

Supplementary Table S1: Significant GO terms (p < 0.01) related to the 2,528 5hmC-containing probes common in brain, blood, and saliva.

Category = Gene ontology category

Over_represented pvalue = p-value of the overrepresented gene ontology term

Number DE In Cat = The number of differentially expressed genes in the gene ontology category

Number In Cat = The total number of genes in the gene ontology category

GO term = Specific gene ontology term in the category

Category	over_represented pvalue	number DE In Cat	number In Cat	GO term
GO:0002376	5.40E-09	280	2574	immune system process
GO:0019899	4.49E-08	225	1691	enzyme binding
GO:0050778	9.33E-08	90	634	positive regulation of immune response
GO:0009607	9.67E-08	106	934	response to biotic stimulus
GO:0002684	1.24E-07	117	902	positive regulation of immune system process
GO:0007159	1.25E-07	74	478	leukocyte cell-cell adhesion
GO:0045321	1.33E-07	98	708	leukocyte activation
GO:0043207	2.02E-07	102	899	response to external biotic stimulus
GO:0051707	2.02E-07	102	899	response to other organism
GO:0070486	2.20E-07	70	445	leukocyte aggregation
GO:0006955	3.03E-07	178	1655	immune response
GO:0034109	6.53E-07	77	507	homotypic cell-cell adhesion
GO:0002252	7.83E-07	93	755	immune effector process
GO:0005515	1.17E-06	933	10458	protein binding
GO:0050776	1.43E-06	121	971	regulation of immune response
GO:0045576	1.85E-06	16	51	mast cell activation
GO:0098542	2.38E-06	62	543	defense response to other organism
GO:0001775	2.83E-06	121	946	cell activation
GO:0002757	2.85E-06	71	456	immune response-activating signal transduction
GO:0046649	3.62E-06	83	603	lymphocyte activation
GO:0002274	3.73E-06	31	157	myeloid leukocyte activation
GO:0033003	6.05E-06	12	34	regulation of mast cell activation
GO:0071593	6.98E-06	65	438	lymphocyte aggregation
GO:0065010	7.11E-06	265	2714	extracellular membrane-bounded organelle
GO:0070062	7.11E-06	265	2714	extracellular exosome
GO:0043230	7.22E-06	266	2727	extracellular organelle
GO:1903561	7.22E-06	266	2727	extracellular vesicle
GO:0042110	1.11E-05	64	437	T cell activation
GO:0070489	1.11E-05	64	437	T cell aggregation
GO:0004674	1.23E-05	77	437	protein serine/threonine kinase activity
GO:0002253	1.41E-05	72	505	activation of immune response
GO:0002682	1.78E-05	168	1499	regulation of immune system process
GO:0002448	1.85E-05	13	43	mast cell mediated immunity
GO:0050865	2.08E-05	65	462	regulation of cell activation
GO:0006952	2.22E-05	180	1789	defense response
GO:0006950	2.57E-05	380	3947	response to stress
GO:0035556	2.87E-05	294	2608	intracellular signal transduction
GO:0043299	3.05E-05	16	61	leukocyte degranulation
GO:0005737	3.26E-05	905	10317	cytoplasm
GO:0031982	3.44E-05	344	3609	vesicle
GO:0002444	4.19E-05	17	75	myeloid leukocyte mediated immunity
GO:0032418	4.71E-05	13	48	lysosome localization
GO:0002443	5.13E-05	38	283	leukocyte mediated immunity
GO:0031988	5.19E-05	331	3486	membrane-bounded vesicle
GO:0002366	5.47E-05	33	205	leukocyte activation involved in immune response
GO:0002694	5.84E-05	59	428	regulation of leukocyte activation
GO:0002279	5.89E-05	12	41	mast cell activation involved in immune response
GO:0043303	5.89E-05	12	41	mast cell degranulation
GO:0016773	6.07E-05	107	698	phosphotransferase activity, alcohol group as acceptor
GO:0002697	6.13E-05	53	411	regulation of immune effector process
GO:0044424	6.15E-05	1093	13248	intracellular part
GO:0002263	6.45E-05	33	207	cell activation involved in immune response
GO:0009617	6.68E-05	59	524	response to bacterium
GO:0005622	7.11E-05	1114	13564	intracellular

