.26E-06	smooth muscle cell proliferation
GO:0051258	260	0.345	4.34E-08	7.72E-06	protein polymerization
GO:0051893	61	0.688	4.51E-08	7.95E-06	regulation of focal adhesion assembly
GO:0090109	61	0.688	4.51E-08	7.95E-06	regulation of cell-substrate junction assembly
GO:0150116	61	0.688	4.51E-08	7.95E-06	regulation of cell-substrate junction organization
GO:0002040	112	0.518	4.64E-08	8.16E-06	sprouting angiogenesis
GO:0000070	144	0.464	4.67E-08	8.17E-06	mitotic sister chromatid segregation
GO:0060537	384	0.282	4.69E-08	8.19E-06	muscle tissue development
GO:0070374	193	0.398	4.75E-08	8.26E-06	positive regulation of ERK1 and ERK2 cascade
GO:0051283	122	0.503	4.77E-08	8.27E-06	negative regulation of sequestering of calcium ion
GO:1903708	179	0.414	5.39E-08	9.29E-06	positive regulation of hemopoiesis
GO:1990266	104	0.536	5.38E-08	9.29E-06	neutrophil migration
GO:0072507	486	0.251	5.47E-08	9.41E-06	divalent inorganic cation homeostasis
GO:0043535	88	0.585	5.62E-08	9.63E-06	regulation of blood vessel endothelial cell migration
GO:0048762	211	0.377	5.81E-08	9.94E-06	mesenchymal cell differentiation
GO:0007179	181	0.406	5.95E-08	1.01E-05	transforming growth factor beta receptor signaling pathway
GO:0044409	126	0.485	6.05E-08	1.03E-05	entry into host
GO:0051924	238	0.356	6.23E-08	1.06E-05	regulation of calcium ion transport
GO:0030593	89	0.571	6.35E-08	1.07E-05	neutrophil chemotaxis
GO:0030183	118	0.503	6.40E-08	1.08E-05	B cell differentiation
GO:0071674	77	0.608	6.58E-08	1.10E-05	mononuclear cell migration
GO:0060759	160	0.434	6.94E-08	1.16E-05	regulation of response to cytokine stimulus
GO:0014706	368	0.284	7.04E-08	1.18E-05	striated muscle tissue development
GO:0002504	83	0.620	7.21E-08	1.20E-05	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II
GO:0071222	181	0.409	7.28E-08	1.21E-05	cellular response to lipopolysaccharide
GO:0045787	359	0.288	7.35E-08	1.22E-05	positive regulation of cell cycle
GO:0002705	119	0.504	7.38E-08	1.22E-05	positive regulation of leukocyte mediated immunity
GO:0045576	57	0.722	7.55E-08	1.24E-05	mast cell activation

GO:0002822	130	0.482	7.64E-08	1.25E-05	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0061900	51	0.751	7.92E-08	1.29E-05	glial cell activation
GO:0014812	79	0.593	7.97E-08	1.30E-05	muscle cell migration
GO:0001774	43	0.811	8.18E-08	1.32E-05	microglial cell activation
GO:0002269	43	0.811	8.18E-08	1.32E-05	leukocyte activation involved in inflammatory response
GO:0051897	163	0.423	8.54E-08	1.38E-05	positive regulation of protein kinase B signaling
GO:0006816	415	0.267	8.60E-08	1.38E-05	calcium ion transport
GO:0014068	86	0.580	9.44E-08	1.51E-05	positive regulation of phosphatidylinositol 3-kinase signaling
GO:0001503	380	0.277	9.51E-08	1.51E-05	ossification
GO:0030101	67	0.644	9.99E-08	1.59E-05	natural killer cell activation
GO:0071621	107	0.515	1.00E-07	1.59E-05	granulocyte chemotaxis
GO:0051896	214	0.370	1.02E-07	1.61E-05	regulation of protein kinase B signaling
GO:0051282	123	0.488	1.05E-07	1.65E-05	regulation of sequestering of calcium ion
GO:0048511	297	0.311	1.09E-07	1.71E-05	rhythmic process
GO:0046847	57	0.687	1.09E-07	1.71E-05	filopodium assembly
GO:0001655	334	0.294	1.10E-07	1.72E-05	urogenital system development
GO:0002495	82	0.615	1.12E-07	1.75E-05	antigen processing and presentation of peptide antigen via MHC class II
GO:0071219	187	0.396	1.14E-07	1.77E-05	cellular response to molecule of bacterial origin
GO:0098813	246	0.343	1.16E-07	1.79E-05	nuclear chromosome segregation
GO:0070838	460	0.251	1.18E-07	1.82E-05	divalent metal ion transport
GO:0032609	75	0.623	1.24E-07	1.92E-05	interferon-gamma production
GO:0061640	95	0.564	1.26E-07	1.94E-05	cytoskeleton-dependent cytokinesis
GO:0031032	191	0.387	1.31E-07	2.01E-05	actomyosin structure organization
GO:0072511	464	0.249	1.36E-07	2.08E-05	divalent inorganic cation transport
GO:0051209	120	0.489	1.38E-07	2.10E-05	release of sequestered calcium ion into cytosol
GO:0048013	85	0.587	1.40E-07	2.12E-05	ephrin receptor signaling pathway
GO:0050772	84	0.568	1.41E-07	2.13E-05	positive regulation of axonogenesis
GO:0050770	182	0.394	1.42E-07	2.14E-05	regulation of axonogenesis

GO:1903034	155	0.430	1.48E-07	2.23E-05	regulation of response to wounding
GO:1902107	141	0.450	1.52E-07	2.29E-05	positive regulation of leukocyte differentiation
GO:0001959	151	0.434	1.54E-07	2.32E-05	regulation of cytokine-mediated signaling pathway
GO:0071214	317	0.299	1.56E-07	2.33E-05	cellular response to abiotic stimulus
GO:0104004	317	0.299	1.56E-07	2.33E-05	cellular response to environmental stimulus
GO:0051208	126	0.474	1.62E-07	2.41E-05	sequestering of calcium ion
GO:0031099	187	0.389	1.67E-07	2.48E-05	regeneration
GO:1903038	112	0.503	1.67E-07	2.48E-05	negative regulation of leukocyte cell-cell adhesion
GO:0002715	35	0.821	1.75E-07	2.58E-05	regulation of natural killer cell mediated immunity
GO:0021700	275	0.317	1.97E-07	2.91E-05	developmental maturation
GO:0010811	119	0.479	1.98E-07	2.92E-05	positive regulation of cell-substrate adhesion
GO:0048732	442	0.250	2.05E-07	3.01E-05	gland development
GO:0033627	67	0.639	2.08E-07	3.05E-05	cell adhesion mediated by integrin
GO:0010718	46	0.780	2.10E-07	3.07E-05	positive regulation of epithelial to mesenchymal transition
GO:0032732	19	1.101	2.11E-07	3.07E-05	positive regulation of interleukin-1 production
GO:0090068	271	0.320	2.12E-07	3.07E-05	positive regulation of cell cycle process
GO:0043112	186	0.383	2.17E-07	3.14E-05	receptor metabolic process
GO:0061028	41	0.805	2.17E-07	3.14E-05	establishment of endothelial barrier
GO:0007088	160	0.415	2.18E-07	3.14E-05	regulation of mitotic nuclear division
GO:0018209	294	0.306	2.24E-07	3.23E-05	peptidyl-serine modification
GO:0002064	207	0.361	2.29E-07	3.29E-05	epithelial cell development
GO:0048871	466	0.243	2.33E-07	3.33E-05	multicellular organismal homeostasis
GO:0007221	18	1.162	2.39E-07	3.41E-05	positive regulation of transcription of Notch receptor target
GO:0000280	397	0.263	2.42E-07	3.44E-05	nuclear division
GO:1903306	24	1.026	2.57E-07	3.64E-05	negative regulation of regulated secretory pathway
GO:0042269	33	0.836	2.61E-07	3.69E-05	regulation of natural killer cell mediated cytotoxicity
GO:0042063	286	0.308	2.66E-07	3.75E-05	gliogenesis
GO:0046635	61	0.653	2.72E-07	3.82E-05	positive regulation of alpha-beta T cell activation
GO:1990138	164	0.404	2.76E-07	3.87E-05	neuron projection extension

GO:0050766	63	0.677	2.78E-07	3.90E-05	positive regulation of phagocytosis
GO:0007411	271	0.315	2.83E-07	3.96E-05	axon guidance
GO:0035710	89	0.549	2.87E-07	3.99E-05	CD4-positive, alpha-beta T cell activation
GO:0021537	249	0.327	3.01E-07	4.19E-05	telencephalon development
GO:0043367	73	0.602	3.10E-07	4.30E-05	CD4-positive, alpha-beta T cell differentiation
GO:0051495	215	0.353	3.23E-07	4.47E-05	positive regulation of cytoskeleton organization
GO:1903555	106	0.512	3.24E-07	4.47E-05	regulation of tumor necrosis factor superfamily cytokine production
GO:0038127	135	0.443	3.35E-07	4.61E-05	ERBB signaling pathway
GO:0032649	69	0.630	3.36E-07	4.61E-05	regulation of interferon-gamma production
GO:0097485	272	0.313	3.41E-07	4.67E-05	neuron projection guidance
GO:0048675	117	0.473	3.47E-07	4.74E-05	axon extension
GO:0046637	62	0.646	3.50E-07	4.77E-05	regulation of alpha-beta T cell differentiation
GO:0097191	215	0.351	3.66E-07	4.98E-05	extrinsic apoptotic signaling pathway
GO:0051656	398	0.259	3.72E-07	5.03E-05	establishment of organelle localization
GO:0019886	79	0.600	3.71E-07	5.03E-05	antigen processing and presentation of exogenous peptide antigen via MHC class II
GO:0090257	226	0.341	3.76E-07	5.07E-05	regulation of muscle system process
GO:0051047	321	0.287	3.85E-07	5.18E-05	positive regulation of secretion
GO:0071706	110	0.500	3.92E-07	5.27E-05	tumor necrosis factor superfamily cytokine production
GO:0050855	26	0.944	3.93E-07	5.27E-05	regulation of B cell receptor signaling pathway
GO:0046328	180	0.383	4.24E-07	5.68E-05	regulation of JNK cascade
GO:0035023	137	0.435	4.35E-07	5.79E-05	regulation of Rho protein signal transduction
GO:0101023	18	1.045	4.36E-07	5.79E-05	vascular endothelial cell proliferation
GO:1905562	18	1.045	4.36E-07	5.79E-05	regulation of vascular endothelial cell proliferation
GO:0060840	88	0.532	4.42E-07	5.86E-05	artery development
GO:0050890	291	0.299	4.52E-07	5.97E-05	cognition
GO:0002708	88	0.552	4.65E-07	6.14E-05	positive regulation of lymphocyte mediated immunity
GO:1901214	308	0.290	4.79E-07	6.30E-05	regulation of neuron death
GO:0048639	169	0.389	4.84E-07	6.36E-05	positive regulation of developmental growth
GO:0019722	204	0.354	5.17E-07	6.78E-05	calcium-mediated signaling

GO:0045216	182	0.376	5.20E-07	6.80E-05	cell-cell junction organization
GO:0001912	42	0.764	5.54E-07	7.23E-05	positive regulation of leukocyte mediated cytotoxicity
GO:0042542	132	0.446	5.67E-07	7.38E-05	response to hydrogen peroxide
GO:0007051	162	0.401	5.72E-07	7.43E-05	spindle organization
GO:0007254	210	0.349	5.95E-07	7.71E-05	JNK cascade
GO:0045621	89	0.533	6.26E-07	8.10E-05	positive regulation of lymphocyte differentiation
GO:0071349	48	0.743	6.31E-07	8.14E-05	cellular response to interleukin-12
GO:0042742	192	0.362	6.84E-07	8.79E-05	defense response to bacterium
GO:0097553	136	0.430	6.95E-07	8.90E-05	calcium ion transmembrane import into cytosol
GO:0007173	113	0.472	7.50E-07	9.59E-05	epidermal growth factor receptor signaling pathway
GO:0070671	49	0.726	7.88E-07	1.01E-04	response to interleukin-12
GO:0045666	358	0.264	8.05E-07	1.03E-04	positive regulation of neuron differentiation
GO:0051092	147	0.413	8.29E-07	1.05E-04	positive regulation of NF-kappaB transcription factor activity
GO:0045428	57	0.654	8.94E-07	1.13E-04	regulation of nitric oxide biosynthetic process
GO:0045446	101	0.489	9.48E-07	1.20E-04	endothelial cell differentiation
GO:0050921	132	0.430	9.65E-07	1.21E-04	positive regulation of chemotaxis
GO:0016049	465	0.230	9.94E-07	1.25E-04	cell growth
GO:0007611	255	0.310	9.92E-07	1.25E-04	learning or memory
GO:0000302	218	0.336	1.02E-06	1.28E-04	response to reactive oxygen species
GO:0060402	155	0.397	1.03E-06	1.28E-04	calcium ion transport into cytosol
GO:0032635	88	0.530	1.03E-06	1.28E-04	interleukin-6 production
GO:0070486	12	1.214	1.09E-06	1.35E-04	leukocyte aggregation
GO:0048002	162	0.389	1.13E-06	1.40E-04	antigen processing and presentation of peptide antigen
GO:0070482	377	0.254	1.14E-06	1.41E-04	response to oxygen levels
GO:0062197	330	0.272	1.15E-06	1.42E-04	cellular response to chemical stress
GO:0032102	333	0.270	1.17E-06	1.44E-04	negative regulation of response to external stimulus
GO:0045058	48	0.706	1.17E-06	1.44E-04	T cell selection
GO:0002687	124	0.441	1.20E-06	1.47E-04	positive regulation of leukocyte migration
GO:0007187	232	0.321	1.20E-06	1.47E-04	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger
GO:0070664	71	0.583	1.23E-06	1.50E-04	negative regulation of leukocyte proliferation
GO:0030316	94	0.509	1.27E-06	1.55E-04	osteoclast differentiation

GO:0051098	356	0.260	1.28E-06	1.55E-04	regulation of binding
GO:0035265	180	0.364	1.28E-06	1.55E-04	organ growth
GO:0002260	60	0.653	1.29E-06	1.56E-04	lymphocyte homeostasis
GO:0046718	113	0.456	1.30E-06	1.57E-04	viral entry into host cell
GO:0018105	274	0.296	1.33E-06	1.60E-04	peptidyl-serine phosphorylation
GO:0010812	60	0.621	1.34E-06	1.61E-04	negative regulation of cell-substrate adhesion
GO:0051651	208	0.339	1.38E-06	1.66E-04	maintenance of location in cell
GO:0051091	255	0.306	1.41E-06	1.69E-04	positive regulation of DNA-binding transcription factor activity
GO:0014909	66	0.583	1.41E-06	1.69E-04	smooth muscle cell migration
GO:0051961	306	0.278	1.48E-06	1.76E-04	negative regulation of nervous system development
GO:0030865	47	0.725	1.50E-06	1.78E-04	cortical cytoskeleton organization
GO:0006606	135	0.419	1.52E-06	1.80E-04	protein import into nucleus
GO:0002292	66	0.599	1.57E-06	1.85E-04	T cell differentiation involved in immune response
GO:0030838	92	0.506	1.60E-06	1.88E-04	positive regulation of actin filament polymerization
GO:0001953	37	0.763	1.60E-06	1.88E-04	negative regulation of cell-matrix adhesion
GO:0045089	190	0.353	1.64E-06	1.93E-04	positive regulation of innate immune response
GO:2000273	34	0.808	1.74E-06	2.03E-04	positive regulation of signaling receptor activity
GO:0051057	73	0.563	1.78E-06	2.07E-04	positive regulation of small GTPase mediated signal transduction
GO:0010770	152	0.389	1.82E-06	2.11E-04	positive regulation of cell morphogenesis involved in differentiation
GO:0032675	83	0.535	1.82E-06	2.11E-04	regulation of interleukin-6 production
GO:0000281	70	0.590	1.92E-06	2.23E-04	mitotic cytokinesis
GO:0002577	16	1.058	1.95E-06	2.26E-04	regulation of antigen processing and presentation
GO:0033047	65	0.594	1.97E-06	2.27E-04	regulation of mitotic sister chromatid segregation
GO:0010595	97	0.485	2.00E-06	2.30E-04	positive regulation of endothelial cell migration
GO:0048545	376	0.248	2.03E-06	2.33E-04	response to steroid hormone
GO:0045773	41	0.719	2.05E-06	2.35E-04	positive regulation of axon extension
GO:1990868	85	0.524	2.07E-06	2.36E-04	response to chemokine
GO:1990869	85	0.524	2.07E-06	2.36E-04	cellular response to chemokine
GO:0001771	14	1.100	2.15E-06	2.45E-04	immunological synapse formation

GO:0038063	10	1.175	2.16E-06	2.45E-04	collagen-activated tyrosine kinase receptor signaling pathway
GO:0032680	103	0.479	2.18E-06	2.47E-04	regulation of tumor necrosis factor production
GO:1901654	194	0.342	2.19E-06	2.48E-04	response to ketone
GO:0007188	205	0.332	2.21E-06	2.49E-04	adenylate cyclase-modulating G protein-coupled receptor signaling pathway
GO:0019935	199	0.337	2.24E-06	2.51E-04	cyclic-nucleotide-mediated signaling
GO:0046824	64	0.587	2.29E-06	2.57E-04	positive regulation of nucleocytoplasmic transport
GO:0042493	394	0.241	2.32E-06	2.60E-04	response to drug
GO:0043536	54	0.641	2.33E-06	2.60E-04	positive regulation of blood vessel endothelial cell migration
GO:0001894	216	0.324	2.34E-06	2.61E-04	tissue homeostasis
GO:0030866	42	0.757	2.36E-06	2.63E-04	cortical actin cytoskeleton organization
GO:0043277	46	0.682	2.37E-06	2.63E-04	apoptotic cell clearance
GO:0030219	74	0.562	2.38E-06	2.64E-04	megakaryocyte differentiation
GO:0045582	78	0.541	2.43E-06	2.68E-04	positive regulation of T cell differentiation
GO:0036005	12	1.140	2.43E-06	2.68E-04	response to macrophage colony-stimulating factor
GO:0036006	12	1.140	2.43E-06	2.68E-04	cellular response to macrophage colony-stimulating factor stimulus
GO:0030010	134	0.411	2.49E-06	2.73E-04	establishment of cell polarity
GO:0016202	132	0.411	2.51E-06	2.75E-04	regulation of striated muscle tissue development
GO:0032640	107	0.468	2.53E-06	2.77E-04	tumor necrosis factor production
GO:0032835	61	0.598	2.58E-06	2.81E-04	glomerulus development
GO:0034103	75	0.530	2.64E-06	2.88E-04	regulation of tissue remodeling
GO:0070997	343	0.256	2.67E-06	2.91E-04	neuron death
GO:0002821	94	0.497	2.70E-06	2.94E-04	positive regulation of adaptive immune response
GO:0002468	12	1.202	2.83E-06	3.06E-04	dendritic cell antigen processing and presentation
GO:0014910	60	0.590	2.84E-06	3.07E-04	regulation of smooth muscle cell migration
GO:1902532	477	0.217	2.96E-06	3.18E-04	negative regulation of intracellular signal transduction
GO:0051261	105	0.469	2.99E-06	3.21E-04	protein depolymerization
GO:1901222	101	0.471	2.99E-06	3.21E-04	regulation of NIK/NF-kappaB signaling
GO:0002548	52	0.634	3.10E-06	3.32E-04	monocyte chemotaxis
GO:0014896	87	0.506	3.14E-06	3.35E-04	muscle hypertrophy
GO:0000187	147	0.386	3.17E-06	3.38E-04	activation of MAPK activity

