

Supplementary Table S2: Significant GO terms ($p < 0.01$) related to the 5hmC-containing probes in DNase Hypersensitivity Sites

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:0071944	1.20E-24	4043	4406	cell periphery
GO:0005886	9.09E-24	3949	4305	plasma membrane
GO:0044459	1.33E-21	2224	2386	plasma membrane part
GO:0044699	2.30E-17	11084	12517	single-organism process
GO:0007154	3.40E-17	5129	5658	cell communication
GO:0044700	3.57E-17	5060	5579	single organism signaling
GO:0023052	4.34E-17	5065	5585	signaling
GO:0050896	4.85E-17	6843	7625	response to stimulus
GO:0044763	3.03E-16	10161	11448	single-organism cellular process
GO:0051179	2.66E-15	4916	5440	localization
GO:0032879	3.25E-15	2162	2336	regulation of localization
GO:0007165	6.55E-15	4640	5122	signal transduction
GO:0031226	3.19E-14	1390	1494	intrinsic component of plasma membrane
GO:0042995	5.00E-14	1647	1765	cell projection
GO:0051716	9.47E-14	5741	6387	cellular response to stimulus
GO:0005887	1.73E-13	1335	1436	integral component of plasma membrane
GO:0010646	8.41E-13	2675	2913	regulation of cell communication
GO:0023051	1.04E-12	2660	2897	regulation of signaling
GO:0051234	1.81E-12	4012	4444	establishment of localization
GO:0044707	2.02E-12	5283	5858	single-multicellular organism process
GO:0006810	2.55E-12	3894	4313	transport
GO:0048583	3.56E-12	3220	3537	regulation of response to stimulus
GO:0016020	8.89E-12	7202	8103	membrane
GO:0051049	1.09E-11	1585	1714	regulation of transport
GO:0032501	1.93E-11	5751	6407	multicellular organismal process
GO:0065008	2.87E-11	3141	3459	regulation of biological quality
GO:0043168	3.66E-11	2336	2556	anion binding
GO:0097458	4.02E-11	1174	1252	neuron part
GO:1902578	4.45E-11	3571	3955	single-organism localization
GO:0009966	6.89E-11	2340	2551	regulation of signal transduction
GO:0012505	7.87E-11	3240	3583	endomembrane system
GO:0003824	1.63E-10	4739	5300	catalytic activity
GO:0044425	1.86E-10	5187	5820	membrane part
GO:0044765	2.17E-10	3414	3784	single-organism transport
GO:0007166	2.21E-10	2477	2710	cell surface receptor signaling pathway
GO:0048518	2.50E-10	4754	5276	positive regulation of biological process
GO:0009611	2.53E-10	949	1014	response to wounding
GO:0035556	3.10E-10	2333	2553	intracellular signal transduction
GO:0005737	4.73E-10	8902	10054	cytoplasm
GO:0048856	6.07E-10	4524	5012	anatomical structure development
GO:0044767	1.28E-09	4980	5535	single-organism developmental process
GO:0006468	1.37E-09	1621	1760	protein phosphorylation
GO:0032559	1.41E-09	1358	1468	adenyl ribonucleotide binding
GO:0098805	1.42E-09	1797	1959	whole membrane
GO:0097367	1.55E-09	1968	2153	carbohydrate derivative binding
GO:0030554	1.60E-09	1364	1475	adenyl nucleotide binding
GO:0032502	1.66E-09	5050	5616	developmental process
GO:0016773	1.73E-09	658	693	phosphotransferase activity alcohol group as acceptor
GO:0016192	1.91E-09	1221	1319	vesicle-mediated transport
GO:0007275	1.96E-09	4324	4790	multicellular organism development

GO:0016301	2.54E-09	714	755	kinase activity
GO:0051239	2.74E-09	2297	2513	regulation of multicellular organismal process
GO:0004672	2.81E-09	562	589	protein kinase activity
GO:0006464	4.22E-09	3373	3739	cellular protein modification process
GO:0036211	4.22E-09	3373	3739	protein modification process
GO:0005524	4.49E-09	1324	1433	ATP binding
GO:0098590	5.79E-09	859	917	plasma membrane region
GO:0042060	1.05E-08	674	715	wound healing
GO:0001775	1.06E-08	853	916	cell activation
GO:0031224	1.11E-08	4240	4765	intrinsic component of membrane
GO:0048522	1.14E-08	4095	4544	positive regulation of cellular process
GO:0065009	1.52E-08	2471	2718	regulation of molecular function
GO:0098589	1.61E-08	1039	1117	membrane region
GO:0030054	1.88E-08	1052	1128	cell junction
GO:1902531	2.17E-08	1467	1596	regulation of intracellular signal transduction
GO:0005215	2.41E-08	1104	1201	transporter activity
GO:0048731	2.53E-08	3847	4257	system development
GO:0030029	3.19E-08	585	616	actin filament-based process
GO:0098797	3.51E-08	465	488	plasma membrane protein complex
GO:0048584	3.54E-08	1796	1968	positive regulation of response to stimulus
GO:0007155	3.63E-08	1277	1385	cell adhesion
GO:0072358	4.20E-08	897	960	cardiovascular system development
GO:0072359	4.20E-08	897	960	circulatory system development
GO:0016023	4.22E-08	1007	1090	cytoplasmic membrane-bounded vesicle
GO:0044444	6.27E-08	6779	7643	cytoplasmic part
GO:0005102	6.37E-08	1255	1368	receptor binding
GO:0043005	6.49E-08	877	937	neuron projection
GO:0016772	6.50E-08	837	897	transferase activity transferring phosphorus-containing groups
GO:0030001	6.73E-08	733	785	metal ion transport
GO:0003779	6.77E-08	369	383	actin binding
GO:0006897	7.22E-08	558	591	endocytosis
GO:0022610	7.49E-08	1280	1390	biological adhesion
GO:0023014	7.71E-08	808	867	signal transduction by protein phosphorylation
GO:0031410	7.81E-08	1099	1194	cytoplasmic vesicle
GO:0002376	7.86E-08	2231	2470	immune system process
GO:0031982	8.22E-08	3152	3515	vesicle
GO:0006793	8.45E-08	2679	2962	phosphorus metabolic process
GO:0005615	8.87E-08	1115	1227	extracellular space
GO:0006796	8.89E-08	2627	2903	phosphate-containing compound metabolic process
GO:0006950	9.15E-08	3418	3812	response to stress
GO:0005576	9.26E-08	3697	4155	extracellular region
GO:0006928	9.64E-08	1747	1905	movement of cell or subcellular component
GO:0016021	9.67E-08	4130	4649	integral component of membrane
GO:0005794	1.08E-07	1258	1369	Golgi apparatus
GO:0055085	1.45E-07	1244	1358	transmembrane transport
GO:0031988	1.56E-07	3041	3392	membrane-bounded vesicle
GO:0043412	1.79E-07	3509	3910	macromolecule modification
GO:0046873	1.82E-07	381	399	metal ion transmembrane transporter activity
GO:0008092	1.83E-07	758	809	cytoskeletal protein binding
GO:0032553	1.89E-07	1647	1805	ribonucleotide binding
GO:0036094	1.94E-07	2290	2532	small molecule binding
GO:0050790	2.30E-07	2045	2250	regulation of catalytic activity
GO:0004674	2.35E-07	416	436	protein serine/threonine kinase activity
GO:0022892	2.42E-07	945	1027	substrate-specific transporter activity
GO:0048869	2.51E-07	3510	3889	cellular developmental process
GO:0006811	2.70E-07	1352	1480	ion transport
GO:0046903	2.72E-07	967	1048	secretion
GO:0044421	2.73E-07	3177	3558	extracellular region part
GO:0050878	3.13E-07	650	695	regulation of body fluid levels