GO:0018193	7.18E-05	159	1331	peptidyl-amino acid modification
GO:0016301	7.66E-05	113	766	kinase activity
GO:0002764	7.90E-05	88	628	immune response-regulating signaling pathway
GO:0016772	8.93E-05	124	908	transferase activity, transferring phosphorus-containing groups
GO:0033006	9.30E-05	9	26	regulation of mast cell activation involved in immune response
GO:0043304	9.30E-05	9	26	regulation of mast cell degranulation
GO:0002250	9.46E-05	42	342	adaptive immune response
GO:0098602	9.47E-05	103	757	single organism cell adhesion
GO:0002429	9.65E-05	50	310	immune response-activating cell surface receptor signaling pathway
GO:0031267	1.06E-04	47	244	small GTPase binding
GO:0051704	1.07E-04	220	2369	multi-organism process
GO:0016032	1.20E-04	90	786	viral process
GO:0017016	1.26E-04	44	226	Ras GTPase binding
GO:0004672	1.28E-04	93	591	protein kinase activity
GO:0042060	1.35E-04	100	734	wound healing
GO:0032765	1.45E-04	3	3	positive regulation of mast cell cytokine production
GO:0002275	1.48E-04	16	66	myeloid cell activation involved in immune response
GO:0071216	1.53E-04	29	178	cellular response to biotic stimulus
GO:0005829	1.54E-04	340	3255	cytosol
GO:0032269	1.55E-04	122	1030	negative regulation of cellular protein metabolic process
GO:0002886	1.56E-04	11	35	regulation of myeloid leukocyte mediated immunity
GO:0051020	1.64E-04	49	266	GTPase binding
GO:0051248	1.67E-04	129	1098	negative regulation of protein metabolic process
GO:0032268	1.70E-04	254	2412	regulation of cellular protein metabolic process
GO:0044403	1.71E-04	92	825	symbiosis, encompassing mutualism through parasitism
GO:0044419	1.71E-04	92	825	interspecies interaction between organisms
GO:0002819	1.76E-04	20	120	regulation of adaptive immune response
GO:0018105	1.77E-04	44	244	peptidyl-serine phosphorylation
GO:0002703	1.87E-04	24	149	regulation of leukocyte mediated immunity
GO:0043300	1.88E-04	11	35	regulation of leukocyte degranulation
GO:0032763	1.99E-04	4	5	regulation of mast cell cytokine production
GO:0051246	2.05E-04	270	2585	regulation of protein metabolic process
GO:0042119	2.08E-04	9	25	neutrophil activation
GO:0016310	2.11E-04	238	2136	phosphorylation
GO:0000166	2.14E-04	249	2286	nucleotide binding
GO:0044764	2.16E-04	90	800	multi-organism cellular process
GO:1901265	2.19E-04	249	2287	nucleoside phosphate binding
GO:0036094	2.31E-04	273	2592	small molecule binding
GO:0042742	2.42E-04	24	223	defense response to bacterium
GO:0002460	2.52E-04	29	213	adaptive immune response
GO:0034110	2.87E-04	44	303	regulation of homotypic cell-cell adhesion
GO:0031347	2.97E-04	86	781	regulation of defense response
GO:0002699	2.99E-04	23	151	positive regulation of immune effector process
GO:0044428	3.22E-04	354	3721	nuclear part
GO:0006909	3.40E-04	37	205	phagocytosis
GO:0048518	3.46E-04	543	5390	positive regulation of biological process
GO:0002431	3.69E-04	21	79	Fc receptor mediated stimulatory signaling pathway
GO:0050817	3.88E-04	77	566	coagulation
GO:0002521	4.15E-04	63	460	leukocyte differentiation
GO:0036230	4.26E-04	9	29	granulocyte activation
GO:0071869	4.39E-04	13	33	response to catecholamine
GO:0007599	4.54E-04	77	566	hemostasis
GO:0043227	4.90E-04	951	11577	membrane-bounded organelle
GO:0009892	4.91E-04	273	2666	negative regulation of metabolic process
GO:0031981	5.06E-04	321	3371	nuclear lumen
GO:0018209	5.12E-04	44	258	peptidyl-serine modification
GO:0032553	5.34E-04	208	1836	ribonucleotide binding
GO:0007596	5.40E-04	76	561	blood coagulation
GO:0071867	5.70E-04	13	35	response to monoamine
GO:0035639	5.92E-04	201	1778	purine ribonucleoside triphosphate binding
GO:0032549	5.96E-04	202	1791	ribonucleoside binding
GO:0045184	5.99E-04	202	1953	establishment of protein localization
GO:0007049	6.06E-04	186	1762	cell cycle