GO:0051701	190	0.341	3.23E-06	3.43E-04	interaction with host
GO:0045920	32	0.869	3.23E-06	3.43E-04	negative regulation of exocytosis
GO:0048661	85	0.515	3.28E-06	3.47E-04	positive regulation of smooth muscle cell proliferation
GO:1901861	135	0.401	3.29E-06	3.47E-04	regulation of muscle tissue development
GO:0001666	343	0.254	3.38E-06	3.56E-04	response to hypoxia
GO:0061041	126	0.422	3.38E-06	3.56E-04	regulation of wound healing
GO:0034446	98	0.474	3.50E-06	3.67E-04	substrate adhesion-dependent cell spreading
GO:0050858	25	0.883	3.58E-06	3.75E-04	negative regulation of antigen receptor-mediated signaling pathway
GO:0031102	57	0.608	3.62E-06	3.78E-04	neuron projection regeneration
GO:0034121	63	0.626	3.64E-06	3.79E-04	regulation of toll-like receptor signaling pathway
GO:0001937	37	0.739	3.68E-06	3.83E-04	negative regulation of endothelial cell proliferation
GO:0099177	433	0.225	3.72E-06	3.87E-04	regulation of trans-synaptic signaling
GO:0007052	103	0.463	3.74E-06	3.88E-04	mitotic spindle organization
GO:0035722	46	0.701	3.80E-06	3.94E-04	interleukin-12-mediated signaling pathway
GO:0046633	31	0.798	3.84E-06	3.97E-04	alpha-beta T cell proliferation
GO:0032388	212	0.322	3.90E-06	4.00E-04	positive regulation of intracellular transport
GO:0010976	273	0.282	3.92E-06	4.02E-04	positive regulation of neuron projection development
GO:0051302	157	0.371	4.05E-06	4.14E-04	regulation of cell division
GO:2000514	58	0.606	4.15E-06	4.23E-04	regulation of CD4-positive, alpha-beta T cell activation
GO:0019884	155	0.376	4.20E-06	4.28E-04	antigen processing and presentation of exogenous antigen
GO:1903557	52	0.682	4.20E-06	4.28E-04	positive regulation of tumor necrosis factor superfamily cytokine production
GO:0061515	70	0.578	4.28E-06	4.35E-04	myeloid cell development
GO:0006968	44	0.729	4.32E-06	4.38E-04	cellular defense response
GO:0007517	383	0.237	4.43E-06	4.49E-04	muscle organ development
GO:0002440	177	0.352	4.46E-06	4.50E-04	production of molecular mediator of immune response
GO:0048634	135	0.396	4.48E-06	4.51E-04	regulation of muscle organ development
GO:0110020	89	0.491	4.62E-06	4.66E-04	regulation of actomyosin structure organization
GO:0036293	353	0.247	4.74E-06	4.77E-04	response to decreased oxygen levels

GO:0150077	34	0.765	4.93E-06	4.95E-04	regulation of neuroinflammatory response
GO:0045471	130	0.401	4.94E-06	4.95E-04	response to ethanol
GO:0043303	45	0.689	5.04E-06	5.04E-04	mast cell degranulation
GO:0032729	41	0.716	5.20E-06	5.18E-04	positive regulation of interferon-gamma production
GO:2000114	21	0.990	5.20E-06	5.18E-04	regulation of establishment of cell polarity
GO:0050804	432	0.222	5.25E-06	5.22E-04	modulation of chemical synaptic transmission
GO:0051783	185	0.338	5.27E-06	5.22E-04	regulation of nuclear division
GO:1901992	77	0.536	5.26E-06	5.22E-04	positive regulation of mitotic cell cycle phase transition
GO:0032945	66	0.566	5.40E-06	5.33E-04	negative regulation of mononuclear cell proliferation
GO:0050672	66	0.566	5.40E-06	5.33E-04	negative regulation of lymphocyte proliferation
GO:0035904	53	0.602	5.50E-06	5.43E-04	aorta development
GO:0050768	285	0.272	5.57E-06	5.46E-04	negative regulation of neurogenesis
GO:0019079	106	0.446	5.56E-06	5.46E-04	viral genome replication
GO:0046579	65	0.568	5.56E-06	5.46E-04	positive regulation of Ras protein signal transduction
GO:0008037	140	0.386	5.59E-06	5.48E-04	cell recognition
GO:0071604	37	0.725	5.61E-06	5.49E-04	transforming growth factor beta production
GO:0030038	94	0.471	5.69E-06	5.55E-04	contractile actin filament bundle assembly
GO:0043149	94	0.471	5.69E-06	5.55E-04	stress fiber assembly
GO:0014897	85	0.498	5.80E-06	5.64E-04	striated muscle hypertrophy
GO:1902850	128	0.407	5.90E-06	5.73E-04	microtubule cytoskeleton organization involved in mitosis
GO:0043588	316	0.257	5.93E-06	5.74E-04	skin development
GO:0050856	37	0.731	5.93E-06	5.74E-04	regulation of T cell receptor signaling pathway
GO:0002062	118	0.417	6.00E-06	5.80E-04	chondrocyte differentiation
GO:0032608	43	0.763	6.01E-06	5.80E-04	interferon-beta production
GO:0007568	302	0.264	6.10E-06	5.88E-04	aging
GO:0048285	438	0.219	6.53E-06	6.26E-04	organelle fission
GO:0061387	107	0.439	6.58E-06	6.28E-04	regulation of extent of cell growth
GO:0003300	82	0.505	6.57E-06	6.28E-04	cardiac muscle hypertrophy
GO:0002604	11	1.226	6.78E-06	6.46E-04	regulation of dendritic cell antigen processing and presentation
GO:2000401	58	0.621	6.84E-06	6.51E-04	regulation of lymphocyte migration
GO:0033045	77	0.520	6.89E-06	6.55E-04	regulation of sister chromatid segregation

GO:1990090	52	0.627	6.92E-06	6.57E-04	cellular response to nerve growth factor stimulus
GO:0035924	54	0.630	7.21E-06	6.82E-04	cellular response to vascular endothelial growth factor stimulus
GO:0030516	92	0.471	7.30E-06	6.89E-04	regulation of axon extension
GO:0098751	34	0.908	7.75E-06	7.30E-04	bone cell development
GO:1902882	82	0.503	7.93E-06	7.41E-04	regulation of response to oxidative stress
GO:0043368	35	0.782	7.92E-06	7.41E-04	positive T cell selection
GO:0033032	28	0.829	7.91E-06	7.41E-04	regulation of myeloid cell apoptotic process
GO:0032731	15	1.067	7.91E-06	7.41E-04	positive regulation of interleukin-1 beta production
GO:0002717	23	0.879	7.97E-06	7.44E-04	positive regulation of natural killer cell mediated immunity
GO:0043500	106	0.436	8.15E-06	7.60E-04	muscle adaptation
GO:2001204	11	1.152	8.28E-06	7.68E-04	regulation of osteoclast development
GO:0034340	70	0.538	8.61E-06	7.98E-04	response to type I interferon
GO:0002456	89	0.479	8.67E-06	8.01E-04	T cell mediated immunity
GO:0070304	166	0.348	8.69E-06	8.02E-04	positive regulation of stress-activated protein kinase signaling cascade
GO:2001236	149	0.368	8.74E-06	8.04E-04	regulation of extrinsic apoptotic signaling pathway
GO:0032606	117	0.422	8.73E-06	8.04E-04	type I interferon production
GO:0050830	67	0.547	8.75E-06	8.04E-04	defense response to Gram-positive bacterium
GO:0071229	75	0.519	8.80E-06	8.07E-04	cellular response to acid chemical
GO:0014911	37	0.708	9.17E-06	8.35E-04	positive regulation of smooth muscle cell migration
GO:0071230	68	0.544	9.25E-06	8.42E-04	cellular response to amino acid stimulus
GO:0061448	263	0.275	9.40E-06	8.52E-04	connective tissue development
GO:0062207	83	0.505	9.57E-06	8.67E-04	regulation of pattern recognition receptor signaling pathway
GO:0018210	122	0.410	9.65E-06	8.72E-04	peptidyl-threonine modification
GO:0032528	24	0.921	9.65E-06	8.72E-04	microvillus organization
GO:0007043	126	0.395	9.86E-06	8.89E-04	cell-cell junction assembly
GO:0001938	92	0.460	9.90E-06	8.92E-04	positive regulation of endothelial cell proliferation
GO:0001822	280	0.266	1.01E-05	9.09E-04	kidney development
GO:0051988	12	1.316	1.01E-05	9.09E-04	regulation of attachment of spindle microtubules to kinetochore
GO:0002279	46	0.658	1.02E-05	9.12E-04	mast cell activation involved in immune response

GO:0052126	150	0.363	1.02E-05	9.14E-04	movement in host environment
GO:2000045	145	0.372	1.03E-05	9.21E-04	regulation of G1/S transition of mitotic cell cycle
GO:0045954	22	0.891	1.05E-05	9.33E-04	positive regulation of natural killer cell mediated cytotoxicity
GO:0006470	305	0.255	1.06E-05	9.38E-04	protein dephosphorylation
GO:0050922	54	0.601	1.07E-05	9.52E-04	negative regulation of chemotaxis
GO:0090287	263	0.273	1.10E-05	9.76E-04	regulation of cellular response to growth factor stimulus
GO:0032479	115	0.420	1.14E-05	1.00E-03	regulation of type I interferon production
GO:0002824	89	0.477	1.15E-05	1.02E-03	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains
GO:0032613	38	0.704	1.21E-05	1.06E-03	interleukin-10 production
GO:0051222	340	0.240	1.22E-05	1.08E-03	positive regulation of protein transport
GO:1901990	399	0.222	1.23E-05	1.08E-03	regulation of mitotic cell cycle phase transition
GO:0050777	129	0.390	1.23E-05	1.08E-03	negative regulation of immune response
GO:0071634	35	0.721	1.23E-05	1.08E-03	regulation of transforming growth factor beta production
GO:0072001	296	0.256	1.24E-05	1.08E-03	renal system development
GO:0045927	251	0.279	1.24E-05	1.08E-03	positive regulation of growth
GO:0001837	133	0.382	1.24E-05	1.08E-03	epithelial to mesenchymal transition
GO:0002791	347	0.237	1.27E-05	1.11E-03	regulation of peptide secretion
GO:0032760	50	0.657	1.29E-05	1.12E-03	positive regulation of tumor necrosis factor production
GO:0022406	177	0.332	1.36E-05	1.18E-03	membrane docking
GO:0071692	422	0.215	1.37E-05	1.19E-03	protein localization to extracellular region
GO:0001954	50	0.616	1.37E-05	1.19E-03	positive regulation of cell-matrix adhesion
GO:0002790	454	0.207	1.38E-05	1.19E-03	peptide secretion
GO:0032878	25	0.889	1.38E-05	1.19E-03	regulation of establishment or maintenance of cell polarity
GO:0060401	172	0.335	1.39E-05	1.20E-03	cytosolic calcium ion transport
GO:0030199	50	0.634	1.42E-05	1.22E-03	collagen fibril organization
GO:0001913	35	0.760	1.43E-05	1.23E-03	T cell mediated cytotoxicity
GO:0001763	195	0.312	1.44E-05	1.23E-03	morphogenesis of a branching structure
GO:0032874	165	0.340	1.46E-05	1.25E-03	positive regulation of stress-activated MAPK cascade

GO:0034599	280	0.262	1.48E-05	1.26E-03	cellular response to oxidative stress
GO:1901136	177	0.328	1.51E-05	1.29E-03	carbohydrate derivative catabolic process
GO:1905477	123	0.399	1.52E-05	1.29E-03	positive regulation of protein localization to membrane
GO:0002478	149	0.360	1.54E-05	1.31E-03	antigen processing and presentation of exogenous peptide antigen
GO:0019933	171	0.332	1.55E-05	1.31E-03	cAMP-mediated signaling
GO:0009595	28	0.815	1.55E-05	1.31E-03	detection of biotic stimulus
GO:0042552	130	0.383	1.58E-05	1.34E-03	myelination
GO:0045670	62	0.560	1.61E-05	1.36E-03	regulation of osteoclast differentiation
GO:0097306	84	0.478	1.62E-05	1.37E-03	cellular response to alcohol
GO:0097581	79	0.492	1.65E-05	1.39E-03	lamellipodium organization
GO:0002761	113	0.410	1.68E-05	1.42E-03	regulation of myeloid leukocyte differentiation
GO:0032869	216	0.295	1.74E-05	1.46E-03	cellular response to insulin stimulus
GO:0007009	99	0.436	1.75E-05	1.47E-03	plasma membrane organization
GO:1904951	356	0.230	1.77E-05	1.48E-03	positive regulation of establishment of protein localization
GO:0001101	131	0.377	1.77E-05	1.48E-03	response to acid chemical
GO:0051048	176	0.327	1.78E-05	1.49E-03	negative regulation of secretion
GO:0051216	202	0.303	1.82E-05	1.51E-03	cartilage development
GO:0017015	110	0.412	1.82E-05	1.51E-03	regulation of transforming growth factor beta receptor signaling pathway
GO:0010522	99	0.434	1.81E-05	1.51E-03	regulation of calcium ion transport into cytosol
GO:1903844	112	0.408	1.84E-05	1.53E-03	regulation of cellular response to transforming growth factor beta stimulus
GO:0010506	317	0.243	1.86E-05	1.54E-03	regulation of autophagy
GO:0032963	98	0.438	1.87E-05	1.54E-03	collagen metabolic process
GO:1990089	55	0.583	1.87E-05	1.54E-03	response to nerve growth factor
GO:0046640	28	0.783	1.86E-05	1.54E-03	regulation of alpha-beta T cell proliferation
GO:0048144	80	0.483	1.88E-05	1.55E-03	fibroblast proliferation
GO:0051494	134	0.377	1.90E-05	1.56E-03	negative regulation of cytoskeleton organization
GO:0021543	166	0.333	1.96E-05	1.61E-03	pallium development
GO:0038065	13	1.023	2.11E-05	1.73E-03	collagen-activated signaling pathway
GO:0060996	93	0.443	2.14E-05	1.74E-03	dendritic spine development

GO:0050857	22	0.882	2.13E-05	1.74E-03	positive regulation of antigen receptor-mediated signaling pathway
GO:0006979	422	0.210	2.15E-05	1.75E-03	response to oxidative stress
GO:0090316	177	0.323	2.23E-05	1.82E-03	positive regulation of intracellular protein transport
GO:0050803	224	0.285	2.27E-05	1.84E-03	regulation of synapse structure or activity
GO:0007272	132	0.372	2.35E-05	1.91E-03	ensheathment of neurons
GO:0008366	132	0.372	2.35E-05	1.91E-03	axon ensheathment
GO:0070266	35	0.741	2.39E-05	1.93E-03	necroptotic process
GO:0046330	138	0.362	2.42E-05	1.95E-03	positive regulation of JNK cascade
GO:0032653	37	0.689	2.45E-05	1.97E-03	regulation of interleukin-10 production
GO:0071352	13	1.011	2.45E-05	1.97E-03	cellular response to interleukin-2
GO:0070228	50	0.623	2.48E-05	1.99E-03	regulation of lymphocyte apoptotic process
GO:0072659	260	0.264	2.49E-05	2.00E-03	protein localization to plasma membrane
GO:0006936	345	0.229	2.55E-05	2.04E-03	muscle contraction
GO:0002011	52	0.573	2.55E-05	2.04E-03	morphogenesis of an epithelial sheet
GO:1903532	298	0.246	2.57E-05	2.05E-03	positive regulation of secretion by cell
GO:0001933	388	0.216	2.59E-05	2.06E-03	negative regulation of protein phosphorylation
GO:0016358	230	0.280	2.62E-05	2.09E-03	dendrite development
GO:0051099	179	0.317	2.65E-05	2.10E-03	positive regulation of binding
GO:0001780	17	1.028	2.68E-05	2.12E-03	neutrophil homeostasis
GO:0019883	14	1.046	2.69E-05	2.13E-03	antigen processing and presentation of endogenous antigen
GO:1904062	325	0.235	2.79E-05	2.21E-03	regulation of cation transmembrane transport
GO:0032570	46	0.605	2.81E-05	2.22E-03	response to progesterone
GO:0034110	25	0.807	2.88E-05	2.27E-03	regulation of homotypic cell-cell adhesion
GO:0048145	79	0.475	2.88E-05	2.27E-03	regulation of fibroblast proliferation
GO:0050708	317	0.238	2.89E-05	2.27E-03	regulation of protein secretion
GO:0050807	215	0.287	2.89E-05	2.27E-03	regulation of synapse organization
GO:0042326	425	0.206	2.93E-05	2.30E-03	negative regulation of phosphorylation
GO:0070588	307	0.241	2.95E-05	2.32E-03	calcium ion transmembrane transport
GO:0051770	15	1.197	2.96E-05	2.32E-03	positive regulation of nitric-oxide synthase biosynthetic process

GO:0032648	41	0.707	2.96E-05	2.32E-03	regulation of interferon-beta production
GO:1903169	144	0.352	2.99E-05	2.34E-03	regulation of calcium ion transmembrane transport
GO:1901224	75	0.493	3.02E-05	2.36E-03	positive regulation of NIK/NF-kappaB signaling
GO:0070527	59	0.544	3.04E-05	2.37E-03	platelet aggregation
GO:0014015	75	0.488	3.07E-05	2.38E-03	positive regulation of gliogenesis
GO:1904377	63	0.531	3.07E-05	2.38E-03	positive regulation of protein localization to cell periphery
GO:1904019	98	0.419	3.10E-05	2.41E-03	epithelial cell apoptotic process
GO:0003170	60	0.546	3.11E-05	2.41E-03	heart valve development
GO:0002287	60	0.543	3.16E-05	2.44E-03	alpha-beta T cell activation involved in immune response
GO:0002293	60	0.543	3.16E-05	2.44E-03	alpha-beta T cell differentiation involved in immune response
GO:0035592	417	0.206	3.19E-05	2.46E-03	establishment of protein localization to extracellular region
GO:0032486	14	1.080	3.20E-05	2.46E-03	Rap protein signal transduction
GO:0048705	236	0.272	3.30E-05	2.54E-03	skeletal system morphogenesis
GO:0050931	35	0.722	3.31E-05	2.54E-03	pigment cell differentiation
GO:0043200	112	0.395	3.32E-05	2.55E-03	response to amino acid
GO:0036119	21	0.878	3.34E-05	2.56E-03	response to platelet-derived growth factor
GO:0009306	416	0.206	3.37E-05	2.58E-03	protein secretion
GO:0007091	54	0.571	3.38E-05	2.58E-03	metaphase/anaphase transition of mitotic cell cycle
GO:0010965	54	0.571	3.38E-05	2.58E-03	regulation of mitotic sister chromatid separation
GO:0071695	224	0.279	3.40E-05	2.59E-03	anatomical structure maturation
GO:0060337	67	0.512	3.48E-05	2.64E-03	type I interferon signaling pathway
GO:0071357	67	0.512	3.48E-05	2.64E-03	cellular response to type I interferon
GO:0002294	59	0.545	3.50E-05	2.65E-03	CD4-positive, alpha-beta T cell differentiation involved in immune response
GO:2000108	25	0.828	3.50E-05	2.65E-03	positive regulation of leukocyte apoptotic process
GO:0046638	46	0.610	3.56E-05	2.69E-03	positive regulation of alpha-beta T cell differentiation
GO:0051894	25	0.783	3.58E-05	2.70E-03	positive regulation of focal adhesion assembly
GO:0060562	323	0.232	3.60E-05	2.72E-03	epithelial tube morphogenesis
GO:0030889	16	0.923	3.61E-05	2.72E-03	negative regulation of B cell proliferation
GO:0051489	43	0.620	3.62E-05	2.72E-03	regulation of filopodium assembly

GO:0036092	14	1.002	3.65E-05	2.74E-03	phosphatidylinositol-3-phosphate biosynthetic process
GO:2000379	94	0.432	3.66E-05	2.74E-03	positive regulation of reactive oxygen species metabolic process
GO:0002688	106	0.404	3.69E-05	2.76E-03	regulation of leukocyte chemotaxis
GO:0070098	77	0.478	3.70E-05	2.76E-03	chemokine-mediated signaling pathway
GO:0033631	16	0.959	3.71E-05	2.77E-03	cell-cell adhesion mediated by integrin
GO:0043502	83	0.454	3.72E-05	2.77E-03	regulation of muscle adaptation
GO:0008544	362	0.218	3.75E-05	2.79E-03	epidermis development
GO:0060420	65	0.510	3.78E-05	2.80E-03	regulation of heart growth
GO:0007156	119	0.377	3.83E-05	2.84E-03	homophilic cell adhesion via plasma membrane adhesion molecules
GO:0003231	126	0.365	3.94E-05	2.91E-03	cardiac ventricle development
GO:0007062	56	0.562	3.96E-05	2.92E-03	sister chromatid cohesion
GO:0006333	168	0.319	3.96E-05	2.92E-03	chromatin assembly or disassembly
GO:0060252	17	0.911	3.99E-05	2.93E-03	positive regulation of glial cell proliferation
GO:0050860	18	0.915	3.98E-05	2.93E-03	negative regulation of T cell receptor signaling pathway
GO:0043370	46	0.610	4.05E-05	2.97E-03	regulation of CD4-positive, alpha-beta T cell differentiation
GO:0007178	327	0.229	4.05E-05	2.97E-03	transmembrane receptor protein serine/threonine kinase signaling pathway
GO:0150117	26	0.762	4.08E-05	2.99E-03	positive regulation of cell-substrate junction organization
GO:0032868	273	0.251	4.09E-05	2.99E-03	response to insulin
GO:0055024	80	0.458	4.10E-05	3.00E-03	regulation of cardiac muscle tissue development
GO:0006338	185	0.305	4.19E-05	3.05E-03	chromatin remodeling
GO:0002367	82	0.465	4.22E-05	3.07E-03	cytokine production involved in immune response
GO:1904705	50	0.585	4.22E-05	3.07E-03	regulation of vascular associated smooth muscle cell proliferation
GO:1990874	50	0.585	4.22E-05	3.07E-03	vascular associated smooth muscle cell proliferation
GO:0043506	84	0.447	4.45E-05	3.22E-03	regulation of JUN kinase activity
GO:0070227	65	0.522	4.45E-05	3.22E-03	lymphocyte apoptotic process
GO:1901184	87	0.442	4.48E-05	3.24E-03	regulation of ERBB signaling pathway
GO:0043331	42	0.632	4.57E-05	3.30E-03	response to dsRNA
GO:1905475	187	0.303	4.59E-05	3.31E-03	regulation of protein localization to membrane