GO:0005057	3.36E-07	151	152	receptor signaling protein activity
GO:0017076	3.73E-07	1639	1798	purine nucleotide binding
GO:0032555	3.83E-07	1631	1789	purine ribonucleotide binding
GO:0000165	3.84E-07	779	838	MAPK cascade
GO:0051128	4.35E-07	1936	2124	regulation of cellular component organization
GO:0032940	4.57E-07	853	922	secretion by cell
GO:0044463	4.76E-07	873	939	cell projection part
GO:0048468	5.19E-07	1967	2149	cell development
GO:0001882	5.63E-07	1611	1768	nucleoside binding
GO:0030036	5.64E-07	511	539	actin cytoskeleton organization
GO:0043087	6.47E-07	509	538	regulation of GTPase activity
GO:0032549	7.11E-07	1605	1762	ribonucleoside binding
GO:0043062	7.17E-07	362	379	extracellular structure organization
GO:0051130	7.22E-07	1019	1104	positive regulation of cellular component organization
GO:0001883	7.51E-07	1604	1761	purine nucleoside binding
GO:0030198	7.52E-07	361	378	extracellular matrix organization
GO:0048471	7.90E-07	590	630	perinuclear region of cytoplasm
GO:0032550	8.06E-07	1602	1759	purine ribonucleoside binding
GO:0005911	8.38E-07	357	374	cell-cell junction
GO:0030155	8.84E-07	579	617	regulation of cell adhesion
GO:0060341	8.90E-07	1125	1227	regulation of cellular localization
GO:0022857	9.04E-07	866	941	transmembrane transporter activity
GO:0019899	9.12E-07	1530	1671	enzyme binding
GO:0016477	9.17E-07	1082	1171	cell migration
GO:0034330	9.34E-07	246	253	cell junction organization
GO:0043269	9.61E-07	548	584	regulation of ion transport
GO:0010647	9.70E-07	1446	1581	positive regulation of cell communication
GO:0031399	1.11E-06	1567	1718	regulation of protein modification process
GO:0035639	1.15E-06	1593	1750	purine ribonucleoside triphosphate binding
GO:0006955	1.20E-06	1422	1571	immune response
GO:0023056	1.37E-06	1427	1561	positive regulation of signaling
GO:0032880	1.47E-06	862	935	regulation of protein localization
GO:0043408	1.55E-06	713	768	regulation of MAPK cascade
GO:0033036	1.65E-06	2419	2686	macromolecule localization
GO:0015267	1.66E-06	412	437	channel activity
GO:0022803	1.66E-06	412	437	passive transmembrane transporter activity
GO:0018193	1.71E-06	1194	1304	peptidyl-amino acid modification
GO:0017124	1.79E-06	114	114	SH3 domain binding
GO:0044431	1.84E-06	774	837	Golgi apparatus part
GO:0006954	1.86E-06	561	608	inflammatory response
GO:0043547	1.86E-06	461	487	positive regulation of GTPase activity
GO:0036477	1.97E-06	607	647	somatodendritic compartment
GO:0048870	2.09E-06	1171	1273	cell motility
GO:0051674	2.09E-06	1171	1273	localization of cell
GO:0007010	2.10E-06	969	1049	cytoskeleton organization
GO:0007599	2.13E-06	517	551	hemostasis
GO:0031589	2.29E-06	287	298	cell-substrate adhesion
GO:0048646	2.39E-06	1065	1154	anatomical structure formation involved in morphogenesis
GO:0005261	2.39E-06	278	290	cation channel activity
GO:0007160	2.67E-06	188	192	cell-matrix adhesion
GO:0007596	2.88E-06	512	546	blood coagulation
GO:0043085	2.97E-06	1366	1491	positive regulation of catalytic activity
GO:0005856	2.97E-06	1706	1879	cytoskeleton
GO:0071702	3.05E-06	2262	2515	organic substance transport
GO:0009967	3.06E-06	1306	1427	positive regulation of signal transduction
GO:1901615	3.17E-06	494	530	organic hydroxy compound metabolic process
GO:0045321	3.79E-06	630	680	leukocyte activation
GO:0031401	4.33E-06	1071	1167	positive regulation of protein modification process
GO:0050817	4.63E-06	514	549	coagulation