GO:0009615	6.09E-04	47	407	response to virus
GO:0044267	6.13E-04	456	4950	cellular protein metabolic process
GO:0032555	6.16E-04	206	1820	purine ribonucleotide binding
GO:0046631	6.19E-04	22	111	alpha-beta T cell activation
GO:0005773	6.51E-04	73	599	vacuole
GO:0045088	6.51E-04	50	397	regulation of innate immune response
GO:0097367	7.04E-04	240	2192	carbohydrate derivative binding
GO:0006464	7.05E-04	380	3831	cellular protein modification process
GO:0036211	7.05E-04	380	3831	protein modification process
GO:0001882	7.13E-04	202	1798	nucleoside binding
GO:0046634	7.19E-04	15	70	regulation of alpha-beta T cell activation
GO:0017076	7.27E-04	206	1829	purine nucleotide binding
GO:0016337	7.32E-04	92	709	single organismal cell-cell adhesion
GO:0032550	7.34E-04	201	1788	purine ribonucleoside binding
GO:0030155	7.44E-04	86	627	regulation of cell adhesion
GO:0071870	7.44E-04	12	30	cellular response to catecholamine stimulus
GO:0001883	7.81E-04	201	1791	purine nucleoside binding
GO:0002822	8.05E-04	17	110	regulation of adaptive immune response
GO:0006796	8.12E-04	309	2975	phosphate-containing compound metabolic process
GO:0018107	8.44E-04	19	79	peptidyl-threonine phosphorylation
GO:0071868	8.51E-04	12	31	cellular response to monoamine stimulus
GO:0010605	8.63E-04	247	2396	negative regulation of macromolecule metabolic process
GO:0032762	8.67E-04	4	7	mast cell cytokine production
GO:0071219	9.24E-04	25	160	cellular response to molecule of bacterial origin
GO:0002520	9.61E-04	100	813	immune system development
GO:0007165	9.90E-04	523	5597	signal transduction
GO:0070488	1.00E-03	2	2	neutrophil aggregation
GO:0050896	1.03E-03	719	8210	response to stimulus
GO:0001772	1.03E-03	10	33	immunological synapse
GO:0071702	1.04E-03	249	2562	organic substance transport
GO:0002683	1.09E-03	48	365	negative regulation of immune system process
GO:0001816	1.11E-03	70	633	cytokine production
GO:0051249	1.12E-03	48	374	regulation of lymphocyte activation
GO:0051716	1.13E-03	620	6898	cellular response to stimulus
GO:1903037	1.13E-03	40	294	regulation of leukocyte cell-cell adhesion
GO:0032559	1.20E-03	178	1491	adenyl ribonucleotide binding
GO:0015031	1.21E-03	183	1808	protein transport
GO:1903729	1.21E-03	16	73	regulation of plasma membrane organization
GO:0009620	1.22E-03	9	54	response to fungus
GO:0007264	1.22E-03	119	912	small GTPase mediated signal transduction
GO:0006793	1.22E-03	312	3037	phosphorus metabolic process
GO:0000323	1.23E-03	63	511	lytic vacuole
GO:0005764	1.23E-03	63	511	lysosome
GO:0031665	1.25E-03	4	8	negative regulation of lipopolysaccharide-mediated signaling pathway
GO:0005524	1.27E-03	173	1454	ATP binding
GO:0005654	1.28E-03	272	2756	nucleoplasm
GO:0002286	1.28E-03	15	86	T cell activation involved in immune response
GO:0010792	1.31E-03	3	4	DNA double-strand break processing involved in repair via single-strand annealing
GO:0071222	1.33E-03	24	153	cellular response to lipopolysaccharide
GO:0002224	1.35E-03	25	153	toll-like receptor signaling pathway
GO:0042326	1.36E-03	62	423	negative regulation of phosphorylation
GO:0030554	1.37E-03	178	1498	adenyl nucleotide binding
GO:0045335	1.38E-03	15	82	phagocytic vesicle
GO:0002758	1.40E-03	39	281	innate immune response-activating signal transduction
GO:0051607	1.48E-03	38	326	defense response to virus
GO:0048534	1.50E-03	95	770	hematopoietic or lymphoid organ development
GO:0030097	1.53E-03	89	723	hemopoiesis
GO:0050878	1.53E-03	89	715	regulation of body fluid levels
GO:0006886	1.54E-03	105	991	intracellular protein transport
GO:0004697	1.54E-03	8	16	protein kinase C activity
GO:0005634	1.54E-03	571	6628	nucleus
GO:0031349	1.55E-03	50	429	positive regulation of defense response
GO:0045089	1.56E-03	43	330	positive regulation of innate immune response