GO:0048738	208	0.285	4.60E-05	3.32E-03	cardiac muscle tissue development
GO:0034332	64	0.508	4.66E-05	3.35E-03	adherens junction organization
GO:0001890	153	0.330	4.75E-05	3.41E-03	placenta development
GO:0032615	39	0.661	4.77E-05	3.42E-03	interleukin-12 production
GO:2000353	18	0.894	4.77E-05	3.42E-03	positive regulation of endothelial cell apoptotic process
GO:0036120	20	0.887	4.84E-05	3.46E-03	cellular response to platelet-derived growth factor stimulus
GO:0030890	41	0.675	4.92E-05	3.51E-03	positive regulation of B cell proliferation
GO:0002042	54	0.552	4.93E-05	3.52E-03	cell migration involved in sprouting angiogenesis
GO:0044319	28	0.735	4.98E-05	3.54E-03	wound healing, spreading of cells
GO:0090505	28	0.735	4.98E-05	3.54E-03	epiboly involved in wound healing
GO:0090504	29	0.720	5.05E-05	3.58E-03	epiboly
GO:1990778	317	0.230	5.12E-05	3.62E-03	protein localization to cell periphery
GO:0070301	88	0.439	5.11E-05	3.62E-03	cellular response to hydrogen peroxide
GO:0032386	336	0.224	5.19E-05	3.67E-03	regulation of intracellular transport
GO:0003208	72	0.468	5.33E-05	3.76E-03	cardiac ventricle morphogenesis
GO:0018107	114	0.385	5.37E-05	3.79E-03	peptidyl-threonine phosphorylation
GO:1903670	67	0.493	5.37E-05	3.79E-03	regulation of sprouting angiogenesis
GO:0051491	30	0.702	5.40E-05	3.80E-03	positive regulation of filopodium assembly
GO:0002262	147	0.335	5.54E-05	3.89E-03	myeloid cell homeostasis
GO:0043552	33	0.677	5.60E-05	3.93E-03	positive regulation of phosphatidylinositol 3-kinase activity
GO:0055021	59	0.524	5.70E-05	3.99E-03	regulation of cardiac muscle tissue growth
GO:0002448	47	0.609	5.71E-05	4.00E-03	mast cell mediated immunity
GO:0050871	72	0.490	5.74E-05	4.01E-03	positive regulation of B cell activation
GO:0050663	61	0.516	5.79E-05	4.04E-03	cytokine secretion
GO:0061138	181	0.300	5.89E-05	4.11E-03	morphogenesis of a branching epithelium
GO:0033157	251	0.257	5.91E-05	4.11E-03	regulation of intracellular protein transport
GO:0033028	32	0.698	5.96E-05	4.15E-03	myeloid cell apoptotic process
GO:0032755	53	0.561	6.02E-05	4.18E-03	positive regulation of interleukin-6 production
GO:0045665	220	0.273	6.07E-05	4.21E-03	negative regulation of neuron differentiation

GO:0060368	12	1.193	6.08E-05	4.21E-03	regulation of Fc receptor mediated stimulatory signaling pathway
GO:0034612	281	0.241	6.23E-05	4.31E-03	response to tumor necrosis factor
GO:1903510	110	0.388	6.26E-05	4.33E-03	mucopolysaccharide metabolic process
GO:1903522	282	0.240	6.30E-05	4.35E-03	regulation of blood circulation
GO:0036037	22	0.781	6.39E-05	4.41E-03	CD8-positive, alpha-beta T cell activation
GO:0042698	71	0.469	6.44E-05	4.43E-03	ovulation cycle
GO:0042771	45	0.592	6.45E-05	4.44E-03	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator
GO:0036035	17	0.948	6.63E-05	4.56E-03	osteoclast development
GO:0070102	19	0.884	6.67E-05	4.58E-03	interleukin-6-mediated signaling pathway
GO:0060249	405	0.201	6.68E-05	4.58E-03	anatomical structure homeostasis
GO:0052548	358	0.213	6.79E-05	4.65E-03	regulation of endopeptidase activity
GO:0030203	155	0.323	6.81E-05	4.66E-03	glycosaminoglycan metabolic process
GO:0052547	383	0.206	6.86E-05	4.69E-03	regulation of peptidase activity
GO:0071786	16	0.920	6.90E-05	4.71E-03	endoplasmic reticulum tubular network organization
GO:0034614	156	0.321	6.94E-05	4.73E-03	cellular response to reactive oxygen species
GO:0051492	80	0.449	7.00E-05	4.77E-03	regulation of stress fiber assembly
GO:2000134	100	0.405	7.10E-05	4.83E-03	negative regulation of G1/S transition of mitotic cell cycle
GO:0050690	30	0.727	7.21E-05	4.90E-03	regulation of defense response to virus by virus
GO:0033077	71	0.476	7.31E-05	4.96E-03	T cell differentiation in thymus
GO:0042692	346	0.216	7.34E-05	4.97E-03	muscle cell differentiation
GO:1901215	204	0.279	7.38E-05	4.99E-03	negative regulation of neuron death
GO:0071675	43	0.600	7.41E-05	5.01E-03	regulation of mononuclear cell migration
GO:0016572	38	0.635	7.49E-05	5.05E-03	histone phosphorylation
GO:0008608	32	0.750	7.49E-05	5.05E-03	attachment of spindle microtubules to kinetochore
GO:0048844	64	0.492	7.53E-05	5.07E-03	artery morphogenesis
GO:0048247	50	0.563	7.56E-05	5.08E-03	lymphocyte chemotaxis
GO:0050852	176	0.302	7.58E-05	5.09E-03	T cell receptor signaling pathway
GO:0014013	123	0.360	7.63E-05	5.12E-03	regulation of gliogenesis
GO:0001701	346	0.215	7.71E-05	5.16E-03	in utero embryonic development

GO:0006925	21	0.875	7.72E-05	5.16E-03	inflammatory cell apoptotic process
GO:0001885	60	0.516	7.78E-05	5.18E-03	endothelial cell development
GO:0003205	166	0.308	7.84E-05	5.22E-03	cardiac chamber development
GO:0120034	99	0.397	7.95E-05	5.28E-03	positive regulation of plasma membrane bounded cell projection assembly
GO:0002686	42	0.622	8.08E-05	5.37E-03	negative regulation of leukocyte migration
GO:0006809	68	0.483	8.16E-05	5.42E-03	nitric oxide biosynthetic process
GO:0031668	231	0.262	8.22E-05	5.45E-03	cellular response to extracellular stimulus
GO:1902904	127	0.355	8.32E-05	5.51E-03	negative regulation of supramolecular fiber organization
GO:0048880	371	0.206	8.49E-05	5.61E-03	sensory system development
GO:0050901	25	0.748	8.51E-05	5.62E-03	leukocyte tethering or rolling
GO:1904037	30	0.689	8.57E-05	5.65E-03	positive regulation of epithelial cell apoptotic process
GO:1903078	56	0.532	8.68E-05	5.72E-03	positive regulation of protein localization to plasma membrane
GO:0042058	80	0.444	8.73E-05	5.74E-03	regulation of epidermal growth factor receptor signaling pathway
GO:0033628	46	0.589	8.74E-05	5.74E-03	regulation of cell adhesion mediated by integrin
GO:0072006	143	0.331	8.77E-05	5.74E-03	nephron development
GO:0006027	61	0.509	8.79E-05	5.74E-03	glycosaminoglycan catabolic process
GO:0014009	50	0.559	8.78E-05	5.74E-03	glial cell proliferation
GO:1904407	41	0.621	8.90E-05	5.81E-03	positive regulation of nitric oxide metabolic process
GO:0060419	87	0.426	8.95E-05	5.83E-03	heart growth
GO:0006929	26	0.759	8.95E-05	5.83E-03	substrate-dependent cell migration
GO:0032231	93	0.411	9.01E-05	5.86E-03	regulation of actin filament bundle assembly
GO:0001570	77	0.443	9.25E-05	6.01E-03	vasculogenesis
GO:0150063	366	0.206	9.69E-05	6.28E-03	visual system development
GO:0045069	80	0.440	9.68E-05	6.28E-03	regulation of viral genome replication
GO:0030856	137	0.335	9.73E-05	6.30E-03	regulation of epithelial cell differentiation
GO:1990253	10	1.099	9.81E-05	6.34E-03	cellular response to leucine starvation
GO:1905564	14	0.942	9.83E-05	6.35E-03	positive regulation of vascular endothelial cell proliferation
GO:0009896	407	0.195	9.85E-05	6.35E-03	positive regulation of catabolic process
GO:0034504	251	0.248	1.00E-04	6.45E-03	protein localization to nucleus

GO:0021987	110	0.371	1.01E-04	6.47E-03	cerebral cortex development
GO:0002507	22	0.837	1.01E-04	6.51E-03	tolerance induction
GO:0046209	73	0.461	1.03E-04	6.63E-03	nitric oxide metabolic process
GO:0007548	263	0.241	1.05E-04	6.73E-03	sex differentiation
GO:0007584	177	0.294	1.05E-04	6.74E-03	response to nutrient
GO:0043201	13	1.029	1.05E-04	6.75E-03	response to leucine
GO:0010717	82	0.436	1.06E-04	6.78E-03	regulation of epithelial to mesenchymal transition
GO:0060043	41	0.608	1.06E-04	6.78E-03	regulation of cardiac muscle cell proliferation
GO:0001649	206	0.272	1.07E-04	6.84E-03	osteoblast differentiation
GO:1903707	132	0.340	1.07E-04	6.84E-03	negative regulation of hemopoiesis
GO:0034105	32	0.660	1.07E-04	6.84E-03	positive regulation of tissue remodeling
GO:0010639	367	0.205	1.08E-04	6.87E-03	negative regulation of organelle organization
GO:1902743	42	0.595	1.10E-04	6.97E-03	regulation of lamellipodium organization
GO:0070168	27	0.739	1.13E-04	7.14E-03	negative regulation of biomineral tissue development
GO:0110150	27	0.739	1.13E-04	7.14E-03	negative regulation of biomineralization
GO:2000116	219	0.264	1.13E-04	7.16E-03	regulation of cysteine-type endopeptidase activity
GO:0022617	74	0.453	1.14E-04	7.22E-03	extracellular matrix disassembly
GO:0006906	94	0.405	1.15E-04	7.28E-03	vesicle fusion
GO:1902806	158	0.310	1.16E-04	7.33E-03	regulation of cell cycle G1/S phase transition
GO:0001654	362	0.205	1.16E-04	7.33E-03	eye development
GO:0046620	95	0.397	1.17E-04	7.34E-03	regulation of organ growth
GO:1902807	102	0.388	1.17E-04	7.35E-03	negative regulation of cell cycle G1/S phase transition
GO:1903531	152	0.316	1.19E-04	7.43E-03	negative regulation of secretion by cell
GO:0002700	119	0.359	1.19E-04	7.43E-03	regulation of production of molecular mediator of immune response
GO:0042306	58	0.509	1.18E-04	7.43E-03	regulation of protein import into nucleus
GO:0042093	57	0.514	1.21E-04	7.56E-03	T-helper cell differentiation
GO:0030071	51	0.543	1.22E-04	7.64E-03	regulation of mitotic metaphase/anaphase transition
GO:2000107	45	0.587	1.23E-04	7.70E-03	negative regulation of leukocyte apoptotic process
GO:0031331	345	0.209	1.24E-04	7.75E-03	positive regulation of cellular catabolic process
GO:0032655	37	0.642	1.25E-04	7.78E-03	regulation of interleukin-12 production

GO:0051279	78	0.440	1.27E-04	7.91E-03	regulation of release of sequestered calcium ion into cytosol
GO:0003007	248	0.245	1.29E-04	7.98E-03	heart morphogenesis
GO:0045137	217	0.262	1.29E-04	7.98E-03	development of primary sexual characteristics
GO:0032355	133	0.334	1.29E-04	8.00E-03	response to estradiol
GO:0006939	103	0.379	1.29E-04	8.00E-03	smooth muscle contraction
GO:0031960	160	0.305	1.30E-04	8.03E-03	response to corticosteroid
GO:0050688	66	0.480	1.31E-04	8.12E-03	regulation of defense response to virus
GO:0046849	91	0.404	1.33E-04	8.19E-03	bone remodeling
GO:0042130	53	0.530	1.36E-04	8.40E-03	negative regulation of T cell proliferation
GO:0032740	14	0.923	1.38E-04	8.48E-03	positive regulation of interleukin-17 production
GO:0030278	187	0.281	1.39E-04	8.55E-03	regulation of ossification
GO:0061383	49	0.534	1.40E-04	8.59E-03	trabecula morphogenesis
GO:2001237	99	0.387	1.40E-04	8.60E-03	negative regulation of extrinsic apoptotic signaling pathway
GO:0140056	168	0.297	1.41E-04	8.62E-03	organelle localization by membrane tethering
GO:0070672	14	0.903	1.41E-04	8.63E-03	response to interleukin-15
GO:0006509	43	0.642	1.42E-04	8.69E-03	membrane protein ectodomain proteolysis
GO:0007565	183	0.283	1.43E-04	8.72E-03	female pregnancy
GO:0030048	137	0.328	1.43E-04	8.73E-03	actin filament-based movement
GO:0043281	196	0.275	1.44E-04	8.75E-03	regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0071233	10	1.134	1.44E-04	8.75E-03	cellular response to leucine
GO:0043393	209	0.265	1.44E-04	8.77E-03	regulation of protein binding
GO:0033046	41	0.604	1.45E-04	8.81E-03	negative regulation of sister chromatid segregation
GO:0031650	13	0.909	1.46E-04	8.84E-03	regulation of heat generation
GO:0097696	139	0.325	1.53E-04	9.25E-03	receptor signaling pathway via STAT
GO:0097300	42	0.605	1.53E-04	9.27E-03	programmed necrotic cell death
GO:0055017	80	0.430	1.55E-04	9.33E-03	cardiac muscle tissue growth
GO:1901987	430	0.185	1.55E-04	9.36E-03	regulation of cell cycle phase transition
GO:0051985	42	0.592	1.56E-04	9.41E-03	negative regulation of chromosome segregation
GO:0045429	40	0.606	1.57E-04	9.46E-03	positive regulation of nitric oxide biosynthetic process
GO:0061097	88	0.406	1.58E-04	9.50E-03	regulation of protein tyrosine kinase activity
GO:0002756	33	0.646	1.61E-04	9.65E-03	MyD88-independent toll-like receptor signaling pathway

GO:0097242	34	0.659	1.61E-04	9.65E-03	amyloid-beta clearance
GO:1901879	80	0.431	1.62E-04	9.70E-03	regulation of protein depolymerization
GO:0006959	190	0.277	1.64E-04	9.83E-03	humoral immune response
GO:0007259	135	0.326	1.71E-04	1.02E-02	receptor signaling pathway via JAK-STAT
GO:1905818	59	0.499	1.72E-04	1.03E-02	regulation of chromosome separation
GO:0016055	499	0.170	1.73E-04	1.03E-02	Wnt signaling pathway
GO:0032728	25	0.788	1.73E-04	1.03E-02	positive regulation of interferon-beta production
GO:0070507	180	0.283	1.73E-04	1.03E-02	regulation of microtubule cytoskeleton organization
GO:0042307	39	0.596	1.77E-04	1.06E-02	positive regulation of protein import into nucleus
GO:0014855	64	0.479	1.78E-04	1.06E-02	striated muscle cell proliferation
GO:0032465	82	0.418	1.83E-04	1.08E-02	regulation of cytokinesis
GO:1901989	91	0.402	1.86E-04	1.10E-02	positive regulation of cell cycle phase transition
GO:0007292	131	0.328	1.88E-04	1.11E-02	female gamete generation
GO:0046850	50	0.512	1.88E-04	1.11E-02	regulation of bone remodeling
GO:0032495	20	0.914	1.90E-04	1.12E-02	response to muramyl dipeptide
GO:0043270	265	0.231	1.91E-04	1.13E-02	positive regulation of ion transport
GO:0043030	55	0.502	1.91E-04	1.13E-02	regulation of macrophage activation
GO:0002371	11	1.083	1.93E-04	1.13E-02	dendritic cell cytokine production
GO:0033003	39	0.608	1.94E-04	1.14E-02	regulation of mast cell activation
GO:0048568	429	0.182	1.96E-04	1.15E-02	embryonic organ development
GO:0071356	263	0.232	1.97E-04	1.16E-02	cellular response to tumor necrosis factor
GO:0003206	125	0.332	1.98E-04	1.16E-02	cardiac chamber morphogenesis
GO:0010742	33	0.647	1.99E-04	1.16E-02	macrophage derived foam cell differentiation
GO:0090077	33	0.647	1.99E-04	1.16E-02	foam cell differentiation
GO:0003179	51	0.530	1.99E-04	1.16E-02	heart valve morphogenesis
GO:0060135	65	0.461	2.00E-04	1.17E-02	maternal process involved in female pregnancy
GO:0060251	33	0.624	2.03E-04	1.18E-02	regulation of glial cell proliferation
GO:1904375	115	0.351	2.06E-04	1.20E-02	regulation of protein localization to cell periphery
GO:2000404	41	0.595	2.06E-04	1.20E-02	regulation of T cell migration
GO:0048813	142	0.314	2.06E-04	1.20E-02	dendrite morphogenesis
GO:0061437	26	0.699	2.07E-04	1.20E-02	renal system vasculature development
GO:0061440	26	0.699	2.07E-04	1.20E-02	kidney vasculature development

GO:0046641	19	0.819	2.07E-04	1.20E-02	positive regulation of alpha-beta T cell proliferation
GO:0007189	127	0.330	2.08E-04	1.21E-02	adenylate cyclase-activating G protein-coupled receptor signaling pathway
GO:0002698	103	0.368	2.08E-04	1.21E-02	negative regulation of immune effector process
GO:0085029	37	0.622	2.09E-04	1.21E-02	extracellular matrix assembly
GO:1902041	54	0.516	2.11E-04	1.22E-02	regulation of extrinsic apoptotic signaling pathway via death domain receptors
GO:2001057	76	0.430	2.11E-04	1.22E-02	reactive nitrogen species metabolic process
GO:0002691	28	0.709	2.12E-04	1.22E-02	regulation of cellular extravasation
GO:0010762	30	0.670	2.13E-04	1.23E-02	regulation of fibroblast migration
GO:0002576	125	0.334	2.13E-04	1.23E-02	platelet degranulation
GO:0090594	11	0.985	2.14E-04	1.23E-02	inflammatory response to wounding
GO:1903727	49	0.534	2.15E-04	1.24E-02	positive regulation of phospholipid metabolic process
GO:0003229	55	0.490	2.16E-04	1.24E-02	ventricular cardiac muscle tissue development
GO:0033619	60	0.506	2.18E-04	1.25E-02	membrane protein proteolysis
GO:0044784	56	0.504	2.27E-04	1.30E-02	metaphase/anaphase transition of cell cycle
GO:0051767	19	0.919	2.29E-04	1.31E-02	nitric-oxide synthase biosynthetic process
GO:0051769	19	0.919	2.29E-04	1.31E-02	regulation of nitric-oxide synthase biosynthetic process
GO:0070757	11	1.001	2.29E-04	1.31E-02	interleukin-35-mediated signaling pathway
GO:0006022	164	0.290	2.30E-04	1.31E-02	aminoglycan metabolic process
GO:0009913	257	0.231	2.31E-04	1.31E-02	epidermal cell differentiation
GO:0022612	123	0.334	2.32E-04	1.32E-02	gland morphogenesis
GO:0051225	99	0.378	2.33E-04	1.32E-02	spindle assembly
GO:0016050	320	0.208	2.35E-04	1.34E-02	vesicle organization
GO:0060349	114	0.345	2.39E-04	1.36E-02	bone morphogenesis
GO:0043116	14	0.849	2.43E-04	1.37E-02	negative regulation of vascular permeability
GO:0003015	279	0.221	2.49E-04	1.40E-02	heart process
GO:0043647	71	0.436	2.49E-04	1.40E-02	inositol phosphate metabolic process
GO:0030318	26	0.743	2.49E-04	1.40E-02	melanocyte differentiation
GO:1903426	84	0.403	2.53E-04	1.42E-02	regulation of reactive oxygen species biosynthetic process
GO:0048146	48	0.532	2.53E-04	1.42E-02	positive regulation of fibroblast proliferation