GO:0004871	4.73E-06	1137	1248	signal transducer activity
GO:0016310	5.07E-06	1890	2083	phosphorylation
GO:0051345	5.53E-06	752	810	positive regulation of hydrolase activity
GO:0045202	5.85E-06	692	740	synapse
GO:0016740	5.86E-06	1928	2136	transferase activity
GO:0009986	6.09E-06	655	708	cell surface
GO:0009605	6.68E-06	2145	2376	response to external stimulus
GO:0005509	6.78E-06	606	654	calcium ion binding
GO:0031252	6.95E-06	339	354	cell leading edge
GO:0001944	6.95E-06	577	617	vasculature development
GO:0001568	7.33E-06	556	594	blood vessel development
GO:0051336	7.54E-06	1107	1208	regulation of hydrolase activity
GO:0032989	7.61E-06	1402	1526	cellular component morphogenesis
GO:0031344	7.87E-06	484	512	regulation of cell projection organization
GO:0030425	8.23E-06	426	450	dendrite
GO:0022838	8.52E-06	383	407	substrate-specific channel activity
GO:0043292	9.09E-06	201	208	contractile fiber
GO:0019898	1.01E-05	235	244	extrinsic component of membrane
GO:0007167	1.07E-05	1128	1224	enzyme linked receptor protein signaling pathway
GO:0034329	1.12E-05	218	225	cell junction assembly
GO:0099568	1.15E-05	244	253	cytoplasmic region
GO:0009653	1.23E-05	2474	2724	anatomical structure morphogenesis
GO:0030695	1.32E-05	260	271	GTPase regulator activity
GO:0003008	1.35E-05	1421	1563	system process
GO:0045216	1.37E-05	214	221	cell-cell junction organization
GO:0022891	1.41E-05	790	861	substrate-specific transmembrane transporter activity
GO:0001932	1.41E-05	1225	1340	regulation of protein phosphorylation
GO:0030154	1.46E-05	3283	3643	cell differentiation
GO:0050865	1.47E-05	423	453	regulation of cell activation
GO:0051641	1.49E-05	2628	2925	cellular localization
GO:0051050	1.62E-05	826	899	positive regulation of transport
GO:0098802	1.71E-05	163	167	plasma membrane receptor complex
GO:0006887	1.74E-05	338	359	exocytosis
GO:0005938	1.79E-05	226	234	cell cortex
GO:0044093	1.81E-05	1595	1750	positive regulation of molecular function
GO:0003012	1.95E-05	362	384	muscle system process
GO:1901265	2.08E-05	2021	2239	nucleoside phosphate binding
GO:0040011	2.15E-05	1621	1778	locomotion
GO:0000166	2.15E-05	2020	2238	nucleotide binding
GO:0007009	2.30E-05	254	265	plasma membrane organization
GO:0030175	2.36E-05	92	92	filopodium
GO:0050839	2.37E-05	172	177	cell adhesion molecule binding
GO:0022804	2.43E-05	316	336	active transmembrane transporter activity
GO:0048878	2.50E-05	902	986	chemical homeostasis
GO:0008610	2.55E-05	575	623	lipid biosynthetic process
GO:0042221	2.59E-05	3484	3896	response to chemical
GO:0032403	2.76E-05	835	906	protein complex binding
GO:0005515	2.89E-05	8986	10190	protein binding
GO:0051247	2.93E-05	1379	1516	positive regulation of protein metabolic process
GO:0005216	2.96E-05	373	397	ion channel activity
GO:0006629	3.01E-05	1159	1278	lipid metabolic process
GO:0009581	3.05E-05	179	186	detection of external stimulus
GO:0098772	3.08E-05	1095	1197	molecular function regulator
GO:0044456	3.13E-05	559	597	synapse part
GO:0005829	3.16E-05	2886	3217	cytosol
GO:0050793	3.23E-05	1898	2086	regulation of developmental process
GO:0051270	3.25E-05	687	740	regulation of cellular component movement
GO:0051246	3.32E-05	2262	2513	regulation of protein metabolic process
GO:0015629	3.38E-05	417	442	actin cytoskeleton

GO:0006814	3.59E-05	193	201	sodium ion transport
GO:0016324	3.67E-05	261	275	apical plasma membrane
GO:0006836	3.67E-05	175	180	neurotransmitter transport
GO:0030016	3.68E-05	190	197	myofibril
GO:0008104	3.91E-05	2114	2349	protein localization
GO:0001934	3.96E-05	884	963	positive regulation of protein phosphorylation
GO:0031032	4.06E-05	141	144	actomyosin structure organization
GO:0031346	4.16E-05	280	293	positive regulation of cell projection organization
GO:0002694	4.17E-05	391	419	regulation of leukocyte activation
GO:0050900	4.22E-05	323	345	leukocyte migration
GO:0007169	4.46E-05	849	918	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0034220	4.50E-05	896	979	ion transmembrane transport
GO:0032970	5.13E-05	288	303	regulation of actin filament-based process
GO:0098602	5.18E-05	675	730	single organism cell adhesion
GO:0031012	5.23E-05	384	409	extracellular matrix
GO:0034332	5.38E-05	115	116	adherens junction organization
GO:0044433	5.60E-05	503	542	cytoplasmic vesicle part
GO:0042592	5.64E-05	1388	1534	homeostatic process
GO:0016787	5.84E-05	2008	2242	hydrolase activity
GO:0001505	5.89E-05	171	176	regulation of neurotransmitter levels
GO:0043167	6.12E-05	5149	5801	ion binding
GO:0044449	6.14E-05	184	191	contractile fiber part
GO:1901565	6.34E-05	328	351	organonitrogen compound catabolic process
GO:0034765	6.41E-05	383	408	regulation of ion transmembrane transport
GO:0000902	6.62E-05	1328	1448	cell morphogenesis
GO:0098858	6.65E-05	165	170	actin-based cell projection
GO:0044057	6.69E-05	470	504	regulation of system process
GO:0042325	6.80E-05	1301	1429	regulation of phosphorylation
GO:0098655	6.81E-05	639	693	cation transmembrane transport
GO:0098552	7.00E-05	386	413	side of membrane
GO:0042127	7.41E-05	1336	1468	regulation of cell proliferation
GO:0008289	7.52E-05	567	613	lipid binding
GO:0044297	7.61E-05	452	483	cell body
GO:0045177	7.90E-05	326	347	apical part of cell
GO:0030030	7.98E-05	1349	1473	cell projection organization
GO:0030334	8.53E-05	600	646	regulation of cell migration
GO:0048513	8.68E-05	2734	3033	animal organ development
GO:0010975	8.83E-05	368	388	regulation of neuron projection development
GO:0005912	9.34E-05	434	461	adherens junction
GO:0046578	9.54E-05	176	181	regulation of Ras protein signal transduction
GO:0007044	9.55E-05	86	86	cell-substrate junction assembly
GO:0008236	1.02E-04	156	164	serine-type peptidase activity
GO:0032270	1.02E-04	1292	1422	positive regulation of cellular protein metabolic process
GO:0098793	1.04E-04	248	260	presynapse
GO:0046649	1.06E-04	535	579	lymphocyte activation
GO:0044255	1.06E-04	905	995	cellular lipid metabolic process
GO:0019220	1.11E-04	1500	1654	regulation of phosphate metabolic process
GO:0000139	1.11E-04	604	655	Golgi membrane
GO:0051240	1.16E-04	1271	1396	positive regulation of multicellular organismal process
GO:0032268	1.19E-04	2107	2343	regulation of cellular protein metabolic process
GO:0015075	1.20E-04	727	794	ion transmembrane transporter activity
GO:0001667	1.22E-04	303	320	ameboidal-type cell migration
GO:0070887	1.22E-04	2500	2786	cellular response to chemical stimulus
GO:0070161	1.22E-04	449	478	anchoring junction
GO:0005768	1.25E-04	695	756	endosome
GO:0002684	1.26E-04	807	885	positive regulation of immune system process
GO:0010562	1.35E-04	1018	1116	positive regulation of phosphorus metabolic process
GO:0045937	1.35E-04	1018	1116	positive regulation of phosphate metabolic process
GO:0006820	1.35E-04	521	565	anion transport

