

Supplementary Table S3: Significant GO terms (p < 0.01) related to the 5hmC-containing probes in Open Chromatin Regions

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:0044700	2.26E-12	3743	4716	single organism signaling
GO:0023052	2.45E-12	3747	4721	signaling
GO:0007165	9.37E-12	3429	4321	signal transduction
GO:0051716	2.19E-11	4214	5363	cellular response to stimulus
GO:0044425	4.63E-11	3735	4767	membrane part
GO:0016020	2.26E-10	5218	6724	membrane
GO:0031224	1.79E-09	3014	3849	intrinsic component of membrane
GO:0048583	4.24E-09	2393	3001	regulation of response to stimulus
GO:0043547	7.28E-09	390	440	positive regulation of GTPase activity
GO:0016021	9.17E-09	2941	3764	integral component of membrane
GO:0010646	4.41E-08	2023	2523	regulation of cell communication
GO:0098589	5.90E-08	805	966	membrane region
GO:0023051	1.24E-07	2004	2503	regulation of signaling
GO:0035556	1.82E-07	1755	2193	intracellular signal transduction
GO:0098590	1.95E-07	666	795	plasma membrane region
GO:0031012	2.65E-07	300	344	extracellular matrix
GO:0044707	4.32E-07	3822	4888	single-multicellular organism process
GO:0032879	4.36E-07	1591	1980	regulation of localization
GO:0043087	4.96E-07	419	483	regulation of GTPase activity
GO:0044763	6.60E-07	7288	9529	single-organism cellular process
GO:0006022	6.75E-07	135	147	aminoglycan metabolic process
GO:0030054	9.04E-07	826	997	cell junction
GO:0005578	1.73E-06	260	298	proteinaceous extracellular matrix
GO:0030203	2.14E-06	129	141	glycosaminoglycan metabolic process
GO:0032502	2.41E-06	3653	4674	developmental process
GO:0032501	2.53E-06	4145	5328	multicellular organismal process
GO:0012505	2.73E-06	2382	3027	endomembrane system
GO:0048856	4.67E-06	3287	4191	anatomical structure development
GO:0009966	5.02E-06	1758	2201	regulation of signal transduction
GO:0051049	6.63E-06	1172	1452	regulation of transport
GO:0098805	6.88E-06	1369	1706	whole membrane
GO:0044699	7.86E-06	7893	10366	single-organism process
GO:0016192	8.34E-06	918	1126	vesicle-mediated transport
GO:0051345	9.14E-06	594	711	positive regulation of hydrolase activity
GO:0044767	9.60E-06	3600	4612	single-organism developmental process
GO:0003824	1.19E-05	3457	4473	catalytic activity
GO:0019898	1.43E-05	188	213	extrinsic component of membrane
GO:0003779	1.46E-05	298	344	actin binding
GO:0043062	1.48E-05	283	329	extracellular structure organization
GO:0030198	1.59E-05	282	328	extracellular matrix organization
GO:0006464	1.83E-05	2495	3189	cellular protein modification process
GO:0036211	1.83E-05	2495	3189	protein modification process
GO:0030001	1.96E-05	550	664	metal ion transport
GO:1903510	2.16E-05	97	105	mucopolysaccharide metabolic process
GO:0016324	2.29E-05	211	242	apical plasma membrane

GO:0006023	2.90E-05	88	95	aminoglycan biosynthetic process
GO:0019897	3.10E-05	104	113	extrinsic component of plasma membrane
GO:0005096	3.33E-05	199	225	GTPase activator activity
GO:0006024	3.79E-05	87	94	glycosaminoglycan biosynthetic process
GO:0022610	3.90E-05	946	1167	biological adhesion
GO:0006897	4.17E-05	419	499	endocytosis
GO:0051239	4.34E-05	1680	2115	regulation of multicellular organismal process
GO:0044456	4.82E-05	457	544	synapse part
GO:0007155	5.21E-05	941	1162	cell adhesion
GO:0050654	5.26E-05	49	50	chondroitin sulfate proteoglycan metabolic process
GO:0043412	5.27E-05	2587	3319	macromolecule modification
GO:0005085	5.48E-05	167	185	guanyl-nucleotide exchange factor activity