GO:0045087	1.56E-03	112	1091	innate immune response
GO:0042581	1.59E-03	5	14	specific granule
GO:0006974	1.65E-03	82	783	cellular response to DNA damage stimulus
GO:0048476	1.66E-03	2	2	Holliday junction resolvase complex
GO:0007249	1.67E-03	34	259	I-kappaB kinase/NF-kappaB signaling
GO:0050866	1.68E-03	25	160	negative regulation of cell activation
GO:0034112	1.69E-03	30	203	positive regulation of homotypic cell-cell adhesion
GO:0018210	1.74E-03	19	83	peptidyl-threonine modification
GO:0010608	1.76E-03	51	436	posttranscriptional regulation of gene expression
GO:0061676	1.77E-03	2	2	importin-alpha family protein binding
GO:1990000	1.78E-03	4	6	amyloid fibril formation
GO:0043412	1.78E-03	387	4002	macromolecule modification
GO:0002695	1.78E-03	22	141	negative regulation of leukocyte activation
GO:0002218	1.82E-03	39	286	activation of innate immune response
GO:0016740	1.86E-03	220	2176	transferase activity
GO:0050863	1.97E-03	38	284	regulation of T cell activation
GO:0008645	2.03E-03	24	146	hexose transport
GO:0002283	2.05E-03	6	14	neutrophil activation involved in immune response
GO:1903039	2.05E-03	30	205	positive regulation of leukocyte cell-cell adhesion
GO:0000798	2.10E-03	3	5	nuclear cohesin complex
GO:0034991	2.10E-03	3	5	nuclear meiotic cohesin complex
GO:0008643	2.19E-03	27	182	carbohydrate transport
GO:0052642	2.23E-03	2	2	lysophosphatidic acid phosphatase activity
GO:0009611	2.24E-03	121	1049	response to wounding
GO:0002768	2.28E-03	68	494	immune response-regulating cell surface receptor signaling pathway
GO:0030312	2.30E-03	4	10	external encapsulating structure
GO:0032609	2.33E-03	16	104	interferon-gamma production
GO:0006302	2.37E-03	28	219	double-strand break repair
GO:0080134	2.39E-03	148	1434	regulation of response to stress
GO:0000726	2.41E-03	13	69	non-recombinational repair
GO:0015749	2.51E-03	24	148	monosaccharide transport
GO:0050851	2.52E-03	31	201	antigen receptor-mediated signaling pathway
GO:0051250	2.52E-03	19	121	negative regulation of lymphocyte activation
GO:0034142	2.53E-03	20	115	toll-like receptor 4 signaling pathway
GO:0050867	2.60E-03	38	286	positive regulation of cell activation
GO:0002702	2.71E-03	11	65	positive regulation of production of molecular mediator of immune response
GO:0019003	2.74E-03	10	53	GDP binding
GO:0043168	2.74E-03	274	2601	anion binding
GO:0032943	2.87E-03	32	259	mononuclear cell proliferation
GO:0002821	2.88E-03	12	73	positive regulation of adaptive immune response
GO:0012501	3.00E-03	197	1853	programmed cell death
GO:0070661	3.01E-03	33	271	leukocyte proliferation
GO:0050832	3.01E-03	7	40	defense response to fungus
GO:0051258	3.04E-03	36	224	protein polymerization
GO:0030217	3.05E-03	32	210	T cell differentiation
GO:0042098	3.05E-03	24	174	T cell proliferation
GO:0032439	3.05E-03	3	3	endosome localization
GO:0045002	3.05E-03	3	5	double-strand break repair via single-strand annealing
GO:0048519	3.09E-03	444	4547	negative regulation of biological process
GO:0043086	3.13E-03	92	846	negative regulation of catalytic activity
GO:0002696	3.14E-03	37	278	positive regulation of leukocyte activation
GO:0032970	3.14E-03	49	306	regulation of actin filament-based process
GO:0008104	3.18E-03	242	2381	protein localization
GO:0008064	3.22E-03	27	155	regulation of actin polymerization or depolymerization
GO:0032947	3.22E-03	17	67	protein complex scaffold
GO:0055037	3.24E-03	22	128	recycling endosome
GO:0002237	3.33E-03	40	333	response to molecule of bacterial origin
GO:0060759	3.33E-03	20	142	regulation of response to cytokine stimulus
GO:0033005	3.36E-03	5	15	positive regulation of mast cell activation
GO:0043560	3.42E-03	6	11	insulin receptor substrate binding
GO:0031625	3.43E-03	37	254	ubiquitin protein ligase binding
GO:0007154	3.45E-03	569	6140	cell communication
GO:0005085	3.52E-03	40	198	guanyl-nucleotide exchange factor activity