GO:0030100	1.37E-04	188	196	regulation of endocytosis
GO:0006812	1.46E-04	914	1003	cation transport
GO:0031984	1.52E-04	269	285	organelle subcompartment
GO:0030424	1.56E-04	398	424	axon
GO:0098588	1.61E-04	2010	2243	bounding membrane of organelle
GO:1903034	1.61E-04	352	379	regulation of response to wounding
GO:0005096	1.61E-04	232	243	GTPase activator activity
GO:0005578	1.62E-04	330	351	proteinaceous extracellular matrix
GO:0006936	1.62E-04	301	320	muscle contraction
GO:0099503	1.64E-04	393	424	secretory vesicle
GO:0042327	1.71E-04	915	1001	positive regulation of phosphorylation
GO:0006952	1.71E-04	1512	1685	defense response
GO:0030027	1.72E-04	167	172	lamellipodium
GO:2000145	1.73E-04	632	683	regulation of cell motility
GO:0016337	1.73E-04	630	683	single organismal cell-cell adhesion
GO:0043025	1.75E-04	400	427	neuronal cell body
GO:0035637	1.77E-04	178	185	multicellular organismal signaling
GO:0051174	1.83E-04	1510	1667	regulation of phosphorus metabolic process
GO:0048871	1.94E-04	302	322	multicellular organismal homeostasis
GO:0051056	2.02E-04	264	277	regulation of small GTPase mediated signal transduction
GO:1903827	2.06E-04	491	531	regulation of cellular protein localization
GO:0034762	2.07E-04	395	423	regulation of transmembrane transport
GO:1901681	2.07E-04	214	226	sulfur compound binding
GO:0010256	2.09E-04	491	529	endomembrane system organization
GO:0042991	2.12E-04	94	96	transcription factor import into nucleus
GO:0048514	2.12E-04	467	501	blood vessel morphogenesis
GO:0009582	2.12E-04	181	190	detection of abiotic stimulus
GO:0010959	2.14E-04	307	326	regulation of metal ion transport
GO:0030168	2.16E-04	241	254	platelet activation
GO:0051249	2.22E-04	341	366	regulation of lymphocyte activation
GO:0070588	2.30E-04	241	254	calcium ion transmembrane transport
GO:0015711	2.32E-04	380	409	organic anion transport
GO:0034333	2.39E-04	79	79	adherens junction assembly
GO:2000026	2.44E-04	1445	1586	regulation of multicellular organismal development
GO:1902533	2.46E-04	884	969	positive regulation of intracellular signal transduction
GO:0006898	2.48E-04	262	278	receptor-mediated endocytosis
GO:0017171	2.50E-04	157	166	serine hydrolase activity
GO:0030031	2.54E-04	342	365	cell projection assembly
GO:0030017	2.54E-04	167	174	sarcomere
GO:0019538	2.57E-04	4751	5364	protein metabolic process
GO:1900180	2.61E-04	197	207	regulation of protein localization to nucleus
GO:0010033	2.63E-04	2621	2926	response to organic substance
GO:0060589	2.69E-04	278	294	nucleoside-triphosphatase regulator activity
GO:0071310	2.76E-04	2086	2318	cellular response to organic substance
GO:0012506	2.77E-04	451	486	vesicle membrane
GO:0018212	2.80E-04	306	325	peptidyl-tyrosine modification
GO:0051649	2.81E-04	2267	2531	establishment of localization in cell
GO:1990778	2.81E-04	195	204	protein localization to cell periphery
GO:0010810	2.89E-04	166	172	regulation of cell-substrate adhesion
GO:0042990	2.91E-04	91	93	regulation of transcription factor import into nucleus
GO:0070201	2.99E-04	731	800	regulation of establishment of protein localization
GO:0008360	3.02E-04	124	127	regulation of cell shape
GO:0005773	3.14E-04	538	585	vacuole
GO:0007268	3.18E-04	647	700	synaptic transmission
GO:0099536	3.18E-04	647	700	synaptic signaling
GO:0099537	3.18E-04	647	700	trans-synaptic signaling
GO:0051648	3.21E-04	221	233	vesicle localization
GO:0018108	3.24E-04	304	323	peptidyl-tyrosine phosphorylation
GO:0032409	3.24E-04	186	194	regulation of transporter activity

GO:0051650	3.31E-04	210	221	establishment of vesicle localization
GO:0097164	3.35E-04	166	174	ammonium ion metabolic process
GO:0034702	3.51E-04	258	273	ion channel complex
GO:0002682	3.52E-04	1310	1453	regulation of immune system process
GO:0022603	3.53E-04	839	910	regulation of anatomical structure morphogenesis
GO:0010648	3.55E-04	1073	1176	negative regulation of cell communication
GO:0040012	3.56E-04	681	739	regulation of locomotion
GO:0006813	3.58E-04	199	209	potassium ion transport
GO:0032956	3.63E-04	254	268	regulation of actin cytoskeleton organization
GO:0045785	3.64E-04	345	369	positive regulation of cell adhesion
GO:1904019	3.70E-04	79	80	epithelial cell apoptotic process
GO:0071804	3.73E-04	166	173	cellular potassium ion transport
GO:0071805	3.73E-04	166	173	potassium ion transmembrane transport
GO:0006066	3.84E-04	348	375	alcohol metabolic process
GO:0004702	4.06E-04	64	64	receptor signaling protein serine/threonine kinase activity
GO:0030659	4.07E-04	433	467	cytoplasmic vesicle membrane
GO:0044087	4.07E-04	654	709	regulation of cellular component biogenesis
GO:0001726	4.07E-04	153	158	ruffle
GO:0007507	4.18E-04	487	523	heart development
GO:0031267	4.29E-04	232	244	small GTPase binding
GO:0001952	4.34E-04	90	91	regulation of cell-matrix adhesion
GO:0072659	4.48E-04	193	202	protein localization to plasma membrane
GO:0050867	4.58E-04	265	283	positive regulation of cell activation
GO:0002460	4.59E-04	196	209	adaptive immune response based on somatic recombination of immune receptors
GO:1903649	4.69E-04	412	445	regulation of cytoplasmic transport
GO:0032412	4.73E-04	169	176	regulation of ion transmembrane transporter activity
GO:0007602	4.78E-04	109	113	phototransduction
GO:0048489	4.81E-04	101	103	synaptic vesicle transport
GO:0097480	4.81E-04	101	103	establishment of synaptic vesicle localization
GO:0015085	4.88E-04	119	122	calcium ion transmembrane transporter activity
GO:0032386	4.91E-04	552	601	regulation of intracellular transport
GO:0015850	4.93E-04	208	221	organic hydroxy compound transport
GO:0044710	5.03E-04	4702	5325	single-organism metabolic process
GO:0098791	5.06E-04	254	270	Golgi subcompartment
GO:0043410	5.07E-04	539	585	positive regulation of MAPK cascade
GO:0002521	5.09E-04	407	439	leukocyte differentiation
GO:0044712	5.17E-04	962	1065	single-organism catabolic process
GO:0007229	5.30E-04	85	86	integrin-mediated signaling pathway
GO:0046822	5.35E-04	200	211	regulation of nucleocytoplasmic transport
GO:0099504	5.42E-04	84	85	synaptic vesicle cycle
GO:0015079	5.56E-04	135	140	potassium ion transmembrane transporter activity
GO:0070665	5.63E-04	123	128	positive regulation of leukocyte proliferation
GO:0051046	5.66E-04	612	668	regulation of secretion
GO:0009583	5.68E-04	122	127	detection of light stimulus
GO:0007399	5.69E-04	2121	2341	nervous system development
GO:0001738	5.81E-04	66	66	morphogenesis of a polarized epithelium
GO:0098660	6.01E-04	649	709	inorganic ion transmembrane transport
GO:0098662	6.06E-04	577	628	inorganic cation transmembrane transport
GO:0060627	6.10E-04	362	389	regulation of vesicle-mediated transport
GO:0090002	6.13E-04	129	133	establishment of protein localization to plasma membrane
GO:0098857	6.19E-04	271	287	membrane microdomain
GO:0004872	6.25E-04	1053	1172	receptor activity
GO:0060089	6.25E-04	1053	1172	molecular transducer activity
GO:0007015	6.32E-04	296	314	actin filament organization
GO:0050727	6.66E-04	248	267	regulation of inflammatory response
GO:0008015	6.74E-04	456	493	blood circulation
GO:0045121	6.74E-04	270	286	membrane raft
GO:0019900	6.82E-04	544	587	kinase binding
GO:0007045	6.86E-04	69	69	cell-substrate adherens junction assembly