GO:0060076	5.99E-05	171	192	excitatory synapse
GO:0008237	6.43E-05	129	144	metallopeptidase activity
GO:0048584	6.90E-05	1316	1658	positive regulation of response to stimulus
GO:0031226	7.89E-05	978	1220	intrinsic component of plasma membrane
GO:0015629	7.99E-05	333	390	actin cytoskeleton
GO:0043197	8.45E-05	103	113	dendritic spine
GO:0098794	8.79E-05	300	351	postsynapse
GO:0030204	9.31E-05	47	48	chondroitin sulfate metabolic process
GO:0043085	9.76E-05	1046	1295	positive regulation of catalytic activity
GO:0045202	1.02E-04	562	674	synapse
GO:0098552	1.04E-04	294	348	side of membrane
GO:0051336	1.05E-04	834	1026	regulation of hydrolase activity
GO:0006029	1.09E-04	78	84	proteoglycan metabolic process
GO:0008092	1.18E-04	598	723	cytoskeletal protein binding
GO:0060627	1.20E-04	281	331	regulation of vesicle-mediated transport
GO:0005887	1.27E-04	941	1176	integral component of plasma membrane
GO:0051179	1.36E-04	3539	4558	localization
GO:0031234	1.36E-04	79	85	extrinsic component of cytoplasmic side of plasma membrane
GO:0010647	1.41E-04	1071	1340	positive regulation of cell communication
GO:0007275	1.43E-04	3124	4000	multicellular organism development
GO:0007166	1.48E-04	1791	2261	cell surface receptor signaling pathway
GO:0007229	1.54E-04	73	78	integrin-mediated signaling pathway
GO:0022603	1.57E-04	637	774	regulation of anatomical structure morphogenesis
GO:0023056	1.60E-04	1057	1322	positive regulation of signaling
GO:0044309	1.61E-04	104	115	neuron spine
GO:0048518	1.72E-04	3488	4487	positive regulation of biological process
GO:0016323	1.78E-04	160	183	basolateral plasma membrane
GO:0045177	1.80E-04	255	301	apical part of cell
GO:0014069	1.82E-04	162	183	postsynaptic density
GO:0099572	1.82E-04	162	183	postsynaptic specialization
GO:0016773	1.87E-04	520	625	phosphotransferase activity alcohol group as acceptor
GO:0006950	1.88E-04	2447	3154	response to stress
GO:0044255	1.92E-04	656	814	cellular lipid metabolic process
GO:0065008	2.02E-04	2252	2872	regulation of biological quality
GO:0046777	2.05E-04	182	207	protein autophosphorylation
GO:0006796	2.06E-04	1942	2474	phosphate-containing compound metabolic process
GO:0071310	3.01E-04	1530	1941	cellular response to organic substance
GO:0006793	3.12E-04	1980	2527	phosphorus metabolic process
GO:0005913	3.41E-04	44	45	cell-cell adherens junction
GO:0016301	3.50E-04	565	684	kinase activity
GO:0004222	3.59E-04	75	81	metalloendopeptidase activity
GO:0006468	3.63E-04	1205	1515	protein phosphorylation
GO:0003008	3.71E-04	1038	1302	system process

GO:0010959	3.84E-04	233	273	regulation of metal ion transport
GO:0048731	4.05E-04	2798	3577	system development
GO:1901615	4.10E-04	357	435	organic hydroxy compound metabolic process
GO:0031252	4.16E-04	277	325	cell leading edge
GO:0006629	4.17E-04	828	1039	lipid metabolic process
GO:0070887	4.26E-04	1809	2312	cellular response to chemical stimulus
GO:0043507	4.30E-04	55	58	positive regulation of JUN kinase activity
GO:0005911	4.42E-04	275	325	cell-cell junction
GO:0006026	4.48E-04	52	55	aminoglycan catabolic process
GO:0005905	4.81E-04	54	57	coated pit
GO:0050793	5.12E-04	1394	1754	regulation of developmental process
GO:0050839	5.13E-04	135	153	cell adhesion molecule binding
GO:0031098	5.22E-04	212	249	stress-activated protein kinase signaling cascade
GO:0008305	5.38E-04	29	29	integrin complex
GO:0098636	5.38E-04	29	29	protein complex involved in cell adhesion