GO:0002755	35	0.667	2.53E-04	1.42E-02	MyD88-dependent toll-like receptor signaling pathway
GO:0050707	48	0.526	2.56E-04	1.44E-02	regulation of cytokine secretion
GO:0021955	35	0.618	2.56E-04	1.44E-02	central nervous system neuron axonogenesis
GO:1901186	31	0.661	2.58E-04	1.45E-02	positive regulation of ERBB signaling pathway
GO:0010591	30	0.666	2.60E-04	1.45E-02	regulation of lamellipodium assembly
GO:0038110	12	0.921	2.62E-04	1.46E-02	interleukin-2-mediated signaling pathway
GO:0031103	48	0.522	2.62E-04	1.46E-02	axon regeneration
GO:0006869	337	0.201	2.65E-04	1.47E-02	lipid transport
GO:0050000	76	0.425	2.67E-04	1.48E-02	chromosome localization
GO:0007569	100	0.370	2.68E-04	1.49E-02	cell aging
GO:1903428	50	0.523	2.68E-04	1.49E-02	positive regulation of reactive oxygen species biosynthetic process
GO:0007143	30	0.665	2.76E-04	1.53E-02	female meiotic nuclear division
GO:0044706	211	0.252	2.80E-04	1.55E-02	multi-multicellular organism process
GO:0001911	12	0.915	2.83E-04	1.57E-02	negative regulation of leukocyte mediated cytotoxicity
GO:0071103	280	0.219	2.85E-04	1.58E-02	DNA conformation change
GO:0003222	16	0.823	2.85E-04	1.58E-02	ventricular trabecula myocardium morphogenesis
GO:0032620	26	0.701	2.86E-04	1.58E-02	interleukin-17 production
GO:0001914	24	0.736	2.86E-04	1.58E-02	regulation of T cell mediated cytotoxicity
GO:0061756	35	0.630	2.95E-04	1.63E-02	leukocyte adhesion to vascular endothelial cell
GO:0055010	48	0.507	2.96E-04	1.63E-02	ventricular cardiac muscle tissue morphogenesis
GO:0035666	29	0.666	2.96E-04	1.63E-02	TRIF-dependent toll-like receptor signaling pathway
GO:0071354	36	0.595	3.02E-04	1.66E-02	cellular response to interleukin-6
GO:0070167	91	0.379	3.05E-04	1.68E-02	regulation of biomineral tissue development
GO:0110149	91	0.379	3.05E-04	1.68E-02	regulation of biomineralization
GO:0045616	39	0.568	3.06E-04	1.68E-02	regulation of keratinocyte differentiation
GO:1901880	63	0.468	3.08E-04	1.68E-02	negative regulation of protein depolymerization
GO:0036473	80	0.412	3.09E-04	1.69E-02	cell death in response to oxidative stress
GO:0010592	20	0.808	3.11E-04	1.70E-02	positive regulation of lamellipodium assembly
GO:0031214	156	0.290	3.13E-04	1.71E-02	biomineral tissue development
GO:0110148	156	0.290	3.13E-04	1.71E-02	biomineralization

GO:0031663	54	0.513	3.13E-04	1.71E-02	lipopolysaccharide-mediated signaling pathway
GO:0061384	34	0.598	3.15E-04	1.71E-02	heart trabecula morphogenesis
GO:1904646	35	0.652	3.15E-04	1.71E-02	cellular response to amyloid-beta
GO:0051303	75	0.423	3.15E-04	1.71E-02	establishment of chromosome localization
GO:0016239	65	0.452	3.22E-04	1.75E-02	positive regulation of macroautophagy
GO:0032886	224	0.243	3.23E-04	1.75E-02	regulation of microtubule-based process
GO:0098543	13	1.089	3.24E-04	1.75E-02	detection of other organism
GO:0002718	63	0.468	3.24E-04	1.75E-02	regulation of cytokine production involved in immune response
GO:0010596	49	0.510	3.31E-04	1.79E-02	negative regulation of endothelial cell migration
GO:0007077	12	1.079	3.33E-04	1.80E-02	mitotic nuclear envelope disassembly
GO:0045124	42	0.537	3.36E-04	1.81E-02	regulation of bone resorption
GO:0061037	26	0.685	3.44E-04	1.85E-02	negative regulation of cartilage development
GO:0019048	31	0.626	3.45E-04	1.86E-02	modulation by virus of host process
GO:0106027	84	0.394	3.47E-04	1.87E-02	neuron projection organization
GO:0032660	24	0.721	3.50E-04	1.88E-02	regulation of interleukin-17 production
GO:0048066	45	0.538	3.51E-04	1.89E-02	developmental pigmentation
GO:0008406	211	0.247	3.53E-04	1.89E-02	gonad development
GO:1900407	73	0.424	3.53E-04	1.89E-02	regulation of cellular response to oxidative stress
GO:0031623	107	0.346	3.57E-04	1.91E-02	receptor internalization
GO:1900182	75	0.416	3.59E-04	1.92E-02	positive regulation of protein localization to nucleus
GO:0051306	57	0.479	3.61E-04	1.93E-02	mitotic sister chromatid separation
GO:0010761	37	0.591	3.63E-04	1.93E-02	fibroblast migration
GO:0034694	31	0.636	3.63E-04	1.93E-02	response to prostaglandin
GO:0071361	13	0.932	3.64E-04	1.94E-02	cellular response to ethanol
GO:0006323	187	0.263	3.66E-04	1.94E-02	DNA packaging
GO:0001558	396	0.181	3.67E-04	1.95E-02	regulation of cell growth
GO:0043242	70	0.435	3.69E-04	1.96E-02	negative regulation of protein-containing complex disassembly
GO:0048008	55	0.489	3.71E-04	1.97E-02	platelet-derived growth factor receptor signaling pathway
GO:0010508	117	0.330	3.77E-04	1.99E-02	positive regulation of autophagy
GO:0008630	103	0.351	3.81E-04	2.02E-02	intrinsic apoptotic signaling pathway in response to DNA damage
GO:0010256	413	0.177	3.83E-04	2.02E-02	endomembrane system organization

GO:0030100	197	0.254	3.88E-04	2.05E-02	regulation of endocytosis
GO:1903201	62	0.457	3.93E-04	2.07E-02	regulation of oxidative stress-induced cell death
GO:0045010	44	0.561	4.01E-04	2.11E-02	actin nucleation
GO:0035313	15	0.865	4.04E-04	2.13E-02	wound healing, spreading of epidermal cells
GO:0003018	161	0.280	4.07E-04	2.14E-02	vascular process in circulatory system
GO:0061098	55	0.480	4.09E-04	2.15E-02	positive regulation of protein tyrosine kinase activity
GO:0070106	11	1.051	4.14E-04	2.17E-02	interleukin-27-mediated signaling pathway
GO:0001660	10	0.975	4.15E-04	2.17E-02	fever generation
GO:0072012	24	0.694	4.16E-04	2.18E-02	glomerulus vasculature development
GO:0003418	24	0.684	4.18E-04	2.18E-02	growth plate cartilage chondrocyte differentiation
GO:0051016	19	0.811	4.19E-04	2.19E-02	barbed-end actin filament capping
GO:0006937	157	0.283	4.22E-04	2.20E-02	regulation of muscle contraction
GO:0070306	31	0.635	4.24E-04	2.21E-02	lens fiber cell differentiation
GO:0010952	172	0.271	4.25E-04	2.21E-02	positive regulation of peptidase activity
GO:0006026	65	0.441	4.25E-04	2.21E-02	aminoglycan catabolic process
GO:0051385	31	0.645	4.29E-04	2.23E-02	response to mineralocorticoid
GO:0043010	321	0.198	4.30E-04	2.23E-02	camera-type eye development
GO:0010611	56	0.478	4.34E-04	2.25E-02	regulation of cardiac muscle hypertrophy
GO:1903900	128	0.314	4.36E-04	2.26E-02	regulation of viral life cycle
GO:0032958	42	0.539	4.39E-04	2.28E-02	inositol phosphate biosynthetic process
GO:0001773	26	0.739	4.41E-04	2.29E-02	myeloid dendritic cell activation
GO:1903978	21	0.739	4.45E-04	2.30E-02	regulation of microglial cell activation
GO:0038061	161	0.279	4.52E-04	2.33E-02	NIK/NF-kappaB signaling
GO:0090174	100	0.356	4.63E-04	2.39E-02	organelle membrane fusion
GO:0016601	34	0.590	4.69E-04	2.42E-02	Rac protein signal transduction
GO:0060760	54	0.489	4.70E-04	2.42E-02	positive regulation of response to cytokine stimulus
GO:0014743	59	0.461	4.72E-04	2.43E-02	regulation of muscle hypertrophy
GO:0051146	273	0.213	4.78E-04	2.46E-02	striated muscle cell differentiation
GO:0098581	17	0.888	4.91E-04	2.52E-02	detection of external biotic stimulus
GO:2000241	151	0.284	4.93E-04	2.53E-02	regulation of reproductive process
GO:1904645	45	0.539	4.93E-04	2.53E-02	response to amyloid-beta
GO:1902117	72	0.418	4.95E-04	2.54E-02	positive regulation of organelle assembly

GO:0072577	54	0.470	4.97E-04	2.54E-02	endothelial cell apoptotic process
GO:0001764	157	0.278	5.04E-04	2.58E-02	neuron migration
GO:0062208	29	0.710	5.06E-04	2.58E-02	positive regulation of pattern recognition receptor signaling pathway
GO:0003177	21	0.712	5.07E-04	2.59E-02	pulmonary valve development
GO:1901890	97	0.353	5.08E-04	2.59E-02	positive regulation of cell junction assembly
GO:0035335	97	0.354	5.10E-04	2.60E-02	peptidyl-tyrosine dephosphorylation
GO:0030042	52	0.501	5.13E-04	2.61E-02	actin filament depolymerization
GO:1903305	160	0.277	5.15E-04	2.62E-02	regulation of regulated secretory pathway
GO:0051497	21	0.798	5.20E-04	2.64E-02	negative regulation of stress fiber assembly
GO:0038095	112	0.331	5.26E-04	2.67E-02	Fc-epsilon receptor signaling pathway
GO:0033622	22	0.735	5.27E-04	2.67E-02	integrin activation
GO:0051169	332	0.192	5.29E-04	2.68E-02	nuclear transport
GO:0030522	267	0.214	5.29E-04	2.68E-02	intracellular receptor signaling pathway
GO:0034764	196	0.250	5.30E-04	2.68E-02	positive regulation of transmembrane transport
GO:0032418	72	0.413	5.30E-04	2.68E-02	lysosome localization
GO:0051310	58	0.463	5.29E-04	2.68E-02	metaphase plate congression
GO:0051984	28	0.702	5.30E-04	2.68E-02	positive regulation of chromosome segregation
GO:0043383	12	0.989	5.29E-04	2.68E-02	negative T cell selection
GO:0043244	106	0.341	5.34E-04	2.69E-02	regulation of protein-containing complex disassembly
GO:0002730	10	1.073	5.38E-04	2.71E-02	regulation of dendritic cell cytokine production
GO:1903203	26	0.732	5.43E-04	2.73E-02	regulation of oxidative stress-induced neuron death
GO:0030224	34	0.639	5.44E-04	2.73E-02	monocyte differentiation
GO:1903131	34	0.639	5.44E-04	2.73E-02	mononuclear cell differentiation
GO:0007219	184	0.256	5.51E-04	2.76E-02	Notch signaling pathway
GO:0016311	459	0.163	5.54E-04	2.78E-02	dephosphorylation
GO:0032722	36	0.612	5.58E-04	2.79E-02	positive regulation of chemokine production
GO:0031100	72	0.416	5.59E-04	2.79E-02	animal organ regeneration
GO:2000249	38	0.569	5.59E-04	2.79E-02	regulation of actin cytoskeleton reorganization
GO:0043374	14	0.826	5.59E-04	2.79E-02	CD8-positive, alpha-beta T cell differentiation
GO:0007223	37	0.561	5.68E-04	2.83E-02	Wnt signaling pathway, calcium modulating pathway
GO:1904589	61	0.446	5.74E-04	2.86E-02	regulation of protein import

GO:1901889	30	0.621	5.79E-04	2.88E-02	negative regulation of cell junction assembly
GO:0070741	40	0.543	5.82E-04	2.90E-02	response to interleukin-6
GO:0043507	72	0.406	5.84E-04	2.90E-02	positive regulation of JUN kinase activity
GO:0032330	47	0.502	5.97E-04	2.97E-02	regulation of chondrocyte differentiation
GO:2001185	14	0.837	6.01E-04	2.98E-02	regulation of CD8-positive, alpha-beta T cell activation
GO:0002063	46	0.498	6.04E-04	3.00E-02	chondrocyte development
GO:0000186	55	0.572	4.20E-05	9.80E-03	activation of MAPKK activity
GO:0032733	25	0.688	6.12E-04	3.03E-02	positive regulation of interleukin-10 production
GO:0120032	168	0.266	6.25E-04	3.09E-02	regulation of plasma membrane bounded cell projection assembly
GO:0033048	39	0.555	6.27E-04	3.10E-02	negative regulation of mitotic sister chromatid segregation
GO:0070265	49	0.502	6.33E-04	3.12E-02	necrotic cell death
GO:0002544	19	0.763	6.36E-04	3.14E-02	chronic inflammatory response
GO:0031116	27	0.656	6.40E-04	3.16E-02	positive regulation of microtubule polymerization
GO:0032409	265	0.212	6.42E-04	3.16E-02	regulation of transporter activity
GO:0048535	16	0.870	6.48E-04	3.19E-02	lymph node development
GO:0045742	29	0.640	6.55E-04	3.22E-02	positive regulation of epidermal growth factor receptor signaling pathway
GO:0090025	22	0.706	6.55E-04	3.22E-02	regulation of monocyte chemotaxis
GO:0031345	177	0.259	6.58E-04	3.23E-02	negative regulation of cell projection organization
GO:0046546	137	0.293	6.60E-04	3.23E-02	development of primary male sexual characteristics
GO:0045639	90	0.366	6.59E-04	3.23E-02	positive regulation of myeloid cell differentiation
GO:0070570	30	0.627	6.60E-04	3.23E-02	regulation of neuron projection regeneration
GO:0035455	18	0.756	6.60E-04	3.23E-02	response to interferon-alpha
GO:0030834	49	0.506	6.63E-04	3.24E-02	regulation of actin filament depolymerization
GO:0002886	53	0.470	6.71E-04	3.28E-02	regulation of myeloid leukocyte mediated immunity
GO:0090630	82	0.384	6.73E-04	3.29E-02	activation of GTPase activity
GO:0002467	15	0.915	6.81E-04	3.32E-02	germinal center formation
GO:0007612	146	0.284	6.88E-04	3.35E-02	learning
GO:0045840	53	0.470	6.93E-04	3.36E-02	positive regulation of mitotic nuclear division
GO:0071677	23	0.706	6.92E-04	3.36E-02	positive regulation of mononuclear cell migration
GO:0031498	21	0.765	7.00E-04	3.40E-02	chromatin disassembly

GO:0006913	329	0.189	7.06E-04	3.42E-02	nucleocytoplasmic transport
GO:0010715	16	0.861	7.08E-04	3.43E-02	regulation of extracellular matrix disassembly
GO:0030879	143	0.284	7.11E-04	3.44E-02	mammary gland development
GO:1902099	53	0.474	7.19E-04	3.48E-02	regulation of metaphase/anaphase transition of cell cycle
GO:0010876	370	0.178	7.24E-04	3.50E-02	lipid localization
GO:0050765	21	0.776	7.42E-04	3.58E-02	negative regulation of phagocytosis
GO:0007623	208	0.235	7.44E-04	3.59E-02	circadian rhythm
GO:0043550	63	0.429	7.52E-04	3.62E-02	regulation of lipid kinase activity
GO:0090218	37	0.560	7.52E-04	3.62E-02	positive regulation of lipid kinase activity
GO:1903053	38	0.561	7.55E-04	3.63E-02	regulation of extracellular matrix organization
GO:0033044	326	0.188	7.60E-04	3.65E-02	regulation of chromosome organization
GO:0060491	170	0.260	7.60E-04	3.65E-02	regulation of cell projection assembly
GO:0090049	38	0.540	7.64E-04	3.67E-02	regulation of cell migration involved in sprouting angiogenesis
GO:0008286	139	0.287	7.74E-04	3.71E-02	insulin receptor signaling pathway
GO:0045059	13	0.961	7.76E-04	3.72E-02	positive thymic T cell selection
GO:0044003	37	0.542	7.78E-04	3.72E-02	modulation by symbiont of host process
GO:0048278	65	0.425	7.80E-04	3.73E-02	vesicle docking
GO:0030512	72	0.398	7.84E-04	3.75E-02	negative regulation of transforming growth factor beta receptor signaling pathway
GO:1903845	74	0.392	7.93E-04	3.78E-02	negative regulation of cellular response to transforming growth factor beta stimulus
GO:2000377	175	0.256	7.94E-04	3.78E-02	regulation of reactive oxygen species metabolic process
GO:0048678	73	0.394	7.94E-04	3.78E-02	response to axon injury
GO:0060142	28	0.641	7.96E-04	3.79E-02	regulation of syncytium formation by plasma membrane fusion
GO:0070669	14	0.862	7.97E-04	3.79E-02	response to interleukin-2
GO:0007492	77	0.381	8.17E-04	3.88E-02	endoderm development
GO:0034162	25	0.748	8.17E-04	3.88E-02	toll-like receptor 9 signaling pathway
GO:0050798	38	0.552	8.20E-04	3.89E-02	activated T cell proliferation
GO:0010977	148	0.278	8.23E-04	3.90E-02	negative regulation of neuron projection development
GO:0030033	16	0.863	8.35E-04	3.95E-02	microvillus assembly

GO:0043551	54	0.453	8.44E-04	3.99E-02	regulation of phosphatidylinositol 3-kinase activity
GO:0001782	28	0.665	8.55E-04	4.04E-02	B cell homeostasis
GO:0016241	167	0.260	8.56E-04	4.04E-02	regulation of macroautophagy
GO:0034113	57	0.451	8.64E-04	4.07E-02	heterotypic cell-cell adhesion
GO:0043297	61	0.426	8.71E-04	4.10E-02	apical junction assembly
GO:0006907	21	0.728	8.71E-04	4.10E-02	pinocytosis
GO:0034724	41	0.531	8.74E-04	4.11E-02	DNA replication-independent nucleosome organization
GO:0010878	16	0.784	8.97E-04	4.21E-02	cholesterol storage
GO:0045841	36	0.561	9.00E-04	4.22E-02	negative regulation of mitotic metaphase/anaphase transition
GO:2000816	36	0.561	9.00E-04	4.22E-02	negative regulation of mitotic sister chromatid separation
GO:0072583	41	0.513	9.10E-04	4.26E-02	clathrin-dependent endocytosis
GO:0008584	136	0.286	9.12E-04	4.27E-02	male gonad development
GO:0060047	270	0.203	9.25E-04	4.33E-02	heart contraction
GO:0045741	10	1.054	9.31E-04	4.35E-02	positive regulation of epidermal growth factor-activated receptor activity
GO:0062033	17	0.779	9.32E-04	4.35E-02	positive regulation of mitotic sister chromatid segregation
GO:0098974	10	0.958	9.35E-04	4.37E-02	postsynaptic actin cytoskeleton organization
GO:0035723	13	0.823	9.44E-04	4.40E-02	interleukin-15-mediated signaling pathway
GO:0071350	13	0.823	9.44E-04	4.40E-02	cellular response to interleukin-15
GO:0043524	147	0.273	9.48E-04	4.41E-02	negative regulation of neuron apoptotic process
GO:0009991	482	0.152	9.59E-04	4.46E-02	response to extracellular stimulus
GO:1902100	37	0.549	9.63E-04	4.47E-02	negative regulation of metaphase/anaphase transition of cell cycle
GO:1905819	37	0.549	9.63E-04	4.47E-02	negative regulation of chromosome separation
GO:0043931	19	0.707	9.72E-04	4.51E-02	ossification involved in bone maturation
GO:0030307	158	0.265	9.73E-04	4.51E-02	positive regulation of cell growth
GO:0030032	62	0.424	9.83E-04	4.55E-02	lamellipodium assembly
GO:0051058	56	0.448	9.84E-04	4.55E-02	negative regulation of small GTPase mediated signal transduction
GO:0006904	44	0.511	9.84E-04	4.55E-02	vesicle docking involved in exocytosis
GO:0034111	15	0.805	9.84E-04	4.55E-02	negative regulation of homotypic cell-cell adhesion

GO:0034123	21	0.833	9.84E-04	4.55E-02	positive regulation of toll-like receptor signaling pathway
GO:0097061	76	0.381	9.92E-04	4.58E-02	dendritic spine organization
GO:0043523	208	0.230	1.01E-03	4.64E-02	regulation of neuron apoptotic process
GO:0035051	146	0.274	1.01E-03	4.64E-02	cardiocyte differentiation
GO:0010950	153	0.268	1.01E-03	4.67E-02	positive regulation of endopeptidase activity
GO:0043044	74	0.385	1.03E-03	4.72E-02	ATP-dependent chromatin remodeling
GO:0008217	174	0.250	1.03E-03	4.72E-02	regulation of blood pressure
GO:1902751	30	0.646	1.04E-03	4.75E-02	positive regulation of cell cycle G2/M phase transition
GO:0008306	79	0.372	1.04E-03	4.77E-02	associative learning
GO:0017157	215	0.226	1.04E-03	4.78E-02	regulation of exocytosis
GO:1903725	84	0.359	1.04E-03	4.78E-02	regulation of phospholipid metabolic process
GO:0061614	45	0.488	1.05E-03	4.81E-02	pri-miRNA transcription by RNA polymerase II
GO:0070232	31	0.620	1.05E-03	4.81E-02	regulation of T cell apoptotic process
GO:0007260	75	0.380	1.06E-03	4.83E-02	tyrosine phosphorylation of STAT protein
GO:0034142	34	0.592	1.06E-03	4.85E-02	toll-like receptor 4 signaling pathway
GO:0002709	59	0.432	1.07E-03	4.86E-02	regulation of T cell mediated immunity
GO:0060998	70	0.391	1.07E-03	4.87E-02	regulation of dendritic spine development
GO:0001569	31	0.573	1.07E-03	4.87E-02	branching involved in blood vessel morphogenesis
GO:0046661	158	0.261	1.08E-03	4.90E-02	male sex differentiation
GO:0001975	34	0.559	1.09E-03	4.96E-02	response to amphetamine
GO:0010743	27	0.618	1.10E-03	4.98E-02	regulation of macrophage derived foam cell differentiation

Molecular functions in Genetic group 1 in the most efficient group.