GO:0048041	6.86E-04	69	69	focal adhesion assembly
GO:0001525	6.91E-04	393	422	angiogenesis
GO:0050776	7.16E-04	848	935	regulation of immune response
GO:0044853	7.20E-04	85	86	plasma membrane raft
GO:0065007	7.26E-04	9134	10379	biological regulation
GO:0005516	7.32E-04	166	173	calmodulin binding
GO:0051235	7.40E-04	268	286	maintenance of location
GO:0061572	7.67E-04	119	122	actin filament bundle organization
GO:0001816	7.73E-04	560	614	cytokine production
GO:0004713	7.74E-04	135	139	protein tyrosine kinase activity
GO:0008324	7.78E-04	541	590	cation transmembrane transporter activity
GO:0046777	7.79E-04	216	227	protein autophosphorylation
GO:0023057	7.91E-04	1061	1165	negative regulation of signaling
GO:0019901	8.11E-04	486	523	protein kinase binding
GO:0007159	8.16E-04	420	455	leukocyte cell-cell adhesion
GO:0008047	8.16E-04	405	436	enzyme activator activity
GO:0004252	8.17E-04	132	140	serine-type endopeptidase activity
GO:0008150	8.18E-04	13342	15286	biological process
GO:0002696	8.24E-04	257	275	positive regulation of leukocyte activation
GO:0099531	8.38E-04	141	146	presynaptic process involved in synaptic transmission
GO:0032946	8.44E-04	119	124	positive regulation of mononuclear cell proliferation
GO:0004620	8.51E-04	83	85	phospholipase activity
GO:0002520	8.55E-04	717	784	immune system development
GO:0010638	8.63E-04	515	560	positive regulation of organelle organization
GO:0044448	8.82E-04	114	117	cell cortex part
GO:0061337	9.12E-04	124	128	cardiac conduction
GO:0050778	9.22E-04	566	620	positive regulation of immune response
GO:0010927	9.29E-04	257	275	cellular component assembly involved in morphogenesis
GO:0055065	9.33E-04	497	542	metal ion homeostasis
GO:0030141	9.36E-04	289	313	secretory granule
GO:0010976	9.46E-04	210	220	positive regulation of neuron projection development
GO:0050671	9.74E-04	117	122	positive regulation of lymphocyte proliferation
GO:0003013	9.78E-04	458	496	circulatory system process
GO:0070727	9.82E-04	1346	1495	cellular macromolecule localization
GO:0000323	9.91E-04	458	498	lytic vacuole
GO:0005764	9.91E-04	458	498	lysosome
GO:0008233	9.94E-04	506	557	peptidase activity
GO:0042439	1.01E-03	83	85	ethanolamine-containing compound metabolic process
GO:0030234	1.02E-03	814	896	enzyme regulator activity
GO:0046942	1.03E-03	274	294	carboxylic acid transport
GO:0030055	1.04E-03	368	393	cell-substrate junction
GO:0006644	1.05E-03	327	352	phospholipid metabolic process
GO:0070011	1.09E-03	489	538	peptidase activity acting on L-amino acid peptides
GO:0051020	1.10E-03	251	266	GTPase binding
GO:0022898	1.11E-03	171	179	regulation of transmembrane transporter activity
GO:0042692	1.12E-03	335	358	muscle cell differentiation
GO:0044089	1.13E-03	370	398	positive regulation of cellular component biogenesis
GO:0019897	1.15E-03	125	129	extrinsic component of plasma membrane
GO:0043235	1.15E-03	297	317	receptor complex
GO:0051251	1.16E-03	235	251	positive regulation of lymphocyte activation
GO:0051017	1.16E-03	115	118	actin filament bundle assembly
GO:0070371	1.16E-03	225	240	ERK1 and ERK2 cascade
GO:0005924	1.17E-03	365	390	cell-substrate adherens junction
GO:0009888	1.17E-03	1570	1733	tissue development
GO:0006816	1.18E-03	344	370	calcium ion transport
GO:0007266	1.19E-03	152	158	Rho protein signal transduction
GO:0030048	1.20E-03	104	107	actin filament-based movement
GO:1904589	1.23E-03	167	176	regulation of protein import
GO:0022836	1.28E-03	285	305	gated channel activity