GO:0004672	5.41E-04	444	533	protein kinase activity
GO:0030695	5.42E-04	217	252	GTPase regulator activity
GO:0044463	5.55E-04	681	834	cell projection part
GO:0009967	5.58E-04	966	1211	positive regulation of signal transduction
GO:1902531	5.60E-04	1092	1369	regulation of intracellular signal transduction
GO:0051015	6.17E-04	96	105	actin filament binding
GO:0014823	6.20E-04	53	57	response to activity
GO:0030029	6.39E-04	450	540	actin filament-based process
GO:0016740	6.53E-04	1447	1845	transferase activity
GO:0044444	6.72E-04	4927	6444	cytoplasmic part
GO:0030155	6.85E-04	421	512	regulation of cell adhesion
GO:0009898	6.95E-04	121	136	cytoplasmic side of plasma membrane
GO:0046903	7.10E-04	705	873	secretion
GO:0008270	7.12E-04	757	947	zinc ion binding
GO:0006810	7.56E-04	2800	3607	transport
GO:0009986	7.60E-04	477	586	cell surface
GO:0036477	7.64E-04	485	586	somatodendritic compartment
GO:0019220	7.65E-04	1115	1407	regulation of phosphate metabolic process
GO:0005794	7.77E-04	952	1195	Golgi apparatus
GO:0007257	7.91E-04	31	31	activation of JUN kinase activity
GO:0070302	8.06E-04	144	166	regulation of stress-activated protein kinase signaling cascade
GO:0032872	8.49E-04	143	165	regulation of stress-activated MAPK cascade
GO:0042327	8.54E-04	691	861	positive regulation of phosphorylation
GO:0004871	8.77E-04	824	1034	signal transducer activity
GO:0060079	8.90E-04	49	51	excitatory postsynaptic potential
GO:0000323	9.10E-04	352	428	lytic vacuole
GO:0005764	9.10E-04	352	428	lysosome
GO:0010562	9.15E-04	764	956	positive regulation of phosphorus metabolic process
GO:0045937	9.15E-04	764	956	positive regulation of phosphate metabolic process
GO:0046914	9.53E-04	896	1132	transition metal ion binding
GO:0006027	9.84E-04	48	51	glycosaminoglycan catabolic process
GO:0000165	1.01E-03	572	708	MAPK cascade
GO:0016310	1.06E-03	1415	1796	phosphorylation
GO:0034329	1.08E-03	173	199	cell junction assembly
GO:0034330	1.11E-03	194	225	cell junction organization
GO:0010033	1.11E-03	1910	2449	response to organic substance
GO:0022604	1.11E-03	379	454	regulation of cell morphogenesis
GO:0051234	1.14E-03	2884	3720	establishment of localization
GO:0005737	1.23E-03	6416	8429	cytoplasm
GO:0023014	1.25E-03	593	736	signal transduction by protein phosphorylation

GO:0046328	1.27E-03	116	132	regulation of JNK cascade
GO:0009268	1.31E-03	32	33	response to pH
GO:0051050	1.31E-03	605	753	positive regulation of transport
GO:0051174	1.34E-03	1121	1418	regulation of phosphorus metabolic process
GO:0006898	1.35E-03	192	226	receptor-mediated endocytosis
GO:0042592	1.36E-03	989	1252	homeostatic process
GO:0016101	1.38E-03	58	64	diterpenoid metabolic process
GO:0005773	1.38E-03	410	504	vacuole
GO:0051403	1.39E-03	192	227	stress-activated MAPK cascade
GO:0098562	1.49E-03	129	147	cytoplasmic side of membrane
GO:0043408	1.51E-03	523	647	regulation of MAPK cascade
GO:0006811	1.51E-03	979	1233	ion transport
GO:0005509	1.55E-03	450	553	calcium ion binding
GO:0009605	1.56E-03	1535	1959	response to external stimulus
GO:0003013	1.57E-03	337	408	circulatory system process
GO:0031589	1.61E-03	215	253	cell-substrate adhesion
GO:0008360	1.67E-03	103	116	regulation of cell shape
GO:0043269	1.68E-03	404	490	regulation of ion transport
GO:0007254	1.71E-03	139	161	JNK cascade
GO:0007169	1.74E-03	652	804	transmembrane receptor protein tyrosine kinase signaling pathway
GO:0032403	1.80E-03	631	780	protein complex binding