Go term	Number of genes	LOR*	pvalue	padj	Molecular functions
GO:0036312	10	1.108	1.45E-06	2.38E-03	phosphatidylinositol 3-kinase regulatory subunit binding
GO:0023026	10	1.089	6.87E-06	7.50E-03	MHC class II protein complex binding
GO:0016303	10	1.038	1.79E-04	1.61E-02	1-phosphatidylinositol-3-kinase activity
GO:0048407	11	1.301	4.05E-10	1.74E-07	platelet-derived growth factor binding
GO:0035004	11	1.035	5.37E-06	7.95E-03	phosphatidylinositol 3-kinase activity

GO:0097493	11	1.035	8.94E-06	9.28E-03	structural molecule activity conferring elasticity
GO:0004115	11	0.967	2.55E-04	2.13E-02	3',5'-cyclic-AMP phosphodiesterase activity
GO:0005522	11	0.981	7.18E-04	4.99E-02	profilin binding
GO:0031005	12	0.943	4.99E-04	3.81E-02	filamin binding
GO:0042834	13	1.026	3.53E-04	2.82E-02	peptidoglycan binding
GO:0017160	15	0.969	2.45E-04	2.07E-02	Ral GTPase binding
GO:0023023	16	1.011	2.99E-07	5.99E-04	MHC protein complex binding
GO:0035173	17	0.916	5.81E-06	6.53E-03	histone kinase activity
GO:0008139	20	0.802	2.09E-04	1.82E-02	nuclear localization sequence binding
GO:0050431	22	0.900	1.01E-04	1.03E-02	transforming growth factor beta binding
GO:0043325	25	0.697	3.80E-04	3.01E-02	phosphatidylinositol-3,4-bisphosphate binding
GO:0042974	26	0.874	4.02E-07	7.54E-04	retinoic acid receptor binding
GO:0042287	27	0.757	4.49E-06	5.69E-03	MHC protein binding
GO:0043236	27	0.671	4.62E-04	3.59E-02	laminin binding
GO:0071889	28	0.711	1.09E-04	1.08E-02	14-3-3 protein binding
GO:0003823	29	0.710	6.31E-04	4.57E-02	antigen binding
GO:0043548	31	0.828	1.26E-07	2.93E-04	phosphatidylinositol 3-kinase binding
GO:0043394	34	0.644	1.51E-04	1.37E-02	proteoglycan binding
GO:0042169	36	0.635	7.06E-06	7.61E-03	SH2 domain binding
GO:0005547	37	0.790	1.44E-07	3.18E-04	phosphatidylinositol-3,4,5-trisphosphate binding
GO:0030020	40	0.641	2.87E-06	4.25E-03	extracellular matrix structural constituent conferring tensile strength
GO:0001102	41	0.573	2.75E-04	2.26E-02	RNA polymerase II activating transcription factor binding
GO:0004715	46	0.896	1.75E-12	1.26E-09	non-membrane spanning protein tyrosine kinase activity
GO:0042379	48	0.496	6.55E-04	4.70E-02	chemokine receptor binding
GO:0045309	49	0.555	1.31E-04	1.25E-02	protein phosphorylated amino acid binding
GO:0050840	53	0.546	5.49E-06	6.53E-03	extracellular matrix binding
GO:0004714	62	0.496	1.14E-04	1.12E-02	transmembrane receptor protein tyrosine kinase activity
GO:0005518	64	0.681	6.84E-09	2.11E-06	collagen binding
GO:0048365	66	0.620	8.51E-08	2.10E-04	Rac GTPase binding
GO:0001618	68	0.490	5.25E-06	6.47E-03	virus receptor activity
GO:0030971	68	0.479	1.24E-04	1.20E-02	receptor tyrosine kinase binding
GO:0140272	69	0.482	6.07E-06	6.70E-03	exogenous protein binding
GO:0003725	72	0.505	3.28E-06	4.42E-03	double-stranded RNA binding
GO:0033613	74	0.511	1.39E-06	2.38E-03	activating transcription factor binding

GO:0038024	75	0.400	5.97E-04	4.38E-02	cargo receptor activity
GO:0005089	77	0.434	1.50E-04	1.37E-02	Rho guanyl-nucleotide exchange factor activity
GO:0019199	80	0.474	3.06E-06	4.25E-03	transmembrane receptor protein kinase activity
GO:0046332	80	0.473	3.02E-06	4.25E-03	SMAD binding
GO:0003777	80	0.459	5.72E-06	6.53E-03	microtubule motor activity
GO:1990782	90	0.524	1.34E-07	3.05E-04	protein tyrosine kinase binding
GO:0035258	91	0.404	1.46E-04	1.35E-02	steroid hormone receptor binding
GO:0004896	94	0.424	4.64E-06	5.79E-03	cytokine receptor activity
GO:0004725	96	0.359	4.66E-04	3.59E-02	protein tyrosine phosphatase activity
GO:1902936	101	0.389	1.04E-04	1.06E-02	phosphatidylinositol biphosphate binding
GO:0140375	109	0.447	3.63E-07	6.98E-04	immune receptor activity
GO:0016922	110	0.402	2.98E-06	4.25E-03	nuclear receptor binding
GO:0019955	122	0.534	9.62E-10	3.73E-07	cytokine binding
GO:0044325	125	0.308	5.97E-04	4.38E-02	ion channel binding
GO:0005178	126	0.700	2.22E-01	4.79E-13	integrin binding
GO:0017124	127	0.552	1.26E-10	6.01E-08	SH3 domain binding
GO:0019838	129	0.384	1.70E-06	2.72E-03	growth factor binding
GO:0003774	132	0.448	4.25E-08	1.08E-04	motor activity
GO:0005088	134	0.419	1.70E-07	3.66E-04	Ras guanyl-nucleotide exchange factor activity
GO:0004713	135	0.462	9.36E-09	2.78E-06	protein tyrosine kinase activity
GO:0019903	135	0.350	5.57E-06	6.53E-03	protein phosphatase binding
GO:0070851	136	0.434	4.02E-08	1.05E-04	growth factor receptor binding
GO:1901981	152	0.432	1.55E-08	4.45E-06	phosphatidylinositol phosphate binding
GO:0035257	152	0.352	1.83E-06	2.86E-03	nuclear hormone receptor binding
GO:0005201	157	0.551	9.50E-13	9.10E-10	extracellular matrix structural constituent
GO:0017048	171	0.488	2.39E-11	1.29E-08	Rho GTPase binding
GO:0004721	176	0.280	2.33E-04	2.01E-02	phosphoprotein phosphatase activity
GO:0019902	180	0.307	4.43E-06	5.69E-03	phosphatase binding
GO:0051427	182	0.355	2.23E-07	4.69E-04	hormone receptor binding
GO:0051015	190	0.437	3.90E-10	1.74E-07	actin filament binding
GO:0005516	195	0.408	1.35E-09	4.30E-07	calmodulin binding
GO:0005539	199	0.336	2.59E-07	5.32E-04	glycosaminoglycan binding
GO:0005085	210	0.304	1.46E-06	2.38E-03	guanyl-nucleotide exchange factor activity
GO:0035091	234	0.450	1.38E-12	1.11E-09	phosphatidylinositol binding
GO:0008017	236	0.324	9.05E-08	2.17E-04	microtubule binding
GO:0030246	237	0.250	1.36E-04	1.27E-02	carbohydrate binding

GO:0005096	242	0.511	1.00E-15	1.44E-12	GTPase activator activity
GO:0005126	249	0.331	2.25E-08	6.26E-06	cytokine receptor binding
GO:0001664	258	0.263	2.90E-06	4.25E-03	G protein-coupled receptor binding
GO:0061629	265	0.230	2.08E-04	1.82E-02	RNA polymerase II-specific DNA-binding transcription factor binding
GO:0030695	272	0.485	5.53E-02	9.53E-13	GTPase regulator activity
GO:0060589	311	0.372	1.34E-12	8.25E-09	nucleoside-triphosphatase regulator activity
GO:0045296	313	0.496	8.69E-04	4.05E-02	cadherin binding
GO:0015631	321	0.210	2.04E-04	1.82E-02	tubulin binding
GO:0140297	336	0.223	5.59E-06	6.53E-03	DNA-binding transcription factor binding
GO:0042578	355	0.188	4.48E-04	3.51E-02	phosphoric ester hydrolase activity
GO:0016887	402	0.175	5.36E-04	4.05E-02	ATPase activity
GO:0017016	403	0.366	6.00E-14	6.46E-11	Ras GTPase binding
GO:0005543	408	0.405	1.54E-12	4.44E-13	phospholipid binding
GO:0003779	414	0.433	9.39E-04	4.05E-02	actin binding
GO:0031267	417	0.367	2.17E-14	2.67E-11	small GTPase binding
GO:0001216	420	0.206	2.97E-06	4.25E-03	DNA-binding transcription activator activity
GO:0001228	420	0.206	2.97E-06	4.25E-03	DNA-binding transcription activator activity, RNA polymerase II-specific
GO:0004674	430	0.300	1.02E-10	5.15E-08	protein serine/threonine kinase activity
GO:0046982	451	0.247	2.40E-08	6.45E-06	protein heterodimerization activity
GO:0008047	476	0.317	1.42E-12	1.11E-09	enzyme activator activity
GO:0016831	34	-0.594	7.15E-04	4.99E-02	carboxy-lyase activity
GO:0034062	41	-0.538	7.03E-04	4.97E-02	5'-3' RNA polymerase activity
GO:0097747	41	-0.538	7.03E-04	4.97E-02	RNA polymerase activity
GO:0051536	61	-0.445	6.00E-04	4.38E-02	iron-sulfur cluster binding
GO:0051540	61	-0.445	6.00E-04	4.38E-02	metal cluster binding
GO:0000030	25	-0.809	3.45E-04	2.78E-02	mannosyltransferase activity
GO:0004519	116	-0.339	2.90E-04	2.36E-02	endonuclease activity
GO:0009982	13	-0.951	2.71E-04	2.25E-02	pseudouridine synthase activity
GO:0008175	33	-0.615	2.38E-04	2.03E-02	tRNA methyltransferase activity
GO:0008320	19	-0.809	1.33E-04	1.26E-02	protein transmembrane transporter activity
GO:0016783	11	-1.041	1.07E-04	1.07E-02	sulfurtransferase activity
GO:0004549	16	-1.059	7.56E-06	7.95E-03	tRNA-specific ribonuclease activity
GO:0008173	63	-0.503	5.73E-06	6.53E-03	RNA methyltransferase activity
GO:0016829	183	-0.300	5.83E-06	6.53E-03	lyase activity

GO:0140318	21	-0.819	4.29E-06	5.61E-03	protein transporter activity
GO:0009055	101	-0.412	3.99E-06	5.30E-03	electron transfer activity
GO:0016779	116	-0.393	3.28E-06	4.42E-03	nucleotidyltransferase activity
GO:0016651	95	-0.449	1.42E-06	2.38E-03	oxidoreductase activity, acting on NAD(P)H
GO:0008168	202	-0.312	1.09E-06	1.92E-03	methyltransferase activity
GO:0016741	212	-0.304	1.09E-06	1.92E-03	transferase activity, transferring one-carbon groups
GO:0004518	190	-0.323	1.01E-06	1.85E-03	nuclease activity
GO:0015651	10	-1.182	3.64E-07	6.98E-04	quaternary ammonium group transmembrane transporter activity
GO:0003735	155	-0.453	1.15E-09	3.80E-07	structural constituent of ribosome
GO:0003954	38	-0.959	1.08E-09	3.73E-07	NADH dehydrogenase activity
GO:0008137	38	-0.959	1.08E-09	3.73E-07	NADH dehydrogenase (ubiquinone) activity
GO:0050136	38	-0.959	1.08E-09	3.73E-07	NADH dehydrogenase (quinone) activity
GO:0016655	50	-0.805	7.20E-10	2.96E-07	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
GO:0140098	300	-0.374	1.78E-11	1.02E-08	catalytic activity, acting on RNA
GO:0140101	119	-0.599	5.86E-12	3.89E-09	catalytic activity, acting on a tRNA

Cellular components in Genetic group 1 in the most efficient group.

Go term	Number of genes	LOR*	pvalue	padj	Cellular components
GO:0005743	435	-0.793	1.90E-57	1.03E-53	mitochondrial inner membrane
GO:0098798	239	-0.958	5.51E-52	1.50E-48	mitochondrial protein complex
GO:0019866	492	-0.677	7.03E-46	1.27E-42	organelle inner membrane
GO:0005759	456	-0.675	1.01E-42	1.37E-39	mitochondrial matrix
GO:0000313	86	-1.131	1.52E-35	1.38E-32	organellar ribosome
GO:0005761	86	-1.131	1.52E-35	1.38E-32	mitochondrial ribosome
GO:0005925	400	0.629	1.48E-34	1.15E-31	focal adhesion
GO:0030055	407	0.619	5.30E-34	3.60E-31	cell-substrate junction
GO:0000315	56	-1.172	7.76E-28	4.21E-25	organellar large ribosomal subunit
GO:0005762	56	-1.172	7.76E-28	4.21E-25	mitochondrial large ribosomal subunit
GO:0098552	466	0.511	3.28E-26	1.62E-23	side of membrane
GO:0098800	116	-0.957	1.36E-25	6.17E-23	inner mitochondrial membrane protein complex
GO:0009897	283	0.565	3.58E-20	1.50E-17	external side of plasma membrane
GO:0031252	398	0.473	4.79E-20	1.86E-17	cell leading edge
GO:0098589	322	0.504	8.65E-19	3.13E-16	membrane region

GO:0098857	310	0.507	2.23E-18	7.57E-16	membrane microdomain
GO:0045121	309	0.507	2.84E-18	9.07E-16	membrane raft
GO:0015629	487	0.397	1.53E-17	4.62E-15	actin cytoskeleton
GO:0030667	277	0.512	6.32E-17	1.81E-14	secretory granule membrane
GO:0070469	81	-0.916	8.03E-17	2.18E-14	respirasome
GO:0098803	69	-0.957	1.60E-15	4.14E-13	respiratory chain complex
GO:0030027	190	0.561	3.24E-14	8.00E-12	lamellipodium
GO:0005746	74	-0.871	3.57E-14	8.42E-12	mitochondrial respirasome
GO:0062023	375	0.397	4.58E-14	1.04E-11	collagen-containing extracellular matrix
GO:0031012	488	0.344	1.06E-13	2.30E-11	extracellular matrix
GO:0044391	182	-0.533	3.56E-13	7.44E-11	ribosomal subunit
GO:0001726	168	0.570	7.80E-13	1.57E-10	ruffle
GO:0005840	229	-0.467	1.65E-12	3.21E-10	ribosome
GO:0030139	277	0.412	1.75E-11	3.28E-09	endocytic vesicle
GO:0015934	115	-0.607	3.02E-11	5.47E-09	large ribosomal subunit
GO:0043235	382	0.338	8.71E-11	1.53E-08	receptor complex
GO:0000775	190	0.479	1.41E-10	2.39E-08	chromosome, centromeric region
GO:0005769	331	0.357	1.85E-10	3.04E-08	early endosome
GO:0098858	197	0.461	2.29E-10	3.66E-08	actin-based cell projection
GO:0005911	417	0.315	2.53E-10	3.67E-08	cell-cell junction
GO:0005747	43	-1.007	2.57E-10	3.67E-08	mitochondrial respiratory chain complex I
GO:0030964	43	-1.007	2.57E-10	3.67E-08	NADH dehydrogenase complex
GO:0045271	43	-1.007	2.57E-10	3.67E-08	respiratory chain complex I
GO:0019897	162	0.497	3.69E-10	5.04E-08	extrinsic component of plasma membrane
GO:0045335	123	0.589	3.71E-10	5.04E-08	phagocytic vesicle
GO:0005938	304	0.363	5.59E-10	7.41E-08	cell cortex
GO:0030175	98	0.639	9.01E-10	1.17E-07	filopodium
GO:0070820	151	0.498	1.17E-09	1.47E-07	tertiary granule
GO:0005884	105	0.604	1.84E-09	2.27E-07	actin filament
GO:0032432	73	0.695	2.08E-09	2.52E-07	actin filament bundle
GO:0042641	77	0.675	2.78E-09	3.29E-07	actomyosin
GO:0005819	338	0.327	4.20E-09	4.85E-07	spindle
GO:0000314	28	-0.973	5.31E-09	5.89E-07	organellar small ribosomal subunit
GO:0005763	28	-0.973	5.31E-09	5.89E-07	mitochondrial small ribosomal subunit
GO:0009898	151	0.478	1.10E-08	1.19E-06	cytoplasmic side of plasma membrane
GO:0001725	67	0.689	1.48E-08	1.55E-06	stress fiber
GO:0097517	67	0.689	1.48E-08	1.55E-06	contractile actin filament bundle
GO:0010008	443	0.273	1.65E-08	1.69E-06	endosome membrane
GO:0001772	37	1.049	2.15E-08	2.14E-06	immunological synapse

GO:0031304	40	-0.838	2.21E-08	2.14E-06	intrinsic component of mitochondrial inner membrane
GO:0031305	40	-0.838	2.21E-08	2.14E-06	integral component of mitochondrial inner membrane
GO:0098687	322	0.316	2.53E-08	2.41E-06	chromosomal region
GO:0035579	86	0.617	2.60E-08	2.43E-06	specific granule membrane
GO:0042581	151	0.463	3.09E-08	2.85E-06	specific granule
GO:0043202	92	0.598	3.94E-08	3.57E-06	lysosomal lumen
GO:0031901	133	0.476	5.28E-08	4.70E-06	early endosome membrane
GO:0005874	399	0.276	5.97E-08	5.23E-06	microtubule
GO:0042629	22	1.077	7.13E-08	6.15E-06	mast cell granule
GO:0070821	66	0.651	7.49E-08	6.36E-06	tertiary granule membrane
GO:0045177	375	0.280	8.96E-08	7.48E-06	apical part of cell
GO:0005902	79	0.616	9.95E-08	8.19E-06	microvillus
GO:0005775	158	0.435	1.02E-07	8.29E-06	vacuolar lumen
GO:0002102	30	1.053	1.07E-07	8.58E-06	podosome
GO:0031234	88	0.571	1.37E-07	1.08E-05	extrinsic component of cytoplasmic side of plasma membrane
GO:0098562	177	0.403	1.53E-07	1.17E-05	cytoplasmic side of membrane
GO:0150034	285	0.314	1.53E-07	1.17E-05	distal axon
GO:0034774	303	0.305	1.87E-07	1.41E-05	secretory granule lumen
GO:0030427	174	0.398	1.97E-07	1.47E-05	site of polarized growth
GO:0016323	212	0.360	2.19E-07	1.61E-05	basolateral plasma membrane
GO:0030426	171	0.398	2.66E-07	1.93E-05	growth cone
GO:0042470	104	0.515	2.78E-07	1.96E-05	melanosome
GO:0048770	104	0.515	2.78E-07	1.96E-05	pigment granule
GO:0005581	93	0.528	2.92E-07	2.03E-05	collagen trimer
GO:0031983	309	0.297	2.95E-07	2.03E-05	vesicle lumen
GO:0000776	132	0.454	3.12E-07	2.12E-05	kinetochore
GO:0060205	307	0.296	3.44E-07	2.31E-05	cytoplasmic vesicle lumen
GO:0098978	358	0.268	5.40E-07	3.58E-05	glutamatergic synapse
GO:0032592	68	-0.596	7.15E-07	4.68E-05	integral component of mitochondrial membrane
GO:0098573	69	-0.584	1.00E-06	6.47E-05	intrinsic component of mitochondrial membrane
GO:0072686	106	0.493	1.13E-06	7.20E-05	mitotic spindle
GO:0005871	52	0.697	1.20E-06	7.61E-05	kinesin complex
GO:0005604	92	0.498	1.26E-06	7.66E-05	basement membrane
GO:0005766	138	0.422	1.24E-06	7.66E-05	primary lysosome
GO:0042582	138	0.422	1.24E-06	7.66E-05	azurophil granule
GO:0031253	313	0.278	1.30E-06	7.86E-05	cell projection membrane
GO:0030136	173	0.370	1.38E-06	8.24E-05	clathrin-coated vesicle
GO:0005875	148	0.402	1.42E-06	8.41E-05	microtubule associated complex
GO:0098852	329	0.268	1.69E-06	9.77E-05	lytic vacuole membrane
GO:1905368	92	-0.505	1.69E-06	9.77E-05	peptidase complex