GO:0030098	3.57E-03	41	307	lymphocyte differentiation
GO:0045121	3.62E-03	46	287	membrane raft
GO:0030832	3.64E-03	27	156	regulation of actin filament length
GO:0002221	3.65E-03	27	187	pattern recognition receptor signaling pathway
GO:0043484	3.67E-03	16	90	regulation of RNA splicing
GO:0022407	3.71E-03	49	379	regulation of cell-cell adhesion
GO:0098857	3.71E-03	46	288	membrane microdomain
GO:0015758	3.72E-03	23	144	glucose transport
GO:0006468	3.72E-03	198	1802	protein phosphorylation
GO:0030833	3.75E-03	24	137	regulation of actin filament polymerization
GO:0033293	3.77E-03	11	55	monocarboxylic acid binding
GO:0022406	3.88E-03	14	67	membrane docking
GO:0042832	3.91E-03	5	18	defense response to protozoan
GO:0038094	3.94E-03	18	77	Fc-gamma receptor signaling pathway
GO:0004905	3.95E-03	2	2	type I interferon receptor activity
GO:0019962	3.95E-03	2	2	type I interferon binding
GO:0009605	3.98E-03	249	2478	response to external stimulus
GO:0006915	4.02E-03	194	1834	apoptotic process
GO:0044389	4.07E-03	37	258	ubiquitin-like protein ligase binding
GO:0070663	4.13E-03	27	202	regulation of leukocyte proliferation
GO:0045159	4.14E-03	3	5	myosin II binding
GO:0046651	4.14E-03	31	256	lymphocyte proliferation
GO:0043231	4.26E-03	856	10449	intracellular membrane-bounded organelle
GO:0019902	4.29E-03	29	161	phosphatase binding
GO:0016604	4.30E-03	44	344	nuclear body
GO:0010563	4.32E-03	73	544	negative regulation of phosphorus metabolic process
GO:0045936	4.32E-03	73	544	negative regulation of phosphate metabolic process
GO:0043254	4.34E-03	48	353	regulation of protein complex assembly
GO:0001913	4.36E-03	7	30	T cell mediated cytotoxicity
GO:0031400	4.38E-03	81	634	negative regulation of protein modification process
GO:0005885	4.55E-03	4	11	Arp2/3 protein complex
GO:0044444	4.64E-03	682	7802	cytoplasmic part
GO:0042113	4.64E-03	29	218	B cell activation
GO:0023052	4.65E-03	563	6064	signaling
GO:0000724	4.66E-03	19	148	double-strand break repair via homologous recombination
GO:0000725	4.66E-03	19	148	recombinational repair
GO:0044093	4.69E-03	206	1784	positive regulation of molecular function
GO:0001959	4.70E-03	19	136	regulation of cytokine-mediated signaling pathway
GO:0035662	4.75E-03	2	3	Toll-like receptor 4 binding
GO:0048013	4.80E-03	21	95	ephrin receptor signaling pathway
GO:0050870	4.83E-03	28	199	positive regulation of T cell activation
GO:0016888	4.84E-03	4	12	endodeoxyribonuclease activity, producing 5'-phosphomonoesters
GO:0050544	4.89E-03	3	5	arachidonic acid binding
GO:0002824	4.90E-03	11	69	positive regulation of adaptive immune response
GO:0032271	4.92E-03	29	172	regulation of protein polymerization
GO:0048522	5.04E-03	460	4635	positive regulation of cellular process
GO:0044822	5.25E-03	104	1156	poly(A) RNA binding
GO:0050789	5.27E-03	889	10521	regulation of biological process
GO:0010543	5.28E-03	9	32	regulation of platelet activation
GO:0043312	5.30E-03	5	11	neutrophil degranulation
GO:0044421	5.35E-03	314	3693	extracellular region part
GO:0065009	5.43E-03	294	2787	regulation of molecular function
GO:0002456	5.43E-03	13	77	T cell mediated immunity
GO:0030893	5.44E-03	3	7	meiotic cohesin complex
GO:0001817	5.45E-03	60	570	regulation of cytokine production
GO:0046635	5.46E-03	11	51	positive regulation of alpha-beta T cell activation
GO:0002440	5.47E-03	19	151	production of molecular mediator of immune response
GO:0051247	5.51E-03	164	1556	positive regulation of protein metabolic process
GO:0017137	5.51E-03	18	89	Rab GTPase binding
GO:0030029	5.53E-03	92	622	actin filament-based process
GO:0044700	5.53E-03	561	6058	single organism signaling
GO:0090330	5.53E-03	7	17	regulation of platelet aggregation
GO:0009057	5.58E-03	113	1149	macromolecule catabolic process