GO:0030016	1.86E-03	143	165	myofibril
GO:0019900	1.86E-03	427	517	kinase binding
GO:0010517	1.90E-03	73	80	regulation of phospholipase activity
GO:0019538	1.94E-03	3445	4493	protein metabolic process
GO:0097458	1.95E-03	905	1121	neuron part
GO:0001934	1.95E-03	662	827	positive regulation of protein phosphorylation
GO:0051240	2.00E-03	918	1156	positive regulation of multicellular organismal process
GO:0042995	2.03E-03	1236	1549	cell projection
GO:0010518	2.03E-03	67	73	positive regulation of phospholipase activity
GO:0008015	2.11E-03	334	405	blood circulation
GO:0043506	2.25E-03	66	72	regulation of JUN kinase activity
GO:0051094	2.38E-03	756	945	positive regulation of developmental process
GO:0044712	2.41E-03	693	878	single-organism catabolic process
GO:0008013	2.52E-03	68	75	beta-catenin binding
GO:0070304	2.62E-03	102	117	positive regulation of stress-activated protein kinase signaling cascade
GO:0030166	2.64E-03	47	51	proteoglycan biosynthetic process
GO:0043406	2.68E-03	153	179	positive regulation of MAP kinase activity
GO:0071216	2.74E-03	123	144	cellular response to biotic stimulus
GO:0042312	2.76E-03	34	36	regulation of vasodilation
GO:0032874	2.76E-03	101	116	positive regulation of stress-activated MAPK cascade
GO:0046330	2.79E-03	85	96	positive regulation of JNK cascade
GO:0050878	2.80E-03	466	575	regulation of body fluid levels
GO:0098588	2.81E-03	1494	1925	bounding membrane of organelle
GO:0050790	2.82E-03	1495	1902	regulation of catalytic activity
GO:0006720	2.91E-03	75	86	isoprenoid metabolic process
GO:0043235	2.91E-03	232	276	receptor complex
GO:0046873	2.95E-03	293	351	metal ion transmembrane transporter activity
GO:0044437	2.97E-03	270	327	vacuolar part
GO:0005086	2.99E-03	23	23	ARF guanyl-nucleotide exchange factor activity
GO:0051056	3.06E-03	222	260	regulation of small GTPase mediated signal transduction
GO:0031399	3.07E-03	1162	1476	regulation of protein modification process
GO:0008194	3.14E-03	93	108	UDP-glycosyltransferase activity
GO:0043292	3.14E-03	149	174	contractile fiber
GO:0044093	3.19E-03	1200	1512	positive regulation of molecular function

GO:0004620	3.20E-03	61	68	phospholipase activity
GO:0031641	3.21E-03	31	32	regulation of myelination
GO:0006066	3.22E-03	249	303	alcohol metabolic process
GO:0055085	3.26E-03	895	1129	transmembrane transport
GO:1901701	3.28E-03	710	891	cellular response to oxygen-containing compound
GO:0005604	3.31E-03	77	86	basement membrane
GO:1990778	3.34E-03	155	181	protein localization to cell periphery
GO:0004674	3.35E-03	331	397	protein serine/threonine kinase activity
GO:0019725	3.38E-03	505	629	cellular homeostasis
GO:0065009	3.44E-03	1800	2298	regulation of molecular function
GO:0031253	3.49E-03	213	253	cell projection membrane
GO:0033173	3.50E-03	22	22	calcineurin-NFAT signaling cascade
GO:0051046	3.53E-03	453	560	regulation of secretion
GO:0044710	3.55E-03	3352	4389	single-organism metabolic process
GO:0060191	3.66E-03	83	93	regulation of lipase activity
GO:0018209	3.74E-03	186	219	peptidyl-serine modification
GO:0031256	3.77E-03	106	121	leading edge membrane
GO:0032940	3.77E-03	618	769	secretion by cell
GO:0016772	3.83E-03	646	800	transferase activity transferring phosphorus-containing groups
GO:0072659	3.85E-03	154	180	protein localization to plasma membrane
GO:0031623	3.88E-03	60	67	receptor internalization
GO:0005088	3.90E-03	108	120	Ras guanyl-nucleotide exchange factor activity