GO:0005765	328	0.267	1.83E-06	1.04E-04	lysosomal membrane
GO:0033643	15	1.053	2.54E-06	1.44E-04	host cell part
GO:0000779	116	0.443	2.81E-06	1.57E-04	condensed chromosome, centromeric region
GO:1990204	101	-0.471	2.83E-06	1.57E-04	oxidoreductase complex
GO:0030496	170	0.366	2.87E-06	1.57E-04	midbody
GO:0005758	76	-0.552	2.88E-06	1.57E-04	mitochondrial intermembrane space
GO:0019898	288	0.278	3.13E-06	1.69E-04	extrinsic component of membrane
GO:0098685	85	0.504	3.39E-06	1.81E-04	Schaffer collateral - CA1 synapse
GO:0030684	73	-0.532	3.46E-06	1.83E-04	preribosome
GO:0000777	103	0.466	3.54E-06	1.85E-04	condensed chromosome kinetochore
GO:0030666	145	0.389	3.86E-06	2.00E-04	endocytic vesicle membrane
GO:0005774	381	0.239	4.12E-06	2.11E-04	vacuolar membrane
GO:0016461	10	1.157	5.65E-06	2.87E-04	unconventional myosin complex
GO:0016324	310	0.260	6.16E-06	3.10E-04	apical plasma membrane
GO:0098644	19	0.956	8.71E-06	4.34E-04	complex of collagen trimers
GO:0031256	166	0.349	9.36E-06	4.62E-04	leading edge membrane
GO:0044853	108	0.424	1.22E-05	5.96E-04	plasma membrane raft
GO:0001891	26	0.860	1.32E-05	6.40E-04	phagocytic cup
GO:0098636	34	0.733	1.39E-05	6.66E-04	protein complex involved in cell adhesion
GO:0030687	23	-0.846	1.78E-05	8.48E-04	preribosome, large subunit precursor
GO:0033646	13	1.048	1.83E-05	8.58E-04	host intracellular part
GO:0043656	13	1.048	1.83E-05	8.58E-04	host intracellular region
GO:0120114	74	-0.498	1.85E-05	8.61E-04	Sm-like protein family complex
GO:0030863	113	0.410	1.92E-05	8.82E-04	cortical cytoskeleton
GO:0005905	68	0.514	2.37E-05	1.08E-03	clathrin-coated pit
GO:0097386	26	0.828	2.39E-05	1.08E-03	glial cell projection
GO:0005876	57	0.604	2.71E-05	1.22E-03	spindle microtubule
GO:0034719	19	-0.886	2.87E-05	1.28E-03	SMN-Sm protein complex
GO:0034399	133	0.363	3.33E-05	1.47E-03	nuclear periphery
GO:0101003	53	0.556	3.69E-05	1.60E-03	ficolin-1-rich granule membrane
GO:0031970	84	-0.459	3.69E-05	1.60E-03	organelle envelope lumen
GO:0005732	22	-0.804	3.91E-05	1.69E-03	small nucleolar ribonucleoprotein complex
GO:0016363	105	0.404	4.10E-05	1.75E-03	nuclear matrix
GO:0000793	211	0.284	4.53E-05	1.92E-03	condensed chromosome
GO:0032587	90	0.441	4.81E-05	2.01E-03	ruffle membrane
GO:0070069	25	-0.777	4.79E-05	2.01E-03	cytochrome complex
GO:0008305	31	0.702	6.59E-05	2.73E-03	integrin complex
GO:0031314	14	-0.935	7.42E-05	3.05E-03	extrinsic component of mitochondrial inner membrane
GO:0032154	53	0.556	7.76E-05	3.17E-03	cleavage furrow

GO:0101002	120	0.364	8.41E-05	3.38E-03	ficolin-1-rich granule
GO:1904813	120	0.364	8.41E-05	3.38E-03	ficolin-1-rich granule lumen
GO:0005753	18	-0.844	8.74E-05	3.46E-03	mitochondrial proton-transporting ATP synthase complex
GO:0045259	18	-0.844	8.74E-05	3.46E-03	proton-transporting ATP synthase complex
GO:0044309	160	0.307	1.12E-04	4.40E-03	neuron spine
GO:0051233	33	0.757	1.17E-04	4.58E-03	spindle midzone
GO:0032797	11	-1.125	1.22E-04	4.71E-03	SMN complex
GO:1990023	12	1.015	1.24E-04	4.79E-03	mitotic spindle midzone
GO:0000790	342	0.208	1.39E-04	5.31E-03	nuclear chromatin
GO:0005838	22	-0.762	1.75E-04	6.64E-03	proteasome regulatory particle
GO:0030665	102	0.370	1.84E-04	6.91E-03	clathrin-coated vesicle membrane
GO:0043197	158	0.299	1.84E-04	6.91E-03	dendritic spine
GO:1990752	29	0.873	1.94E-04	7.23E-03	microtubule end
GO:0042734	162	0.293	2.09E-04	7.73E-03	presynaptic membrane
GO:0045178	50	0.537	2.26E-04	8.30E-03	basal part of cell
GO:0005744	13	-1.072	2.38E-04	8.67E-03	TIM23 mitochondrial import inner membrane translocase complex
GO:0017053	76	0.421	2.86E-04	1.04E-02	transcription repressor complex
GO:0030864	84	0.404	2.93E-04	1.05E-02	cortical actin cytoskeleton
GO:0030914	12	-0.973	3.07E-04	1.10E-02	STAGA complex
GO:0018995	66	0.448	3.45E-04	1.22E-02	host cellular component
GO:0043657	66	0.448	3.45E-04	1.22E-02	host cell
GO:0097525	56	-0.470	3.54E-04	1.24E-02	spliceosomal snRNP complex
GO:0005583	11	1.037	4.07E-04	1.41E-02	fibrillar collagen trimer
GO:0098643	11	1.037	4.07E-04	1.41E-02	banded collagen fibril
GO:0099056	73	0.408	4.61E-04	1.58E-02	integral component of presynaptic membrane
GO:1902911	104	0.348	4.63E-04	1.58E-02	protein kinase complex
GO:0030479	16	0.904	4.69E-04	1.58E-02	actin cortical patch
GO:0061645	16	0.904	4.69E-04	1.58E-02	endocytic patch
GO:0043292	233	0.230	5.01E-04	1.68E-02	contractile fiber
GO:0005770	239	0.227	5.27E-04	1.76E-02	late endosome
GO:0035578	80	0.393	5.92E-04	1.94E-02	azurophil granule lumen
GO:0071437	16	0.943	5.95E-04	1.94E-02	invadopodium
GO:0005665	13	-0.884	5.92E-04	1.94E-02	RNA polymerase II, core complex
GO:0016591	76	-0.394	5.96E-04	1.94E-02	RNA polymerase II, holoenzyme
GO:0005750	10	-0.947	6.20E-04	1.98E-02	mitochondrial respiratory chain complex III
GO:0015935	70	-0.405	6.14E-04	1.98E-02	small ribosomal subunit
GO:0045275	10	-0.947	6.20E-04	1.98E-02	respiratory chain complex III
GO:0031091	90	0.362	6.28E-04	1.99E-02	platelet alpha granule

GO:0005813	500	0.155	6.48E-04	2.05E-02	centrosome
GO:0098799	16	-0.798	6.57E-04	2.06E-02	outer mitochondrial membrane protein complex
GO:0097504	11	-1.055	6.72E-04	2.10E-02	Gemini of coiled bodies
GO:0005788	299	0.197	7.37E-04	2.28E-02	endoplasmic reticulum lumen
GO:0042101	17	0.949	7.38E-04	2.28E-02	T cell receptor complex
GO:1902554	84	0.370	8.27E-04	2.54E-02	serine/threonine protein kinase complex
GO:0042383	135	0.289	8.47E-04	2.58E-02	sarcolemma
GO:0030532	62	-0.421	9.06E-04	2.75E-02	small nuclear ribonucleoprotein complex
GO:0098802	181	0.248	9.48E-04	2.86E-02	plasma membrane signaling receptor complex
GO:0001931	12	0.978	9.88E-04	2.95E-02	uropod
GO:0031254	12	0.978	9.88E-04	2.95E-02	cell trailing edge
GO:0009925	34	0.581	1.00E-03	2.97E-02	basal plasma membrane
GO:0097449	14	0.929	1.02E-03	3.00E-02	astrocyte projection
GO:0031527	17	0.741	1.07E-03	3.13E-02	filopodium membrane
GO:0032153	66	0.402	1.20E-03	3.49E-02	cell division site
GO:0098984	349	0.175	1.20E-03	3.49E-02	neuron to neuron synapse
GO:0036019	19	0.757	1.24E-03	3.57E-02	endolysosome
GO:0097060	429	0.157	1.30E-03	3.74E-02	synaptic membrane
GO:0000307	42	0.519	1.33E-03	3.81E-02	cyclin-dependent protein kinase holoenzyme complex
GO:0098793	491	0.146	1.35E-03	3.85E-02	presynapse
GO:0035577	53	0.439	1.40E-03	3.95E-02	azurophil granule membrane
GO:0032009	12	0.848	1.48E-03	4.17E-02	early phagosome
GO:0030016	222	0.214	1.51E-03	4.23E-02	myofibril
GO:0055029	99	-0.320	1.55E-03	4.33E-02	nuclear DNA-directed RNA polymerase complex
GO:0044295	28	0.614	1.60E-03	4.43E-02	axonal growth cone
GO:0030670	67	0.394	1.65E-03	4.56E-02	phagocytic vesicle membrane
GO:0030904	20	0.719	1.66E-03	4.56E-02	retromer complex
GO:0045277	14	-0.814	1.76E-03	4.80E-02	respiratory chain complex IV
GO:0016327	19	0.665	1.83E-03	4.97E-02	apicolateral plasma membrane
The significant biological processes in Genetic group 2 in the most efficient group.					
Go term	Number of genes	LOR*	pvalue	padj	Biological process
GO:0045047	107	1.016	1.55E-18	7.43E-14	protein targeting to ER
GO:0006613	98	1.103	2.57E-18	7.43E-14	cotranslational protein targeting to membrane
GO:0006614	94	1.139	6.26E-18	1.21E-13	SRP-dependent cotranslational protein targeting to membrane
GO:0006119	121	0.803	6.69E-16	9.67E-12	oxidative phosphorylation
GO:0022900	164	0.646	1.65E-15	1.91E-11	electron transport chain
GO:0006612	188	0.603	7.84E-15	5.03E-11	protein targeting to membrane

GO:0071346	146	0.670	6.33E-15	5.03E-11	cellular response to interferon-gamma
GO:0072599	111	0.920	7.06E-15	5.03E-11	establishment of protein localization to endoplasmic reticulum
GO:0042773	81	0.957	5.76E-15	5.03E-11	ATP synthesis coupled electron transport
GO:0042775	80	0.959	9.35E-15	5.40E-11	mitochondrial ATP synthesis coupled electron transport
GO:0043299	493	0.359	1.15E-14	6.04E-11	leukocyte degranulation
GO:0000184	117	0.856	1.79E-14	8.62E-11	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
GO:0070972	135	0.777	3.14E-14	1.39E-10	protein localization to endoplasmic reticulum
GO:0022904	100	0.812	5.16E-14	2.13E-10	respiratory electron transport chain
GO:0035459	19	-1.276	8.96E-14	3.45E-10	vesicle cargo loading
GO:0034341	163	0.599	1.42E-13	5.11E-10	response to interferon-gamma
GO:0050900	400	0.380	1.63E-13	5.54E-10	leukocyte migration
GO:0006397	474	-0.341	3.03E-13	9.73E-10	mRNA processing
GO:0010257	58	0.961	8.84E-13	2.56E-09	NADH dehydrogenase complex assembly
GO:0032981	58	0.961	8.84E-13	2.56E-09	mitochondrial respiratory chain complex I assembly
GO:0034976	274	-0.439	1.58E-12	4.17E-09	response to endoplasmic reticulum stress
GO:0036230	464	0.337	1.59E-12	4.17E-09	granulocyte activation
GO:0042119	458	0.336	2.70E-12	6.77E-09	neutrophil activation
GO:0007030	122	-0.654	2.94E-12	6.80E-09	Golgi organization
GO:0006120	46	1.141	2.88E-12	6.80E-09	mitochondrial electron transport, NADH to ubiquinone
GO:0002446	460	0.329	6.43E-12	1.43E-08	neutrophil mediated immunity
GO:0043062	355	0.367	1.12E-11	2.40E-08	extracellular structure organization
GO:0002283	449	0.328	1.29E-11	2.56E-08	neutrophil activation involved in immune response
GO:0043312	447	0.329	1.26E-11	2.56E-08	neutrophil degranulation
GO:0030198	354	0.364	1.69E-11	3.26E-08	extracellular matrix organization
GO:0033108	87	0.750	2.20E-11	4.11E-08	mitochondrial respiratory chain complex assembly
GO:0016570	434	-0.327	2.70E-11	4.88E-08	histone modification
GO:0016569	448	-0.319	3.78E-11	6.63E-08	covalent chromatin modification
GO:0050684	128	-0.576	6.38E-11	1.08E-07	regulation of mRNA processing
GO:0006909	256	0.416	1.05E-10	1.74E-07	phagocytosis
GO:0019083	173	0.525	1.20E-10	1.93E-07	viral transcription
GO:0090110	14	-1.283	2.24E-10	3.50E-07	COPII-coated vesicle cargo loading

GO:1903311	308	-0.367	2.56E-10	3.90E-07	regulation of mRNA metabolic process
GO:0090150	317	0.358	5.33E-10	7.90E-07	establishment of protein localization to membrane
GO:0030433	75	-0.754	6.32E-10	9.13E-07	ubiquitin-dependent ERAD pathway
GO:0048193	352	-0.339	6.58E-10	9.28E-07	Golgi vesicle transport
GO:0002237	318	0.351	8.76E-10	1.21E-06	response to molecule of bacterial origin
GO:0002685	185	0.463	1.04E-09	1.40E-06	regulation of leukocyte migration
GO:0002694	476	0.283	1.59E-09	2.08E-06	regulation of leukocyte activation
GO:0050867	306	0.349	2.32E-09	2.98E-06	positive regulation of cell activation
GO:0019080	187	0.458	2.60E-09	3.27E-06	viral gene expression
GO:0035966	190	-0.438	3.17E-09	3.90E-06	response to topologically incorrect protein
GO:0070661	271	0.367	3.31E-09	3.99E-06	leukocyte proliferation
GO:0006413	186	0.449	5.54E-09	6.54E-06	translational initiation
GO:0060333	65	0.753	5.65E-09	6.54E-06	interferon-gamma-mediated signaling pathway
GO:0032963	98	0.594	7.76E-09	8.80E-06	collagen metabolic process
GO:0070126	89	0.621	9.65E-09	1.07E-05	mitochondrial translational termination
GO:0008380	407	-0.288	1.07E-08	1.17E-05	RNA splicing
GO:0043414	295	-0.336	1.15E-08	1.23E-05	macromolecule methylation
GO:0070125	88	0.626	1.25E-08	1.31E-05	mitochondrial translational elongation
GO:0010256	413	-0.285	1.35E-08	1.39E-05	endomembrane system organization
GO:0051650	182	-0.431	1.58E-08	1.57E-05	establishment of vesicle localization
GO:0032496	307	0.329	1.55E-08	1.57E-05	response to lipopolysaccharide
GO:0002696	297	0.334	1.65E-08	1.62E-05	positive regulation of leukocyte activation
GO:0010498	459	-0.269	1.71E-08	1.65E-05	proteasomal protein catabolic process
GO:0036503	97	-0.599	1.82E-08	1.73E-05	ERAD pathway
GO:0006888	203	-0.408	1.89E-08	1.76E-05	endoplasmic reticulum to Golgi vesicle-mediated transport
GO:0032943	250	0.363	2.03E-08	1.86E-05	mononuclear cell proliferation
GO:0043161	406	-0.284	2.10E-08	1.90E-05	proteasome-mediated ubiquitin-dependent protein catabolic process
GO:0006986	169	-0.435	2.81E-08	2.49E-05	response to unfolded protein
GO:0046651	248	0.360	2.84E-08	2.49E-05	lymphocyte proliferation
GO:0002687	124	0.499	5.55E-08	4.79E-05	positive regulation of leukocyte migration
GO:0035967	153	-0.445	6.72E-08	5.71E-05	cellular response to topologically incorrect protein

GO:0015985	20	1.201	8.03E-08	6.63E-05	energy coupled proton transport, down electrochemical gradient
GO:0015986	20	1.201	8.03E-08	6.63E-05	ATP synthesis coupled proton transport
GO:0002683	376	0.281	8.77E-08	7.14E-05	negative regulation of immune system process
GO:0060326	268	0.330	1.15E-07	9.21E-05	cell chemotaxis
GO:1901685	19	1.047	1.30E-07	1.01E-04	glutathione derivative metabolic process
GO:1901687	19	1.047	1.30E-07	1.01E-04	glutathione derivative biosynthetic process
GO:0016458	202	-0.377	1.36E-07	1.05E-04	gene silencing
GO:0051648	201	-0.379	1.39E-07	1.06E-04	vesicle localization
GO:0048194	79	-0.657	1.59E-07	1.18E-04	Golgi vesicle budding
GO:0016441	129	-0.470	1.58E-07	1.18E-04	posttranscriptional gene silencing
GO:0006900	100	-0.561	1.63E-07	1.19E-04	vesicle budding from membrane
GO:0045333	177	0.404	1.68E-07	1.22E-04	cellular respiration
GO:0032259	347	-0.281	2.25E-07	1.61E-04	methylation
GO:0050866	181	0.392	2.29E-07	1.62E-04	negative regulation of cell activation
GO:0042776	19	1.200	2.46E-07	1.71E-04	mitochondrial ATP synthesis coupled proton transport
GO:0031047	150	-0.426	2.55E-07	1.76E-04	gene silencing by RNA
GO:0070663	207	0.366	2.62E-07	1.78E-04	regulation of leukocyte proliferation
GO:0002250	352	0.279	2.77E-07	1.86E-04	adaptive immune response
GO:0060628	16	-1.139	3.08E-07	2.04E-04	regulation of ER to Golgi vesicle-mediated transport
GO:0032944	197	0.373	3.21E-07	2.11E-04	regulation of mononuclear cell proliferation
GO:0035194	128	-0.457	3.71E-07	2.41E-04	post-transcriptional gene silencing by RNA
GO:0048024	90	-0.530	3.86E-07	2.45E-04	regulation of mRNA splicing, via spliceosome
GO:0050920	202	0.363	3.82E-07	2.45E-04	regulation of chemotaxis
GO:0043484	126	-0.451	4.01E-07	2.52E-04	regulation of RNA splicing
GO:0006903	91	-0.570	4.17E-07	2.59E-04	vesicle targeting
GO:0050670	196	0.370	4.26E-07	2.62E-04	regulation of lymphocyte proliferation
GO:0033044	326	-0.284	4.50E-07	2.74E-04	regulation of chromosome organization
GO:0002695	160	0.407	4.70E-07	2.83E-04	negative regulation of leukocyte activation
GO:0042752	112	-0.481	4.80E-07	2.86E-04	regulation of circadian rhythm
GO:0071219	187	0.376	5.04E-07	2.97E-04	cellular response to molecule of bacterial origin
GO:0006403	219	-0.343	5.17E-07	3.02E-04	RNA localization
GO:0042742	192	0.367	5.79E-07	3.35E-04	defense response to bacterium