GO:0044092	5.60E-03	115	1096	negative regulation of molecular function
GO:0032944	5.65E-03	26	195	regulation of mononuclear cell proliferation
GO:0031054	5.70E-03	4	14	pre-miRNA processing
GO:0070820	5.72E-03	3	6	tertiary granule
GO:0030866	5.72E-03	8	28	cortical actin cytoskeleton organization
GO:0002573	5.73E-03	30	190	myeloid leukocyte differentiation
GO:0048583	5.77E-03	364	3626	regulation of response to stimulus
GO:0071638	5.80E-03	2	3	negative regulation of monocyte chemotactic protein-1 production
GO:0051015	5.90E-03	26	116	actin filament binding
GO:0044351	5.92E-03	4	7	macropinocytosis
GO:0002832	6.03E-03	7	28	negative regulation of response to biotic stimulus
GO:0032956	6.10E-03	42	271	regulation of actin cytoskeleton organization
GO:0043901	6.15E-03	20	153	negative regulation of multi-organism process
GO:0019900	6.16E-03	82	596	kinase binding
GO:0035259	6.20E-03	5	13	glucocorticoid receptor binding
GO:1902743	6.21E-03	11	37	regulation of lamellipodium organization
GO:0050794	6.26E-03	850	9980	regulation of cellular process
GO:1903012	6.33E-03	3	6	positive regulation of bone development
GO:0043085	6.43E-03	177	1523	positive regulation of catalytic activity
GO:0017048	6.50E-03	18	84	Rho GTPase binding
GO:0019901	6.51E-03	75	531	protein kinase binding
GO:0001933	6.51E-03	54	386	negative regulation of protein phosphorylation
GO:1903708	6.66E-03	24	162	positive regulation of hemopoiesis
GO:0032088	6.69E-03	12	66	negative regulation of NF-kappaB transcription factor activity
GO:0001767	6.70E-03	4	8	establishment of lymphocyte polarity
GO:0031324	6.76E-03	235	2362	negative regulation of cellular metabolic process
GO:0050542	6.82E-03	3	6	icosanoid binding
GO:1901567	6.82E-03	3	6	fatty acid derivative binding
GO:0050900	6.93E-03	40	352	leukocyte migration
GO:0006837	6.95E-03	5	17	serotonin transport
GO:1902563	7.02E-03	4	6	regulation of neutrophil activation
GO:0002449	7.06E-03	24	212	lymphocyte mediated immunity
GO:0051128	7.10E-03	238	2149	regulation of cellular component organization
GO:1900034	7.15E-03	14	75	regulation of cellular response to heat
GO:0031334	7.23E-03	28	197	positive regulation of protein complex assembly
GO:0005504	7.25E-03	6	28	fatty acid binding
GO:0002433	7.45E-03	17	73	immune response-regulating cell surface receptor signaling pathway involved in phagocytosis
GO:0038096	7.45E-03	17	73	Fc-gamma receptor signaling pathway involved in phagocytosis
GO:0050543	7.50E-03	3	6	icosatetraenoic acid binding
GO:0032270	7.58E-03	154	1461	positive regulation of cellular protein metabolic process
GO:0050777	7.73E-03	17	118	negative regulation of immune response
GO:0010828	7.80E-03	10	43	positive regulation of glucose transport
GO:0050790	7.85E-03	245	2315	regulation of catalytic activity
GO:0009893	7.87E-03	366	3565	positive regulation of metabolic process
GO:0008219	7.94E-03	202	1957	cell death
GO:0016265	7.94E-03	202	1957	death
GO:0044445	7.94E-03	20	211	cytosolic part
GO:0051234	7.99E-03	424	4531	establishment of localization
GO:1990923	7.99E-03	2	3	PET complex
GO:0006622	8.08E-03	5	15	protein targeting to lysosome
GO:0046627	8.18E-03	9	31	negative regulation of insulin receptor signaling pathway
GO:0019538	8.23E-03	486	5514	protein metabolic process
GO:0001562	8.24E-03	5	21	response to protozoan
GO:2001204	8.25E-03	3	7	regulation of osteoclast development
GO:0006897	8.29E-03	76	598	endocytosis
GO:0034121	8.33E-03	9	40	regulation of toll-like receptor signaling pathway
GO:0031399	8.38E-03	189	1768	regulation of protein modification process
GO:0008360	8.44E-03	24	128	regulation of cell shape
GO:0061081	8.44E-03	4	12	positive regulation of myeloid leukocyte cytokine production involved in immune response
GO:0030218	8.46E-03	17	96	erythrocyte differentiation
GO:0097190	8.46E-03	74	630	apoptotic signaling pathway
GO:0032649	8.52E-03	13	93	regulation of interferon-gamma production
GO:0071986	8.54E-03	2	6	Regulator complex