GO:0055082	3.94E-03	425	527	cellular chemical homeostasis
GO:0030036	3.95E-03	393	475	actin cytoskeleton organization
GO:0042221	4.00E-03	2507	3242	response to chemical
GO:0099568	4.02E-03	191	226	cytoplasmic region
GO:0048016	4.08E-03	30	31	inositol phosphate-mediated signaling
GO:0008610	4.11E-03	422	527	lipid biosynthetic process
GO:0005089	4.14E-03	68	73	Rho guanyl-nucleotide exchange factor activity
GO:0044449	4.16E-03	139	162	contractile fiber part
GO:0043410	4.23E-03	405	501	positive regulation of MAPK cascade
GO:0007202	4.25E-03	49	53	activation of phospholipase C activity
GO:0042325	4.27E-03	965	1224	regulation of phosphorylation
GO:0005912	4.32E-03	340	411	adherens junction
GO:0045597	4.35E-03	557	692	positive regulation of cell differentiation
GO:0038083	4.35E-03	38	40	peptidyl-tyrosine autophosphorylation
GO:0016757	4.36E-03	181	221	transferase activity transferring glycosyl groups
GO:0098772	4.41E-03	807	1010	molecular function regulator
GO:0006816	4.42E-03	261	314	calcium ion transport
GO:0098602	4.46E-03	499	618	single organism cell adhesion
GO:0019901	4.48E-03	379	460	protein kinase binding
GO:0006812	4.63E-03	659	826	cation transport
GO:0005516	4.71E-03	139	161	calmodulin binding
GO:0030276	4.81E-03	52	57	clathrin binding
GO:0005903	4.83E-03	76	85	brush border
GO:0080135	4.90E-03	437	544	regulation of cellular response to stress
GO:0042127	4.93E-03	945	1204	regulation of cell proliferation
GO:0048878	5.02E-03	644	809	chemical homeostasis
GO:0016787	5.04E-03	1462	1885	hydrolase activity
GO:0050806	5.06E-03	96	110	positive regulation of synaptic transmission
GO:0030201	5.28E-03	27	28	heparan sulfate proteoglycan metabolic process
GO:0098797	5.34E-03	350	425	plasma membrane protein complex
GO:0008047	5.41E-03	312	379	enzyme activator activity
GO:0050840	5.43E-03	37	40	extracellular matrix binding
GO:0006887	5.56E-03	251	303	exocytosis

GO:0001523	5.56E-03	52	58	retinoid metabolic process
GO:0060078	5.57E-03	58	63	regulation of postsynaptic membrane potential
GO:0007009	5.58E-03	198	234	plasma membrane organization
GO:1901136	5.58E-03	125	148	carbohydrate derivative catabolic process
GO:0005938	5.58E-03	176	208	cell cortex
GO:0009628	5.70E-03	766	970	response to abiotic stimulus
GO:1900274	5.77E-03	58	64	regulation of phospholipase C activity
GO:0018105	5.92E-03	177	209	peptidyl-serine phosphorylation
GO:0009611	5.99E-03	662	831	response to wounding
GO:0008289	6.03E-03	418	517	lipid binding
GO:0009653	6.08E-03	1811	2310	anatomical structure morphogenesis
GO:1902533	6.11E-03	649	817	positive regulation of intracellular signal transduction
GO:0007610	6.24E-03	503	622	behavior
GO:0044420	6.32E-03	98	112	extracellular matrix component
GO:0045807	6.32E-03	81	93	positive regulation of endocytosis
GO:0006955	6.33E-03	995	1277	immune response
GO:0044877	6.35E-03	943	1187	macromolecular complex binding
GO:0048771	6.36E-03	104	122	tissue remodeling
GO:0070161	6.37E-03	351	426	anchoring junction
GO:0030100	6.49E-03	139	164	regulation of endocytosis
GO:0072511	6.51E-03	292	356	divalent inorganic cation transport
GO:0042060	6.52E-03	474	588	wound healing
GO:0031410	6.62E-03	810	1027	cytoplasmic vesicle
GO:0051020	6.63E-03	207	246	GTPase binding
GO:0072358	6.72E-03	638	797	cardiovascular system development
GO:0072359	6.72E-03	638	797	circulatory system development
GO:0098862	6.74E-03	102	117	cluster of actin-based cell projections
GO:0001948	6.77E-03	72	81	glycoprotein binding