GO:0008283	1.32E-03	1685	1871	cell proliferation
GO:0034613	1.32E-03	1337	1486	cellular protein localization
GO:0045055	1.32E-03	158	166	regulated exocytosis
GO:1902495	1.34E-03	286	306	transmembrane transporter complex
GO:1903037	1.34E-03	267	287	regulation of leukocyte cell-cell adhesion
GO:0002526	1.35E-03	124	131	acute inflammatory response
GO:0022890	1.36E-03	458	498	inorganic cation transmembrane transporter activity
GO:0005160	1.37E-03	49	49	transforming growth factor beta receptor binding
GO:0098609	1.38E-03	774	850	cell-cell adhesion
GO:1904062	1.40E-03	198	209	regulation of cation transmembrane transport
GO:0017016	1.41E-03	214	226	Ras GTPase binding
GO:0040007	1.44E-03	879	963	growth
GO:1903829	1.44E-03	313	338	positive regulation of cellular protein localization
GO:0051493	1.47E-03	376	405	regulation of cytoskeleton organization
GO:0031253	1.47E-03	275	294	cell projection membrane
GO:0008081	1.48E-03	84	86	phosphoric diester hydrolase activity
GO:0097479	1.48E-03	106	109	synaptic vesicle localization
GO:0008285	1.52E-03	590	642	negative regulation of cell proliferation
GO:0051015	1.53E-03	112	115	actin filament binding
GO:0005802	1.53E-03	158	166	trans-Golgi network
GO:0045807	1.55E-03	110	114	positive regulation of endocytosis
GO:0010469	1.55E-03	116	120	regulation of receptor activity
GO:0033043	1.55E-03	941	1037	regulation of organelle organization
GO:0007267	1.55E-03	1067	1176	cell-cell signaling
GO:0042306	1.56E-03	164	173	regulation of protein import into nucleus
GO:0046470	1.56E-03	65	66	phosphatidylcholine metabolic process
GO:0032101	1.58E-03	775	856	regulation of response to external stimulus
GO:0048534	1.58E-03	679	743	hematopoietic or lymphoid organ development
GO:0031234	1.58E-03	93	95	extrinsic component of cytoplasmic side of plasma membrane
GO:0015849	1.63E-03	276	297	organic acid transport
GO:0022843	1.63E-03	137	143	voltage-gated cation channel activity
GO:1903522	1.64E-03	276	295	regulation of blood circulation
GO:0005178	1.65E-03	100	103	integrin binding
GO:0051094	1.66E-03	1034	1135	positive regulation of developmental process
GO:0070302	1.67E-03	183	193	regulation of stress-activated protein kinase signaling cascade
GO:0005925	1.70E-03	360	385	focal adhesion
GO:0043230	1.70E-03	2356	2652	extracellular organelle
GO:1903561	1.70E-03	2356	2652	extracellular vesicle
GO:0007269	1.72E-03	133	138	neurotransmitter secretion
GO:0034110	1.72E-03	275	296	regulation of homotypic cell-cell adhesion
GO:0001508	1.73E-03	114	118	action potential
GO:0032231	1.75E-03	74	75	regulation of actin filament bundle assembly
GO:0005262	1.75E-03	104	107	calcium channel activity
GO:0032872	1.75E-03	182	192	regulation of stress-activated MAPK cascade
GO:0009416	1.81E-03	329	356	response to light stimulus
GO:0002274	1.81E-03	145	153	myeloid leukocyte activation
GO:0034109	1.88E-03	444	483	homotypic cell-cell adhesion
GO:0050801	1.89E-03	600	659	ion homeostasis
GO:0044282	1.89E-03	314	341	small molecule catabolic process
GO:0005539	1.89E-03	185	197	glycosaminoglycan binding
GO:0008654	1.90E-03	216	231	phospholipid biosynthetic process
GO:0048585	1.90E-03	1208	1335	negative regulation of response to stimulus
GO:0051223	1.92E-03	662	728	regulation of protein transport
GO:0007164	1.93E-03	56	56	establishment of tissue polarity
GO:0030139	1.94E-03	228	243	endocytic vesicle
GO:0065010	1.95E-03	2344	2639	extracellular membrane-bounded organelle
GO:0070062	1.95E-03	2344	2639	extracellular exosome
GO:0010631	1.95E-03	206	218	epithelial cell migration
GO:0031674	1.96E-03	113	117	I band

GO:0009100	1.96E-03	491	537	glycoprotein metabolic process
GO:0005901	2.01E-03	75	76	caveola
GO:0030098	2.01E-03	270	290	lymphocyte differentiation
GO:0046474	2.05E-03	188	200	glycerophospholipid biosynthetic process
GO:0042391	2.05E-03	326	350	regulation of membrane potential
GO:0072511	2.06E-03	386	418	divalent inorganic cation transport
GO:1903530	2.06E-03	559	612	regulation of secretion by cell
GO:0001736	2.13E-03	55	55	establishment of planar polarity
GO:0048699	2.14E-03	1454	1598	generation of neurons
GO:0009719	2.24E-03	1570	1742	response to endogenous stimulus
GO:0005884	2.27E-03	75	76	actin filament
GO:0048666	2.28E-03	1121	1227	neuron development
GO:0034394	2.29E-03	48	48	protein localization to cell surface
GO:0009584	2.31E-03	108	113	detection of visible light
GO:0022604	2.31E-03	468	503	regulation of cell morphogenesis
GO:0043491	2.32E-03	140	147	protein kinase B signaling
GO:0001570	2.32E-03	71	72	vasculogenesis
GO:0031098	2.33E-03	266	284	stress-activated protein kinase signaling cascade
GO:0070838	2.37E-03	384	416	divalent metal ion transport
GO:0007603	2.39E-03	94	98	phototransduction visible light
GO:0042113	2.41E-03	188	200	B cell activation
GO:0050709	2.42E-03	100	104	negative regulation of protein secretion
GO:0030335	2.43E-03	350	378	positive regulation of cell migration
GO:0044273	2.44E-03	44	44	sulfur compound catabolic process
GO:0045184	2.44E-03	1720	1924	establishment of protein localization
GO:0071705	2.49E-03	696	767	nitrogen compound transport
GO:0090130	2.49E-03	213	226	tissue migration
GO:0050863	2.50E-03	257	277	regulation of T cell activation
GO:0005518	2.55E-03	65	66	collagen binding
GO:0098771	2.56E-03	549	603	inorganic ion homeostasis
GO:0030018	2.57E-03	99	102	Z disc
GO:0072562	2.58E-03	100	106	blood microparticle
GO:0030097	2.59E-03	636	697	hemopoiesis
GO:0045597	2.61E-03	750	819	positive regulation of cell differentiation
GO:0051640	2.65E-03	412	447	organelle localization
GO:0050804	2.68E-03	265	282	modulation of synaptic transmission
GO:0005913	2.69E-03	53	53	cell-cell adherens junction
GO:0044283	2.72E-03	477	524	small molecule biosynthetic process
GO:0015291	2.78E-03	202	216	secondary active transmembrane transporter activity
GO:0016298	2.84E-03	94	98	lipase activity
GO:0042044	2.85E-03	46	46	fluid transport
GO:0009968	2.85E-03	958	1054	negative regulation of signal transduction
GO:0006869	2.87E-03	269	291	lipid transport
GO:0022008	2.88E-03	1525	1679	neurogenesis
GO:0015081	2.92E-03	122	128	sodium ion transmembrane transporter activity
GO:0070372	2.93E-03	212	227	regulation of ERK1 and ERK2 cascade
GO:0043406	2.97E-03	194	206	positive regulation of MAP kinase activity
GO:0055001	2.97E-03	145	152	muscle cell development
GO:0045087	2.98E-03	922	1025	innate immune response
GO:0045017	3.00E-03	248	267	glycerolipid biosynthetic process
GO:0005244	3.00E-03	173	183	voltage-gated ion channel activity
GO:0022832	3.00E-03	173	183	voltage-gated channel activity
GO:0005088	3.03E-03	122	126	Ras guanyl-nucleotide exchange factor activity
GO:0005543	3.05E-03	312	336	phospholipid binding
GO:0070304	3.08E-03	128	134	positive regulation of stress-activated protein kinase signaling cascade
GO:0006875	3.12E-03	437	478	cellular metal ion homeostasis
GO:0016050	3.15E-03	258	278	vesicle organization
GO:0030182	3.17E-03	1355	1489	neuron differentiation
GO:0070486	3.18E-03	388	422	leukocyte aggregation