GO:0071222	181	0.379	6.09E-07	3.48E-04	cellular response to lipopolysaccharide
GO:0006415	102	0.504	6.33E-07	3.59E-04	translational termination
GO:0030518	125	-0.454	6.42E-07	3.60E-04	intracellular steroid hormone receptor signaling pathway
GO:0006607	16	-1.034	6.83E-07	3.80E-04	NLS-bearing protein import into nucleus
GO:0006405	129	-0.441	7.13E-07	3.92E-04	RNA export from nucleus
GO:0031124	96	-0.507	7.22E-07	3.94E-04	mRNA 3'-end processing
GO:0032946	127	0.446	7.95E-07	4.29E-04	positive regulation of mononuclear cell proliferation
GO:0050727	317	0.280	9.22E-07	4.93E-04	regulation of inflammatory response
GO:0051168	188	-0.360	1.08E-06	5.70E-04	nuclear export
GO:0071674	77	0.563	1.09E-06	5.70E-04	mononuclear cell migration
GO:0050671	126	0.442	1.11E-06	5.76E-04	positive regulation of lymphocyte proliferation
GO:0035456	25	0.985	1.22E-06	6.32E-04	response to interferon-beta
GO:0032103	469	0.228	1.31E-06	6.66E-04	positive regulation of response to external stimulus
GO:0050921	132	0.429	1.32E-06	6.66E-04	positive regulation of chemotaxis
GO:0000028	16	1.331	1.33E-06	6.66E-04	ribosomal small subunit assembly
GO:0070665	132	0.428	1.36E-06	6.78E-04	positive regulation of leukocyte proliferation
GO:0002576	125	0.446	1.38E-06	6.83E-04	platelet degranulation
GO:0002886	53	0.703	1.43E-06	6.98E-04	regulation of myeloid leukocyte mediated immunity
GO:0016579	258	-0.305	1.60E-06	7.78E-04	protein deubiquitination
GO:0046034	270	0.298	1.68E-06	8.11E-04	ATP metabolic process
GO:0045576	57	0.652	1.73E-06	8.28E-04	mast cell activation
GO:0034620	134	-0.420	1.79E-06	8.42E-04	cellular response to unfolded protein
GO:0030098	332	0.266	1.79E-06	8.42E-04	lymphocyte differentiation
GO:0007623	208	-0.334	2.02E-06	9.41E-04	circadian rhythm
GO:0009048	17	-1.075	2.09E-06	9.68E-04	dosage compensation by inactivation of X chromosome
GO:0000375	324	-0.265	2.29E-06	1.05E-03	RNA splicing, via transesterification reactions
GO:1900034	76	-0.546	2.33E-06	1.06E-03	regulation of cellular response to heat
GO:0002521	488	0.217	2.55E-06	1.15E-03	leukocyte differentiation
GO:0050707	48	0.688	2.56E-06	1.15E-03	regulation of cytokine secretion
GO:0002448	47	0.716	2.62E-06	1.17E-03	mast cell mediated immunity
GO:2000249	38	0.836	2.68E-06	1.18E-03	regulation of actin cytoskeleton reorganization
GO:2001056	135	0.408	2.86E-06	1.25E-03	positive regulation of cysteine-type endopeptidase activity

GO:0070646	274	-0.288	2.98E-06	1.30E-03	protein modification by small protein removal
GO:0002279	46	0.704	3.29E-06	1.42E-03	mast cell activation involved in immune response
GO:0006479	175	-0.354	3.45E-06	1.47E-03	protein methylation
GO:0008213	175	-0.354	3.45E-06	1.47E-03	protein alkylation
GO:0000377	321	-0.261	3.76E-06	1.57E-03	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
GO:0000398	321	-0.261	3.76E-06	1.57E-03	mRNA splicing, via spliceosome
GO:0048199	73	-0.589	3.84E-06	1.59E-03	vesicle targeting, to, from or within Golgi
GO:0042110	431	0.226	3.84E-06	1.59E-03	T cell activation
GO:1901568	140	0.394	4.00E-06	1.64E-03	fatty acid derivative metabolic process
GO:0016571	137	-0.398	4.08E-06	1.66E-03	histone methylation
GO:0030968	117	-0.435	4.16E-06	1.68E-03	endoplasmic reticulum unfolded protein response
GO:0052547	383	0.238	4.63E-06	1.86E-03	regulation of peptidase activity
GO:0043303	45	0.702	4.68E-06	1.87E-03	mast cell degranulation
GO:0006605	417	0.228	4.73E-06	1.87E-03	protein targeting
GO:0018205	378	-0.239	4.80E-06	1.89E-03	peptidyl-lysine modification
GO:0051236	185	-0.340	4.93E-06	1.93E-03	establishment of RNA localization
GO:0046185	13	1.069	5.24E-06	2.03E-03	aldehyde catabolic process
GO:0001819	356	0.245	5.32E-06	2.05E-03	positive regulation of cytokine production
GO:0006901	69	-0.605	5.45E-06	2.08E-03	vesicle coating
GO:0035195	119	-0.423	5.46E-06	2.08E-03	gene silencing by miRNA
GO:0051251	254	0.289	5.96E-06	2.25E-03	positive regulation of lymphocyte activation
GO:1905517	46	0.701	6.01E-06	2.26E-03	macrophage migration
GO:0036500	10	-1.246	6.44E-06	2.39E-03	ATF6-mediated unfolded protein response
GO:0010952	172	0.350	6.41E-06	2.39E-03	positive regulation of peptidase activity
GO:0032527	44	-0.732	6.65E-06	2.45E-03	protein exit from endoplasmic reticulum
GO:0006378	43	-0.696	6.74E-06	2.45E-03	mRNA polyadenylation
GO:0043631	43	-0.696	6.74E-06	2.45E-03	RNA polyadenylation
GO:0030522	267	-0.279	7.15E-06	2.58E-03	intracellular receptor signaling pathway
GO:0042116	88	0.495	7.22E-06	2.59E-03	macrophage activation
GO:0042098	173	0.346	7.34E-06	2.62E-03	T cell proliferation
GO:0033003	39	0.739	7.39E-06	2.62E-03	regulation of mast cell activation
GO:0033006	30	0.863	7.47E-06	2.63E-03	regulation of mast cell activation involved in immune response
GO:2000116	219	0.307	7.70E-06	2.70E-03	regulation of cysteine-type endopeptidase activity

GO:0097529	184	0.334	7.83E-06	2.73E-03	myeloid leukocyte migration
GO:0010950	153	0.365	8.13E-06	2.81E-03	positive regulation of endopeptidase activity
GO:0000956	194	0.330	8.33E-06	2.87E-03	nuclear-transcribed mRNA catabolic process
GO:0042149	40	-0.697	8.72E-06	2.95E-03	cellular response to glucose starvation
GO:0002697	351	0.241	8.69E-06	2.95E-03	regulation of immune effector process
GO:0002699	188	0.330	8.65E-06	2.95E-03	positive regulation of immune effector process
GO:0030595	196	0.322	9.71E-06	3.26E-03	leukocyte chemotaxis
GO:0032786	28	-0.808	9.95E-06	3.32E-03	positive regulation of DNA-templated transcription, elongation
GO:0006611	173	-0.340	1.02E-05	3.34E-03	protein export from nucleus
GO:0045785	386	0.228	1.02E-05	3.34E-03	positive regulation of cell adhesion
GO:0031532	99	0.456	1.02E-05	3.34E-03	actin cytoskeleton reorganization
GO:0006913	329	-0.246	1.05E-05	3.44E-03	nucleocytoplasmic transport
GO:0050663	61	0.576	1.07E-05	3.48E-03	cytokine secretion
GO:0006409	32	-0.795	1.14E-05	3.63E-03	tRNA export from nucleus
GO:0071431	32	-0.795	1.14E-05	3.63E-03	tRNA-containing ribonucleoprotein complex export from nucleus
GO:0071426	121	-0.402	1.13E-05	3.63E-03	ribonucleoprotein complex export from nucleus
GO:0043304	29	0.866	1.15E-05	3.64E-03	regulation of mast cell degranulation
GO:0043280	118	0.408	1.20E-05	3.80E-03	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0031123	133	-0.381	1.22E-05	3.82E-03	RNA 3'-end processing
GO:0007229	106	0.436	1.29E-05	4.04E-03	integrin-mediated signaling pathway
GO:0000380	72	-0.519	1.33E-05	4.11E-03	alternative mRNA splicing, via spliceosome
GO:0007599	311	0.250	1.33E-05	4.11E-03	hemostasis
GO:0051169	332	-0.241	1.40E-05	4.29E-03	nuclear transport
GO:0045766	161	0.345	1.45E-05	4.44E-03	positive regulation of angiogenesis
GO:0017148	123	-0.401	1.52E-05	4.62E-03	negative regulation of translation
GO:0051249	395	0.221	1.53E-05	4.64E-03	regulation of lymphocyte activation
GO:0006110	72	-0.524	1.54E-05	4.65E-03	regulation of glycolytic process
GO:0090114	71	-0.548	1.61E-05	4.79E-03	COPII-coated vesicle budding
GO:0050657	182	-0.323	1.62E-05	4.79E-03	nucleic acid transport
GO:0050658	182	-0.323	1.62E-05	4.79E-03	RNA transport

GO:0002688	106	0.426	1.75E-05	5.15E-03	regulation of leukocyte chemotaxis
GO:0150076	63	0.572	1.81E-05	5.31E-03	neuroinflammatory response
GO:0031331	345	-0.233	2.01E-05	5.84E-03	positive regulation of cellular catabolic process
GO:0034248	381	-0.222	2.00E-05	5.84E-03	regulation of cellular amide metabolic process
GO:0006406	105	-0.418	2.07E-05	5.87E-03	mRNA export from nucleus
GO:0071427	105	-0.418	2.07E-05	5.87E-03	mRNA-containing ribonucleoprotein complex export from nucleus
GO:0071166	122	-0.388	2.07E-05	5.87E-03	ribonucleoprotein complex localization
GO:0034504	251	-0.272	2.06E-05	5.87E-03	protein localization to nucleus
GO:0007596	306	0.247	2.06E-05	5.87E-03	blood coagulation
GO:0006801	66	0.537	2.15E-05	6.05E-03	superoxide metabolic process
GO:0030970	28	-0.809	2.17E-05	6.06E-03	retrograde protein transport, ER to cytosol
GO:1903513	28	-0.809	2.17E-05	6.06E-03	endoplasmic reticulum to cytosol transport
GO:1901342	310	0.243	2.23E-05	6.17E-03	regulation of vasculature development
GO:0050764	91	0.455	2.23E-05	6.17E-03	regulation of phagocytosis
GO:0043401	176	-0.324	2.27E-05	6.24E-03	steroid hormone mediated signaling pathway
GO:0072676	94	0.454	2.29E-05	6.27E-03	lymphocyte migration
GO:0048511	297	-0.249	2.33E-05	6.33E-03	rhythmic process
GO:0032543	134	0.370	2.33E-05	6.33E-03	mitochondrial translation
GO:0050728	128	0.381	2.35E-05	6.33E-03	negative regulation of inflammatory response
GO:0002431	84	0.481	2.36E-05	6.33E-03	Fc receptor mediated stimulatory signaling pathway
GO:1905521	35	0.786	2.37E-05	6.35E-03	regulation of macrophage migration
GO:0007159	313	0.242	2.46E-05	6.53E-03	leukocyte cell-cell adhesion
GO:0009595	28	0.803	2.46E-05	6.53E-03	detection of biotic stimulus
GO:0071216	211	0.295	2.48E-05	6.55E-03	cellular response to biotic stimulus
GO:1904356	59	-0.555	2.50E-05	6.57E-03	regulation of telomere maintenance via telomere lengthening
GO:0150079	10	1.198	2.53E-05	6.62E-03	negative regulation of neuroinflammatory response
GO:0097064	36	-0.713	2.57E-05	6.65E-03	ncRNA export from nucleus
GO:0052548	358	0.225	2.58E-05	6.65E-03	regulation of endopeptidase activity
GO:0050817	310	0.242	2.56E-05	6.65E-03	coagulation
GO:0000381	61	-0.533	2.66E-05	6.80E-03	regulation of alternative mRNA splicing, via spliceosome

GO:0042102	90	0.451	2.66E-05	6.80E-03	positive regulation of T cell proliferation
GO:1903039	205	0.298	2.71E-05	6.90E-03	positive regulation of leukocyte cell-cell adhesion
GO:0045765	280	0.253	2.73E-05	6.91E-03	regulation of angiogenesis
GO:0015931	227	-0.280	2.83E-05	7.14E-03	nucleobase-containing compound transport
GO:0043300	43	0.677	2.85E-05	7.15E-03	regulation of leukocyte degranulation
GO:0060968	108	-0.408	2.89E-05	7.19E-03	regulation of gene silencing
GO:0001774	43	0.691	2.90E-05	7.19E-03	microglial cell activation
GO:0002269	43	0.691	2.90E-05	7.19E-03	leukocyte activation involved in inflammatory response
GO:0006487	77	-0.482	2.97E-05	7.35E-03	protein N-linked glycosylation
GO:0002888	32	0.773	3.07E-05	7.55E-03	positive regulation of myeloid leukocyte mediated immunity
GO:0051028	141	-0.353	3.27E-05	8.01E-03	mRNA transport
GO:0034660	436	-0.202	3.30E-05	8.04E-03	ncRNA metabolic process
GO:0006417	331	-0.231	3.47E-05	8.42E-03	regulation of translation
GO:0016573	149	-0.343	3.49E-05	8.44E-03	histone acetylation
GO:0032210	52	-0.579	3.64E-05	8.76E-03	regulation of telomere maintenance via telomerase
GO:0002690	84	0.460	3.86E-05	9.26E-03	positive regulation of leukocyte chemotaxis
GO:0034968	113	-0.392	3.88E-05	9.27E-03	histone lysine methylation
GO:0018210	122	-0.379	4.12E-05	9.77E-03	peptidyl-threonine modification
GO:0034249	140	-0.354	4.12E-05	9.77E-03	negative regulation of cellular amide metabolic process
GO:0006984	46	-0.617	4.16E-05	9.77E-03	ER-nucleus signaling pathway
GO:0038094	82	0.472	4.15E-05	9.77E-03	Fc-gamma receptor signaling pathway
GO:0000186	55	-0.572	4.22E-05	9.83E-03	activation of MAPKK activity
GO:0022409	241	0.267	4.22E-05	9.83E-03	positive regulation of cell-cell adhesion
GO:0060147	90	-0.438	4.32E-05	9.98E-03	regulation of posttranscriptional gene silencing
GO:0060966	90	-0.438	4.32E-05	9.98E-03	regulation of gene silencing by RNA
GO:0060337	67	0.520	4.37E-05	1.00E-02	type I interferon signaling pathway
GO:0071357	67	0.520	4.37E-05	1.00E-02	cellular response to type I interferon
GO:0051031	34	-0.732	4.40E-05	1.01E-02	tRNA transport
GO:0000209	299	-0.239	4.43E-05	1.01E-02	protein polyubiquitination
GO:0032102	333	0.227	4.44E-05	1.01E-02	negative regulation of response to external stimulus
GO:0007007	41	0.659	4.54E-05	1.03E-02	inner mitochondrial membrane organization

GO:0071108	33	-0.826	4.74E-05	1.06E-02	protein K48-linked deubiquitination
GO:0043470	81	-0.461	4.74E-05	1.06E-02	regulation of carbohydrate catabolic process
GO:0032680	103	0.408	4.96E-05	1.11E-02	regulation of tumor necrosis factor production
GO:0045943	22	-0.907	5.12E-05	1.14E-02	positive regulation of transcription by RNA polymerase I
GO:0002703	180	0.306	5.18E-05	1.14E-02	regulation of leukocyte mediated immunity
GO:0006690	87	0.439	5.17E-05	1.14E-02	icosanoid metabolic process
GO:0030574	42	0.619	5.22E-05	1.15E-02	collagen catabolic process
GO:0010935	12	1.264	5.36E-05	1.17E-02	regulation of macrophage cytokine production
GO:0007004	66	-0.497	5.44E-05	1.18E-02	telomere maintenance via telomerase
GO:0030335	479	0.187	5.43E-05	1.18E-02	positive regulation of cell migration
GO:0071887	99	0.409	5.45E-05	1.18E-02	leukocyte apoptotic process
GO:0043543	233	-0.267	5.58E-05	1.20E-02	protein acylation
GO:0050830	67	0.504	5.82E-05	1.25E-02	defense response to Gram-positive bacterium
GO:1904358	37	-0.654	5.93E-05	1.27E-02	positive regulation of telomere maintenance via telomere lengthening
GO:0031663	54	0.570	5.93E-05	1.27E-02	lipopolysaccharide-mediated signaling pathway
GO:0032204	77	-0.464	6.08E-05	1.29E-02	regulation of telomere maintenance
GO:0002433	78	0.472	6.28E-05	1.32E-02	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
GO:0038096	78	0.472	6.28E-05	1.32E-02	Fc-gamma receptor signaling pathway involved in phagocytosis
GO:0018393	153	-0.327	6.33E-05	1.33E-02	internal peptidyl-lysine acetylation
GO:0032640	107	0.394	6.32E-05	1.33E-02	tumor necrosis factor production
GO:0010833	77	-0.457	6.36E-05	1.33E-02	telomere maintenance via telomere lengthening
GO:0001776	84	0.444	6.40E-05	1.33E-02	leukocyte homeostasis
GO:0043624	211	0.278	6.64E-05	1.37E-02	cellular protein complex disassembly
GO:0002335	24	0.802	6.65E-05	1.37E-02	mature B cell differentiation
GO:0006109	190	-0.293	6.76E-05	1.39E-02	regulation of carbohydrate metabolic process
GO:0048207	65	-0.526	7.50E-05	1.53E-02	vesicle targeting, rough ER to cis-Golgi
GO:0048208	65	-0.526	7.50E-05	1.53E-02	COPII vesicle coating
GO:0022617	74	0.469	7.78E-05	1.58E-02	extracellular matrix disassembly

GO:0006959	190	0.289	8.13E-05	1.65E-02	humoral immune response
GO:0150077	34	0.735	8.25E-05	1.67E-02	regulation of neuroinflammatory response
GO:0046456	43	0.599	8.40E-05	1.69E-02	icosanoid biosynthetic process
GO:1903555	106	0.388	8.68E-05	1.74E-02	regulation of tumor necrosis factor superfamily cytokine production
GO:1903312	73	-0.464	8.73E-05	1.75E-02	negative regulation of mRNA metabolic process
GO:2000147	500	0.178	8.90E-05	1.77E-02	positive regulation of cell motility
GO:0050829	58	0.519	8.97E-05	1.78E-02	defense response to Gram-negative bacterium
GO:0050777	129	0.349	9.30E-05	1.84E-02	negative regulation of immune response
GO:0043534	112	0.372	9.40E-05	1.85E-02	blood vessel endothelial cell migration
GO:0018022	126	-0.350	9.91E-05	1.95E-02	peptidyl-lysine methylation
GO:1904018	180	0.292	1.01E-04	1.97E-02	positive regulation of vasculature development
GO:0043542	197	0.279	1.03E-04	2.01E-02	endothelial cell migration
GO:0042129	145	0.327	1.05E-04	2.04E-02	regulation of T cell proliferation
GO:0071706	110	0.375	1.08E-04	2.10E-02	tumor necrosis factor superfamily cytokine production
GO:0019371	11	1.118	1.09E-04	2.11E-02	cyclooxygenase pathway
GO:0043281	196	0.280	1.10E-04	2.12E-02	regulation of cysteine-type endopeptidase activity involved in apoptotic process
GO:0009755	221	-0.262	1.14E-04	2.18E-02	hormone-mediated signaling pathway
GO:0018209	294	-0.227	1.18E-04	2.25E-02	peptidyl-serine modification
GO:0036507	20	-1.023	1.21E-04	2.29E-02	protein demannosylation
GO:0036508	20	-1.023	1.21E-04	2.29E-02	protein alpha-1,2-demannosylation
GO:0043984	20	-0.775	1.24E-04	2.34E-02	histone H4-K16 acetylation
GO:2001252	167	-0.300	1.24E-04	2.34E-02	positive regulation of chromosome organization
GO:0045471	130	0.340	1.23E-04	2.34E-02	response to ethanol
GO:0006278	68	-0.466	1.25E-04	2.34E-02	RNA-dependent DNA biosynthetic process
GO:0099024	58	0.512	1.25E-04	2.35E-02	plasma membrane invagination
GO:0009206	55	0.533	1.28E-04	2.38E-02	purine ribonucleoside triphosphate biosynthetic process
GO:0009145	56	0.527	1.29E-04	2.39E-02	purine nucleoside triphosphate biosynthetic process
GO:0043031	15	0.982	1.31E-04	2.42E-02	negative regulation of macrophage activation
GO:0033962	20	-0.845	1.32E-04	2.44E-02	P-body assembly