GO:0044265	8.64E-03	89	917	cellular macromolecule catabolic process
GO:0050670	8.73E-03	25	193	regulation of lymphocyte proliferation
GO:0090234	8.87E-03	2	2	regulation of kinetochore assembly
GO:0006469	8.88E-03	34	234	negative regulation of protein kinase activity
GO:1902580	8.88E-03	130	1246	single-organism cellular localization
GO:0030838	8.99E-03	16	88	positive regulation of actin filament polymerization
GO:0006810	9.01E-03	409	4399	transport
GO:0003729	9.12E-03	20	150	mRNA binding
GO:0050852	9.26E-03	24	163	T cell receptor signaling pathway
GO:0044446	9.29E-03	654	7742	intracellular organelle part
GO:0071871	9.31E-03	7	16	response to epinephrine
GO:0019961	9.32E-03	2	3	interferon binding
GO:0002285	9.42E-03	19	145	lymphocyte activation involved in immune response
GO:0051251	9.53E-03	33	254	positive regulation of lymphocyte activation
GO:0065007	9.58E-03	923	11019	biological regulation
GO:0005527	9.58E-03	5	18	macrolide binding
GO:0005528	9.58E-03	5	18	FK506 binding
GO:0050786	9.66E-03	3	11	RAGE receptor binding
GO:0030036	9.72E-03	80	542	actin cytoskeleton organization
GO:0070664	9.72E-03	12	68	negative regulation of leukocyte proliferation
GO:1900077	9.73E-03	9	33	negative regulation of cellular response to insulin stimulus
GO:0045730	9.75E-03	6	27	respiratory burst
GO:0032184	9.76E-03	3	6	SUMO polymer binding
GO:0042102	9.78E-03	13	92	positive regulation of T cell proliferation
GO:1902105	9.81E-03	32	235	regulation of leukocyte differentiation
GO:0042325	9.93E-03	159	1473	regulation of phosphorylation
GO:0034350	9.96E-03	4	7	regulation of glial cell apoptotic process
GO:0034351	9.96E-03	4	7	negative regulation of glial cell apoptotic process
GO:0002698	9.97E-03	15	100	negative regulation of immune effector process