GO:0044430	3.19E-03	1221	1359	cytoskeletal part
GO:0042445	3.19E-03	166	177	hormone metabolic process
GO:0002576	3.20E-03	82	85	platelet degranulation
GO:0014069	3.20E-03	185	194	postsynaptic density
GO:0099572	3.20E-03	185	194	postsynaptic specialization
GO:0032874	3.24E-03	127	133	positive regulation of stress-activated MAPK cascade
GO:0009306	3.24E-03	434	474	protein secretion
GO:0001817	3.25E-03	503	554	regulation of cytokine production
GO:0043500	3.36E-03	79	81	muscle adaptation
GO:0071495	3.36E-03	1220	1348	cellular response to endogenous stimulus
GO:0072376	3.37E-03	67	70	protein activation cascade
GO:0032388	3.39E-03	324	352	positive regulation of intracellular transport
GO:0097190	3.41E-03	568	622	apoptotic signaling pathway
GO:0000149	3.42E-03	112	117	SNARE binding
GO:1904035	3.46E-03	57	58	regulation of epithelial cell apoptotic process
GO:0022407	3.47E-03	343	372	regulation of cell-cell adhesion
GO:1903533	3.49E-03	271	293	regulation of protein targeting
GO:0070663	3.49E-03	184	197	regulation of leukocyte proliferation
GO:0080134	3.51E-03	1250	1393	regulation of response to stress
GO:0090132	3.52E-03	208	221	epithelium migration
GO:0097581	3.59E-03	70	71	lamellipodium organization
GO:0055074	3.72E-03	342	372	calcium ion homeostasis
GO:0006892	3.74E-03	111	116	post-Golgi vesicle-mediated transport
GO:0019932	3.84E-03	222	237	second-messenger-mediated signaling
GO:0090066	3.86E-03	422	457	regulation of anatomical structure size
GO:1901700	3.87E-03	1421	1582	response to oxygen-containing compound
GO:0061061	3.88E-03	529	575	muscle structure development
GO:0002250	3.93E-03	293	321	adaptive immune response
GO:0005267	4.00E-03	112	117	potassium channel activity
GO:0018209	4.01E-03	229	244	peptidyl-serine modification
GO:0051588	4.06E-03	63	64	regulation of neurotransmitter transport
GO:0001725	4.07E-03	52	52	stress fiber
GO:0097517	4.07E-03	52	52	contractile actin filament bundle
GO:0042102	4.11E-03	87	91	positive regulation of T cell proliferation
GO:0009898	4.12E-03	145	152	cytoplasmic side of plasma membrane
GO:0051098	4.14E-03	261	280	regulation of binding
GO:0006874	4.21E-03	331	360	cellular calcium ion homeostasis
GO:0002440	4.25E-03	136	145	production of molecular mediator of immune response
GO:0030218	4.27E-03	91	94	erythrocyte differentiation
GO:0071593	4.39E-03	381	415	lymphocyte aggregation
GO:0005769	4.41E-03	266	286	early endosome
GO:0014068	4.44E-03	60	61	positive regulation of phosphatidylinositol 3-kinase signaling
GO:0008284	4.46E-03	725	798	positive regulation of cell proliferation
GO:0042110	4.49E-03	380	414	T cell activation
GO:0070489	4.49E-03	380	414	T cell aggregation
GO:0046434	4.52E-03	142	150	organophosphate catabolic process
GO:0042470	4.58E-03	98	102	melanosome
GO:0048770	4.58E-03	98	102	pigment granule
GO:0046530	4.59E-03	58	59	photoreceptor cell differentiation
GO:0031175	4.59E-03	997	1091	neuron projection development
GO:0015293	4.65E-03	126	133	symporter activity
GO:0010038	4.67E-03	305	330	response to metal ion
GO:0055080	4.68E-03	536	590	cation homeostasis
GO:0072509	4.74E-03	150	158	divalent inorganic cation transmembrane transporter activity
GO:0048519	4.78E-03	3951	4448	negative regulation of biological process
GO:0003015	4.80E-03	240	257	heart process
GO:0035091	4.82E-03	180	191	phosphatidylinositol binding
GO:1903391	4.85E-03	50	50	regulation of adherens junction organization
GO:0051492	4.87E-03	64	65	regulation of stress fiber assembly

GO:0010876	4.94E-03	297	323	lipid localization
GO:0090175	4.98E-03	48	48	regulation of establishment of planar polarity
GO:0098657	5.04E-03	45	45	import into cell
GO:0001819	5.04E-03	350	384	positive regulation of cytokine production
GO:2001236	5.06E-03	146	154	regulation of extrinsic apoptotic signaling pathway
GO:0019722	5.06E-03	140	148	calcium-mediated signaling
GO:0070252	5.07E-03	85	88	actin-mediated cell contraction
GO:0007162	5.12E-03	205	219	negative regulation of cell adhesion
GO:0002237	5.12E-03	302	329	response to molecule of bacterial origin
GO:0006941	5.12E-03	138	146	striated muscle contraction
GO:0038023	5.13E-03	836	933	signaling receptor activity
GO:0006873	5.24E-03	481	529	cellular ion homeostasis
GO:0031503	5.28E-03	98	103	protein complex localization
GO:0097191	5.30E-03	214	229	extrinsic apoptotic signaling pathway
GO:0044437	5.30E-03	345	376	vacuolar part
GO:1901616	5.31E-03	64	66	organic hydroxy compound catabolic process
GO:0004715	5.32E-03	45	45	non-membrane spanning protein tyrosine kinase activity
GO:0098794	5.32E-03	359	386	postsynapse
GO:0060047	5.36E-03	238	255	heart contraction
GO:1990351	5.57E-03	289	312	transporter complex
GO:0002443	5.59E-03	252	275	leukocyte mediated immunity
GO:0044877	5.70E-03	1248	1382	macromolecular complex binding
GO:0048592	5.70E-03	143	150	eye morphogenesis
GO:0042578	5.70E-03	307	332	phosphoric ester hydrolase activity
GO:0008328	5.72E-03	47	47	ionotropic glutamate receptor complex
GO:1903651	5.74E-03	244	264	positive regulation of cytoplasmic transport
GO:1901618	5.79E-03	48	49	organic hydroxy compound transmembrane transporter activity
GO:0060071	5.80E-03	47	47	Wnt signaling pathway planar cell polarity pathway
GO:0006023	5.86E-03	109	114	aminoglycan biosynthetic process
GO:0032944	5.99E-03	177	190	regulation of mononuclear cell proliferation
GO:0007215	6.04E-03	67	68	glutamate receptor signaling pathway
GO:0051893	6.05E-03	48	48	regulation of focal adhesion assembly
GO:0090109	6.05E-03	48	48	regulation of cell-substrate junction assembly
GO:1901617	6.12E-03	205	221	organic hydroxy compound biosynthetic process
GO:0032844	6.13E-03	402	438	regulation of homeostatic process
GO:0005975	6.20E-03	865	962	carbohydrate metabolic process
GO:0070851	6.21E-03	118	125	growth factor receptor binding
GO:2000147	6.24E-03	358	389	positive regulation of cell motility
GO:0016358	6.26E-03	183	193	dendrite development
GO:0045859	6.26E-03	770	847	regulation of protein kinase activity
GO:0035567	6.29E-03	62	63	non-canonical Wnt signaling pathway
GO:0002702	6.51E-03	60	62	positive regulation of production of molecular mediator of immune response
GO:1903039	6.54E-03	189	203	positive regulation of leukocyte cell-cell adhesion
GO:0014888	6.55E-03	41	41	striated muscle adaptation
GO:0015031	6.56E-03	1587	1780	protein transport
GO:0006024	6.57E-03	108	113	glycosaminoglycan biosynthetic process
GO:0045595	6.59E-03	1316	1454	regulation of cell differentiation
GO:0043270	6.63E-03	216	232	positive regulation of ion transport
GO:0050670	6.64E-03	175	188	regulation of lymphocyte proliferation
GO:0051272	6.67E-03	368	400	positive regulation of cellular component movement
GO:1902532	6.68E-03	399	435	negative regulation of intracellular signal transduction
GO:0034703	6.71E-03	157	166	cation channel complex
GO:0006833	6.73E-03	39	39	water transport
GO:0048017	6.86E-03	192	205	inositol lipid-mediated signaling
GO:0060395	6.87E-03	56	57	SMAD protein signal transduction
GO:0009893	6.91E-03	3117	3493	positive regulation of metabolic process
GO:0008238	6.94E-03	93	98	exopeptidase activity
GO:0035725	6.96E-03	117	123	sodium ion transmembrane transport
GO:0051495	7.08E-03	172	183	positive regulation of cytoskeleton organization