GO:0050729	135	0.333	1.33E-04	2.44E-02	positive regulation of inflammatory response
GO:0033169	13	-0.993	1.35E-04	2.47E-02	histone H3-K9 demethylation
GO:0001525	481	0.177	1.35E-04	2.47E-02	angiogenesis
GO:0032212	34	-0.648	1.37E-04	2.49E-02	positive regulation of telomere maintenance via telomerase
GO:0018105	274	-0.233	1.37E-04	2.49E-02	peptidyl-serine phosphorylation
GO:0034453	26	-0.752	1.39E-04	2.52E-02	microtubule anchoring
GO:0018107	114	-0.364	1.40E-04	2.52E-02	peptidyl-threonine phosphorylation
GO:0050870	191	0.278	1.48E-04	2.66E-02	positive regulation of T cell activation
GO:0005978	49	-0.549	1.51E-04	2.69E-02	glycogen biosynthetic process
GO:0009250	49	-0.549	1.51E-04	2.69E-02	glucan biosynthetic process
GO:0042407	29	0.741	1.55E-04	2.76E-02	cristae formation
GO:0060964	87	-0.411	1.55E-04	2.76E-02	regulation of gene silencing by miRNA
GO:0001516	24	0.794	1.61E-04	2.84E-02	prostaglandin biosynthetic process
GO:0046457	24	0.794	1.61E-04	2.84E-02	prostanoid biosynthetic process
GO:0006414	138	0.326	1.62E-04	2.86E-02	translational elongation
GO:0018279	33	-0.688	1.65E-04	2.89E-02	protein N-linked glycosylation via asparagine
GO:0007029	62	-0.504	1.65E-04	2.89E-02	endoplasmic reticulum organization
GO:0045730	34	0.736	1.66E-04	2.89E-02	respiratory burst
GO:0002679	13	1.168	1.69E-04	2.94E-02	respiratory burst involved in defense response
GO:0042246	70	0.448	1.70E-04	2.95E-02	tissue regeneration
GO:0051250	132	0.332	1.74E-04	3.02E-02	negative regulation of lymphocyte activation
GO:0016050	320	-0.212	1.81E-04	3.13E-02	vesicle organization
GO:0097237	110	0.357	1.87E-04	3.21E-02	cellular response to toxic substance
GO:0043302	23	0.801	1.93E-04	3.31E-02	positive regulation of leukocyte degranulation
GO:0043537	32	0.649	1.95E-04	3.34E-02	negative regulation of blood vessel endothelial cell migration
GO:0002700	119	0.348	1.98E-04	3.38E-02	regulation of production of molecular mediator of immune response
GO:2000251	19	0.827	2.05E-04	3.49E-02	positive regulation of actin cytoskeleton reorganization
GO:0007020	25	-0.726	2.19E-04	3.69E-02	microtubule nucleation
GO:0018196	34	-0.660	2.18E-04	3.69E-02	peptidyl-asparagine modification
GO:1901570	88	0.397	2.19E-04	3.69E-02	fatty acid derivative biosynthetic process
GO:0043535	88	0.398	2.19E-04	3.69E-02	regulation of blood vessel endothelial cell migration

GO:0031348	185	0.275	2.25E-04	3.77E-02	negative regulation of defense response
GO:0006911	49	0.539	2.26E-04	3.78E-02	phagocytosis, engulfment
GO:0018394	161	-0.294	2.27E-04	3.79E-02	peptidyl-lysine acetylation
GO:0032956	317	0.210	2.29E-04	3.81E-02	regulation of actin cytoskeleton organization
GO:0009620	37	0.657	2.36E-04	3.90E-02	response to fungus
GO:0048246	34	0.661	2.37E-04	3.92E-02	macrophage chemotaxis
GO:0050832	24	0.776	2.39E-04	3.93E-02	defense response to fungus
GO:0030521	57	-0.497	2.44E-04	4.00E-02	androgen receptor signaling pathway
GO:0006892	101	-0.376	2.48E-04	4.05E-02	post-Golgi vesicle-mediated transport
GO:0006475	158	-0.294	2.50E-04	4.07E-02	internal protein amino acid acetylation
GO:0030258	228	-0.244	2.50E-04	4.07E-02	lipid modification
GO:0034340	70	0.454	2.54E-04	4.13E-02	response to type I interferon
GO:0001510	76	-0.418	2.57E-04	4.17E-02	RNA methylation
GO:1990748	102	0.362	2.61E-04	4.21E-02	cellular detoxification
GO:0035329	37	-0.589	2.67E-04	4.28E-02	hippo signaling
GO:0033143	74	-0.434	2.66E-04	4.28E-02	regulation of intracellular steroid hormone receptor signaling pathway
GO:0042060	462	0.172	2.68E-04	4.29E-02	wound healing
GO:0031440	28	-0.706	2.74E-04	4.36E-02	regulation of mRNA 3'-end processing
GO:0001906	128	0.325	2.73E-04	4.36E-02	cell killing
GO:0033008	15	0.890	2.79E-04	4.42E-02	positive regulation of mast cell activation involved in immune response
GO:0043306	15	0.890	2.79E-04	4.42E-02	positive regulation of mast cell degranulation
GO:0045619	160	0.290	2.84E-04	4.49E-02	regulation of lymphocyte differentiation
GO:0043123	176	0.276	2.86E-04	4.51E-02	positive regulation of I-kappaB kinase/NF-kappaB signaling
GO:0071675	43	0.565	2.88E-04	4.52E-02	regulation of mononuclear cell migration
GO:0016574	45	-0.551	2.90E-04	4.54E-02	histone ubiquitination
GO:0046831	13	-1.010	2.95E-04	4.61E-02	regulation of RNA export from nucleus
GO:0032784	45	-0.547	2.99E-04	4.66E-02	regulation of DNA-templated transcription, elongation
GO:0016577	25	-0.715	3.02E-04	4.69E-02	histone demethylation
GO:0000723	141	-0.306	3.07E-04	4.75E-02	telomere maintenance
GO:0009451	149	-0.297	3.08E-04	4.76E-02	RNA modification
GO:0043255	87	-0.391	3.23E-04	4.97E-02	regulation of carbohydrate biosynthetic process

Molecular functions in Genetic group 2 in the most efficient group.					
Go term	Number of genes	LOR*	pvalue	padj	Molecular functions
GO:0003735	155	1.165	4.37E-25	3.76E-20	structural constituent of ribosome
GO:0003954	38	1.355	9.97E-09	2.15E-05	NADH dehydrogenase activity
GO:0008137	38	1.355	9.97E-09	2.15E-05	NADH dehydrogenase (ubiquinone) activity
GO:0050136	38	1.355	9.97E-09	2.15E-05	NADH dehydrogenase (quinone) activity
GO:0016655	50	1.171	2.22E-02	3.83E-13	oxidoreductase activity, acting on NAD(P)H, quinone or similar compound as acceptor
GO:0101005	83	-0.783	2.71E-13	3.89E-10	ubiquitinyl hydrolase activity
GO:0004843	80	-0.775	1.29E-12	1.59E-09	thiol-dependent ubiquitin-specific protease activity
GO:0008242	90	-0.711	3.03E+03	3.26E-09	omega peptidase activity
GO:0005201	157	0.480	1.71E-11	1.64E-07	extracellular matrix structural constituent
GO:0004842	367	-0.317	2.48E-10	2.14E-07	ubiquitin-protein transferase activity
GO:0016651	95	0.618	3.45E-10	2.48E-07	oxidoreductase activity, acting on NAD(P)H
GO:0019787	390	-0.306	3.25E-10	2.48E-07	ubiquitin-like protein transferase activity
GO:0003729	235	-0.386	6.56E-10	4.35E-07	mRNA binding
GO:0030545	444	0.273	1.31E-09	8.05E-07	receptor regulator activity
GO:0030546	418	0.280	1.48E-09	8.50E-07	signaling receptor activator activity
GO:0048018	412	0.280	1.87E-09	1.01E-06	receptor ligand activity
GO:0008139	20	-1.074	3.65E-09	1.85E-06	nuclear localization sequence binding
GO:0043021	130	-0.483	7.02E-09	3.36E-06	ribonucleoprotein complex binding
GO:0009055	101	0.544	8.44E-09	3.83E-06	electron transfer activity
GO:0046933	15	1.187	1.08E-08	4.64E-06	proton-transporting ATP synthase activity, rotational mechanism
GO:0038187	12	1.256	2.72E-08	1.12E-04	pattern recognition receptor activity
GO:0042393	185	-0.374	5.20E-08	2.04E-04	histone binding
GO:0004386	139	-0.425	9.99E-08	3.75E-04	helicase activity
GO:0004402	60	-0.624	1.07E-07	3.84E-04	histone acetyltransferase activity
GO:0005539	199	0.342	1.72E-07	5.75E-04	glycosaminoglycan binding
GO:0019865	20	1.025	1.80E-07	5.75E-04	immunoglobulin binding
GO:1990380	14	-1.369	1.75E-07	5.75E-04	Lys48-specific deubiquitinase activity

GO:0016887	402	-0.241	1.96E-07	6.04E-04	ATPase activity
GO:0031624	31	-0.894	2.44E-07	7.25E-04	ubiquitin conjugating enzyme binding
GO:0004674	430	-0.228	3.15E-07	9.04E-04	protein serine/threonine kinase activity
GO:0061659	221	-0.315	4.16E-07	1.16E-03	ubiquitin-like protein ligase activity
GO:0003713	313	-0.258	6.30E-07	1.70E-03	transcription coactivator activity
GO:0005178	126	0.406	6.75E-07	1.76E-03	integrin binding
GO:0140030	138	-0.391	7.40E-07	1.88E-03	modification-dependent protein binding
GO:0043022	56	-0.605	9.22E-07	2.21E-03	ribosome binding
GO:0061630	216	-0.307	9.22E-07	2.21E-03	ubiquitin protein ligase activity
GO:0061733	62	-0.561	9.86E-07	2.30E-03	peptide-lysine-N-acetyltransferase activity
GO:0070492	11	1.194	1.23E-06	2.79E-03	oligosaccharide binding
GO:0044390	37	-0.747	1.96E-06	4.33E-03	ubiquitin-like protein conjugating enzyme binding
GO:0034212	71	-0.512	2.02E-06	4.36E-03	peptide N-acetyltransferase activity
GO:0032452	23	-0.845	2.69E-06	5.52E-03	histone demethylase activity
GO:0140457	23	-0.845	2.69E-06	5.52E-03	protein demethylase activity
GO:0004364	24	0.796	4.65E-06	9.33E-03	glutathione transferase activity
GO:0043295	10	1.109	5.55E-06	1.06E-02	glutathione binding
GO:1900750	10	1.109	5.55E-06	1.06E-02	oligopeptide binding
GO:0019843	61	0.536	5.85E-06	1.10E-02	rRNA binding
GO:0032454	11	-1.060	6.85E-06	1.26E-02	histone demethylase activity (H3-K9 specific)
GO:0070063	59	-0.535	7.41E-06	1.33E-02	RNA polymerase binding
GO:0140098	300	-0.225	1.16E-04	2.04E-02	catalytic activity, acting on RNA
GO:0008757	148	-0.317	1.29E-04	2.20E-02	S-adenosylmethionine-dependent methyltransferase activity
GO:0016741	212	-0.265	1.30E-04	2.20E-02	transferase activity, transferring one-carbon groups
GO:0005125	185	0.282	1.36E-04	2.25E-02	cytokine activity
GO:0008201	146	0.316	1.47E-04	2.39E-02	heparin binding
GO:0001540	73	0.453	1.71E-04	2.71E-02	amyloid-beta binding
GO:0008168	202	-0.266	1.73E-04	2.71E-02	methyltransferase activity
GO:0001098	56	-0.510	1.98E-04	2.95E-02	basal transcription machinery binding
GO:0001099	56	-0.510	1.98E-04	2.95E-02	basal RNA polymerase II transcription machinery binding
GO:0043175	44	-0.581	1.95E-04	2.95E-02	RNA polymerase core enzyme binding
GO:0016790	35	0.615	2.12E-04	3.09E-02	thiolester hydrolase activity
GO:0000993	37	-0.630	2.15E-04	3.09E-02	RNA polymerase II complex binding

GO:0016811	67	0.447	2.53E-04	3.55E-02	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides
GO:0008080	83	-0.405	2.55E-04	3.55E-02	N-acetyltransferase activity
GO:0019213	41	0.578	2.91E-04	3.99E-02	deacetylase activity
GO:0042800	16	-0.940	3.12E-04	4.14E-02	histone methyltransferase activity (H3-K4 specific)
GO:0050681	43	-0.559	3.08E-04	4.14E-02	androgen receptor binding
Cellular components in Genetic group 2 in the most efficient group.					
Go term	Number of genes	LOR*	pvalue	padj	Cellular components
GO:0044391	182	1.007	7.02E-20	3.81E-17	ribosomal subunit
GO:0098798	239	0.692	5.93E-24	1.61E-20	mitochondrial protein complex
GO:0005840	229	0.723	2.60E-23	4.71E-20	ribosome
GO:0098800	116	0.996	6.21E-23	8.43E-20	inner mitochondrial membrane protein complex
GO:0015934	115	0.937	1.16E-22	1.26E-19	large ribosomal subunit
GO:0022625	58	1.194	1.22E-19	1.10E-16	cytosolic large ribosomal subunit
GO:0005747	43	1.288	7.20E-18	5.59E-15	mitochondrial respiratory chain complex I
GO:0030964	43	1.288	1.46E-17	9.93E-15	NADH dehydrogenase complex
GO:0045271	43	1.288	6.69E-17	3.31E-14	respiratory chain complex I
GO:0022626	105	1.114	6.69E-17	3.31E-14	cytosolic ribosome
GO:0098803	69	1.159	6.69E-17	3.31E-14	respiratory chain complex
GO:0005746	74	1.041	1.29E-16	5.83E-14	mitochondrial respirasome
GO:0070469	81	0.997	2.92E-16	1.22E-13	respirasome
GO:0062023	375	0.425	5.11E-16	1.98E-13	collagen-containing extracellular matrix
GO:0031012	488	0.368	1.48E-15	5.36E-13	extracellular matrix
GO:0005743	435	0.380	9.92E-15	3.37E-12	mitochondrial inner membrane
GO:0005753	18	1.524	2.03E-14	6.11E-12	mitochondrial proton-transporting ATP synthase complex
GO:0045259	18	1.524	2.03E-14	6.11E-12	proton-transporting ATP synthase complex
GO:0015935	70	1.092	4.97E-14	1.42E-11	small ribosomal subunit
GO:1990204	101	0.726	2.31E-13	6.27E-10	oxidoreductase complex
GO:0019866	492	0.299	8.54E-12	2.21E-09	organelle inner membrane
GO:0000313	86	0.703	1.47E-11	3.47E-09	organellar ribosome
GO:0005761	86	0.703	1.47E-11	3.47E-09	mitochondrial ribosome
GO:0060205	307	0.331	1.42E-09	3.20E-07	cytoplasmic vesicle lumen
GO:0005925	400	0.283	3.10E-09	6.74E-07	focal adhesion
GO:0034774	303	0.322	3.93E-09	8.22E-07	secretory granule lumen
GO:0030055	407	0.277	4.85E-09	9.50E-07	cell-substrate junction
GO:0031983	309	0.317	4.90E-09	9.50E-07	vesicle lumen
GO:0005775	158	0.433	1.01E-08	1.90E-06	vacuolar lumen

GO:0034708	108	-0.522	1.29E-08	2.33E-05	methyltransferase complex
GO:0022627	42	1.331	1.39E-08	2.43E-06	cytosolic small ribosomal subunit
GO:0070820	151	0.425	3.38E-08	5.73E-06	tertiary granule
GO:0000315	56	0.671	4.96E-08	7.81E-06	organellar large ribosomal subunit
GO:0005762	56	0.671	4.96E-08	7.81E-06	mitochondrial large ribosomal subunit
GO:0016607	380	-0.262	5.03E-08	7.81E-06	nuclear speck
GO:0005798	157	-0.404	8.54E-08	1.29E-04	Golgi-associated vesicle
GO:0043202	92	0.520	8.90E-08	1.31E-04	lysosomal lumen
GO:0008023	52	-0.687	1.65E-07	2.36E-04	transcription elongation factor complex
GO:0000151	272	-0.294	1.86E-07	2.59E-04	ubiquitin ligase complex
GO:0035097	81	-0.551	1.97E-07	2.68E-04	histone methyltransferase complex
GO:0098552	466	0.223	2.34E-07	3.10E-04	side of membrane
GO:0035770	206	-0.332	2.64E-07	3.41E-04	ribonucleoprotein granule
GO:0005581	93	0.484	3.68E-07	4.65E-04	collagen trimer
GO:0031965	289	-0.274	4.09E-07	5.05E-04	nuclear membrane
GO:0042581	151	0.374	5.66E-07	6.83E-04	specific granule
GO:1904724	52	0.634	6.43E-07	7.59E-04	tertiary granule lumen
GO:0010494	58	-0.621	7.67E-07	8.86E-04	cytoplasmic stress granule
GO:0016469	46	0.722	8.61E-07	9.54E-04	proton-transporting two-sector ATPase complex
GO:0036464	195	-0.323	8.45E-07	9.54E-04	cytoplasmic ribonucleoprotein granule
GO:0034399	133	-0.386	1.25E-06	1.36E-03	nuclear periphery
GO:0070971	19	-1.157	1.38E-06	1.47E-03	endoplasmic reticulum exit site
GO:0031248	91	-0.460	1.70E-06	1.75E-03	protein acetyltransferase complex
GO:1902493	91	-0.460	1.70E-06	1.75E-03	acetyltransferase complex
GO:0016234	80	-0.481	2.25E-06	2.26E-03	inclusion body
GO:0000123	81	-0.477	2.52E-06	2.49E-03	histone acetyltransferase complex
GO:0042788	30	0.990	4.09E-06	3.97E-03	polysomal ribosome
GO:0005635	436	-0.195	5.92E-06	5.64E-03	nuclear envelope
GO:0005766	138	0.343	7.37E-06	6.56E-03	primary lysosome
GO:0042582	138	0.343	7.37E-06	6.56E-03	azurophil granule
GO:0005643	75	-0.463	7.36E-06	6.56E-03	nuclear pore
GO:0044322	23	-0.957	7.28E-06	6.56E-03	endoplasmic reticulum quality control compartment
GO:1902911	104	-0.398	8.06E-06	7.06E-03	protein kinase complex
GO:0030134	73	-0.483	1.03E-04	8.89E-03	COPII-coated ER to Golgi transport vesicle
GO:0016363	105	-0.385	1.05E-04	8.94E-03	nuclear matrix
GO:0005667	405	-0.195	1.08E-04	9.03E-03	transcription regulator complex
GO:0030667	277	0.235	1.15E-04	9.46E-03	secretory granule membrane

GO:0061695	245	-0.248	1.26E-04	1.02E-02	transferase complex, transferring phosphorus-containing groups
GO:1904949	76	-0.451	1.33E-04	1.06E-02	ATPase complex
GO:0005750	10	1.026	1.84E-04	1.42E-02	mitochondrial respiratory chain complex III
GO:0045275	10	1.026	1.84E-04	1.42E-02	respiratory chain complex III
GO:0030660	94	-0.398	1.86E-04	1.42E-02	Golgi-associated vesicle membrane
GO:0000314	28	0.730	2.20E-04	1.64E-02	organellar small ribosomal subunit
GO:0005763	28	0.730	2.20E-04	1.64E-02	mitochondrial small ribosomal subunit
GO:0070069	25	0.797	2.25E-04	1.65E-02	cytochrome complex
GO:0031984	337	-0.203	2.28E-04	1.65E-02	organelle subcompartment
GO:0045335	123	0.336	2.62E-04	1.87E-02	phagocytic vesicle
GO:0098791	317	-0.205	3.13E-04	2.21E-02	Golgi apparatus subcompartment
GO:0019908	12	-1.119	3.20E-04	2.23E-02	nuclear cyclin-dependent protein kinase holoenzyme complex
GO:0030135	264	-0.220	4.18E-04	2.88E-02	coated vesicle
GO:0009295	43	-0.536	4.39E-04	2.94E-02	nucleoid
GO:0042645	43	-0.536	4.39E-04	2.94E-02	mitochondrial nucleoid
GO:0043235	382	0.181	4.65E-04	3.04E-02	receptor complex
GO:0070603	72	-0.423	4.61E-04	3.04E-02	SWI/SNF superfamily-type complex
GO:0016605	94	-0.362	5.18E-04	3.35E-02	PML body
GO:0012507	43	-0.583	5.32E-04	3.40E-02	ER to Golgi transport vesicle membrane
GO:0009897	283	0.207	5.55E-04	3.50E-02	external side of plasma membrane
GO:0005788	299	0.201	5.73E-04	3.58E-02	endoplasmic reticulum lumen
GO:0030120	56	-0.483	6.33E-04	3.91E-02	vesicle coat
GO:0000790	342	-0.186	6.65E-04	4.06E-02	nuclear chromatin
GO:0031588	13	-0.943	7.69E-04	4.64E-02	nucleotide-activated protein kinase complex