GO:0044765	6.93E-03	2441	3159	single-organism transport
GO:0000187	6.95E-03	98	113	activation of MAPK activity
GO:0031401	7.05E-03	795	1005	positive regulation of protein modification process
GO:0007272	7.06E-03	86	98	ensheathment of neurons
GO:0008366	7.06E-03	86	98	axon ensheathment
GO:0031526	7.09E-03	40	43	brush border membrane
GO:0065007	7.12E-03	6550	8610	biological regulation
GO:0043236	7.17E-03	24	25	laminin binding
GO:0033003	7.21E-03	26	27	regulation of mast cell activation
GO:0046916	7.30E-03	69	80	cellular transition metal ion homeostasis
GO:0050650	7.33E-03	25	26	chondroitin sulfate proteoglycan biosynthetic process
GO:0031674	7.37E-03	91	103	I band
GO:0002761	7.38E-03	77	88	regulation of myeloid leukocyte differentiation
GO:0030316	7.52E-03	64	72	osteoclast differentiation
GO:0007268	7.54E-03	500	614	synaptic transmission
GO:0099536	7.54E-03	500	614	synaptic signaling
GO:0099537	7.54E-03	500	614	trans-synaptic signaling
GO:0001817	7.59E-03	364	458	regulation of cytokine production
GO:0071219	7.63E-03	108	127	cellular response to molecule of bacterial origin
GO:0030425	7.67E-03	346	419	dendrite
GO:0010863	7.78E-03	56	62	positive regulation of phospholipase C activity
GO:0070838	7.84E-03	290	354	divalent metal ion transport
GO:0045017	7.88E-03	190	229	glycerolipid biosynthetic process
GO:0060589	7.89E-03	227	271	nucleoside-triphosphatase regulator activity
GO:0016337	7.92E-03	465	578	single organismal cell-cell adhesion
GO:2000036	8.04E-03	19	19	regulation of stem cell population maintenance
GO:0046578	8.05E-03	149	172	regulation of Ras protein signal transduction

GO:0010043	8.05E-03	37	41	response to zinc ion
GO:0046486	8.08E-03	253	309	glycerolipid metabolic process
GO:0010506	8.25E-03	144	172	regulation of autophagy
GO:0060193	8.25E-03	73	82	positive regulation of lipase activity
GO:0022617	8.25E-03	94	109	extracellular matrix disassembly
GO:0005576	8.31E-03	2522	3309	extracellular region
GO:0030018	8.32E-03	81	91	Z disc
GO:0006836	8.36E-03	141	165	neurotransmitter transport
GO:0006721	8.41E-03	61	70	terpenoid metabolic process
GO:0016298	8.45E-03	69	79	lipase activity
GO:0042641	8.57E-03	52	56	actomyosin
GO:0005856	8.57E-03	1256	1598	cytoskeleton
GO:0045216	8.59E-03	167	197	cell-cell junction organization
GO:0004629	8.61E-03	25	26	phospholipase C activity
GO:0002448	8.68E-03	31	33	mast cell mediated immunity
GO:0031267	8.87E-03	190	225	small GTPase binding
GO:0042578	8.90E-03	234	286	phosphoric ester hydrolase activity
GO:0050865	8.92E-03	301	372	regulation of cell activation
GO:0001725	9.06E-03	44	47	stress fiber
GO:0097517	9.06E-03	44	47	contractile actin filament bundle
GO:1903530	9.17E-03	413	513	regulation of secretion by cell
GO:0030017	9.19E-03	125	146	sarcomere
GO:0071214	9.22E-03	201	246	cellular response to abiotic stimulus
GO:0005615	9.25E-03	712	921	extracellular space
GO:0071222	9.30E-03	103	121	cellular response to lipopolysaccharide
GO:0045670	9.36E-03	45	50	regulation of osteoclast differentiation
GO:0071495	9.37E-03	905	1148	cellular response to endogenous stimulus
GO:0010038	9.54E-03	220	269	response to metal ion
GO:0005102	9.56E-03	874	1116	receptor binding
GO:0008233	9.57E-03	366	461	peptidase activity
GO:0010975	9.61E-03	296	355	regulation of neuron projection development
GO:0010447	9.81E-03	16	16	response to acidic pH
GO:0043168	9.84E-03	1718	2202	anion binding
GO:0016788	9.92E-03	432	544	hydrolase activity acting on ester bonds