GO:0002700	7.09E-03	91	96	regulation of production of molecular mediator of immune response
GO:0045335	7.15E-03	78	81	phagocytic vesicle
GO:0051403	7.17E-03	245	263	stress-activated MAPK cascade
GO:0034112	7.20E-03	187	201	positive regulation of homotypic cell-cell adhesion
GO:0043492	7.20E-03	113	119	ATPase activity coupled to movement of substances
GO:0006801	7.24E-03	51	52	superoxide metabolic process
GO:0030863	7.25E-03	77	79	cortical cytoskeleton
GO:0072507	7.33E-03	365	399	divalent inorganic cation homeostasis
GO:0055002	7.38E-03	132	139	striated muscle cell development
GO:0015399	7.43E-03	108	114	primary active transmembrane transporter activity
GO:0015405	7.43E-03	108	114	P-P-bond-hydrolysis-driven transmembrane transporter activity
GO:0002064	7.46E-03	205	218	epithelial cell development
GO:0017038	7.46E-03	290	315	protein import
GO:0016042	7.48E-03	253	276	lipid catabolic process
GO:0000118	7.53E-03	58	59	histone deacetylase complex
GO:0001523	7.61E-03	80	84	retinoid metabolic process
GO:0034504	7.61E-03	314	341	protein localization to nucleus
GO:0051896	7.66E-03	116	122	regulation of protein kinase B signaling
GO:0002819	7.87E-03	110	117	regulation of adaptive immune response
GO:0032271	7.89E-03	161	171	regulation of protein polymerization
GO:0009897	7.94E-03	213	231	external side of plasma membrane
GO:0006508	7.97E-03	1333	1499	proteolysis
GO:0048015	8.13E-03	189	202	phosphatidylinositol-mediated signaling
GO:0045664	8.15E-03	499	540	regulation of neuron differentiation
GO:0030239	8.17E-03	53	54	myofibril assembly
GO:0007292	8.22E-03	97	102	female gamete generation
GO:1904950	8.25E-03	195	210	negative regulation of establishment of protein localization
GO:0009101	8.25E-03	441	485	glycoprotein biosynthetic process
GO:0051129	8.33E-03	552	604	negative regulation of cellular component organization
GO:0098562	8.37E-03	156	165	cytoplasmic side of membrane
GO:0034101	8.38E-03	96	100	erythrocyte homeostasis
GO:0019905	8.39E-03	80	83	syntaxin binding
GO:0002697	8.45E-03	364	401	regulation of immune effector process
GO:0002699	8.61E-03	137	147	positive regulation of immune effector process
GO:0052689	8.63E-03	108	115	carboxylic ester hydrolase activity
GO:0038083	8.65E-03	44	44	peptidyl-tyrosine autophosphorylation
GO:0045185	8.73E-03	89	93	maintenance of protein location
GO:2001233	8.73E-03	343	374	regulation of apoptotic signaling pathway
GO:0048278	8.95E-03	54	55	vesicle docking
GO:0031091	8.98E-03	59	61	platelet alpha granule
GO:0006606	8.98E-03	247	267	protein import into nucleus
GO:0044744	8.98E-03	247	267	protein targeting to nucleus
GO:1902593	8.98E-03	247	267	single-organism nuclear import
GO:0030217	9.01E-03	192	206	T cell differentiation
GO:0043393	9.01E-03	159	169	regulation of protein binding
GO:0006790	9.05E-03	334	365	sulfur compound metabolic process
GO:0030003	9.06E-03	469	517	cellular cation homeostasis
GO:0032535	9.20E-03	300	323	regulation of cellular component size
GO:0050870	9.35E-03	183	197	positive regulation of T cell activation
GO:0050764	9.36E-03	64	66	regulation of phagocytosis
GO:0005085	9.42E-03	185	196	guanyl-nucleotide exchange factor activity
GO:0015672	9.42E-03	504	555	monovalent inorganic cation transport
GO:0030038	9.45E-03	74	76	contractile actin filament bundle assembly
GO:0043149	9.45E-03	74	76	stress fiber assembly
GO:0051924	9.48E-03	193	207	regulation of calcium ion transport
GO:0043068	9.50E-03	534	585	positive regulation of programmed cell death
GO:0055082	9.51E-03	588	650	cellular chemical homeostasis
GO:0080135	9.52E-03	576	634	regulation of cellular response to stress
GO:0006650	9.66E-03	241	261	glycerophospholipid metabolic process

GO:0002456	9.70E-03	72	75	T cell mediated immunity
GO:0010035	9.75E-03	454	498	response to inorganic substance
GO:0048872	9.80E-03	208	224	homeostasis of number of cells
GO:0043409	9.83E-03	137	145	negative regulation of MAPK cascade
GO:2001257	9.83E-03	83	86	regulation of cation channel activity
GO:0048589	9.87E-03	538	586	developmental growth
GO:0050892	9.88E-03	31	31	intestinal absorption
GO:0001948	9.94E-03	94	98	glycoprotein binding