

GO_Enrich_mfment_C4_wk5_wk11

	ID	Description	GeneRatio	BgRatio	RichFactor	FoldEnrichment	zScore	pvalue	p.adjust	qvalue
GO:0003735	GO:0003735	structural constituent of ribosome	17/400	167/9272	0.1017964071856287	2.35964071856287	3.76465291702607	0.000856885104136053	0.275423904276247	0.274803032983651
GO:0016628	GO:0016628	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	5/400	19/9272	0.263157894736842		6.1	4.7248520629707	0.275423904276247	0.274803032983651
GO:0016229	GO:0016229	protein dehydrogenase activity	5/400	21/9272	0.238095238095238	5.51904761904762	4.4019463404164	0.00167168030323422	0.299230774278925	0.298556236612707
GO:0002091	GO:0002091	protein serine/threonine kinase inhibitor activity	5/400	23/9272	0.217391304347826	5.03913043478261	4.11800553383336	0.00257459991605179	0.335096870097051	0.33434148168068
GO:0004869	GO:0004869	cysteine-type endopeptidase inhibitor activity	4/400	15/9272	0.266666666666667	6.18133333333333	4.26417039030028	0.00318768318281533	0.335096870097051	0.33434148168068
GO:0003764	GO:0003764	steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	4/400	16/9272		0.25	5.795	4.07586179537489	0.00410727059452975	0.335096870097051
GO:0004860	GO:0004860	protein kinase inhibitor activity	6/400	37/9272	0.162162162162162	3.75881891891892	3.57029308764066	0.0046339170529763	0.335096870097051	0.33434148168068
GO:0016620	GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	5/400	28/9272	0.178571428571429	4.13928571428571	3.53233927904723	0.00629889536194111	0.335096870097051	0.33434148168068
GO:0051537	GO:0051537	2 iron, 2 sulfur cluster binding	4/400	18/9272	0.222222222222222	5.15111111111111	3.74298755139829	0.00644989179406967	0.335096870097051	0.33434148168068
GO:0140678	GO:0140678	molecular function inhibitor activity	18/400	220/9272	0.0818181818181818	1.89654545454545	2.85755040948378	0.00679994550166556	0.335096870097051	0.33434148168068
GO:0019210	GO:0019210	kinase inhibitor activity	6/400	40/9272		0.15	3.477	0.00686418169658764	0.335096870097051	0.33434148168068
GO:0004303	GO:0004303	estradiol 17-beta-dehydrogenase [NAD(P)+] activity	3/400	10/9272		0.3	6.954	0.00762272703751098	0.341117034928616	0.340348075622201
GO:0051536	GO:0051536	iron-sulfur cluster binding	6/400	47/9272	0.127659574468085	2.95914893617021	2.85801025984422	0.0149250953586759	0.546102458922216	0.54487141348899
GO:0051540	GO:0051540	metal cluster binding	6/400	47/9272	0.127659574468085	2.95914893617021	2.85901025984422	0.0149250953586759	0.546102458922216	0.54487141348899
GO:0016627	GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	5/400	35/9272	0.142857142857143	3.31142857142857	2.90891845708105	0.0162712092043863	0.546102458922216	0.54487141348899
GO:0033293	GO:0033293	monocarboxylic acid binding	5/400	35/9272	0.142857142857143	3.31142857142857	2.90891845708105	0.0162712092043863	0.546102458922216	0.54487141348899
GO:0016903	GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	5/400	36/9272	0.138888888888889	3.21944444444444	2.83293158472879	0.0182462847349054	0.546171559459812	0.544940358257463
GO:0004857	GO:0004857	enzyme inhibitor activity	14/400	175/9272		0.08	1.8544	0.0190360102914586	0.546171559459812	0.544940358257463
GO:0008139	GO:0008139	nuclear localization sequence binding	3/400	14/9272	0.214285714285714	4.96714285714286	3.15402975772025	0.0203415850823021	0.546171559459812	0.544940358257463
GO:0008373	GO:0008373	sialyltransferase activity	3/400	14/9272	0.214285714285714	4.96714285714286	3.15402975772025	0.0203415850823021	0.546171559459812	0.544940358257463
GO:0019207	GO:0019207	kinase regulator activity	12/400	146/9272	0.0821917808219178	1.90520547945205	2.34080851990364	0.0238165672279239	0.575058370400103	0.573762051423409
GO:0005504	GO:0005504	fatty acid binding	4/400	26/9272	0.153846153846154	3.56615384615385	2.78211410914924	0.024034263972541	0.575058370400103	0.573762051423409
GO:0061608	GO:0061608	nuclear import signal receptor activity	3/400	15/9272		0.2	4.636	0.0246300605571739	0.575058370400103	0.573762051423409
GO:0140101	GO:0140101	catalytic activity, acting on a tRNA	7/400	71/9272	0.0885915492957746	2.28535211267606	2.3084277923252	0.0327802021329598	0.70211892915428	0.70053618531712
GO:0004022	GO:0004022	alcohol dehydrogenase (NAD+) activity	3/400	17/9272	0.176470588235294	4.09058823529412	2.70807018554782	0.0345465402675122	0.70211892915428	0.70053618531712
GO:0008138	GO:0008138	protein tyrosine/serine/threonine phosphatase activity	3/400	17/9272	0.176470588235294	4.09058823529412	2.70807018554782	0.0345465402675122	0.70211892915428	0.70053618531712
GO:0140104	GO:0140104	molecular carrier activity	6/400	57/9272	0.105263157894737		2.44	0.035302069036323	0.70211892915428	0.70053618531712
GO:0003725	GO:0003725	double-stranded RNA binding	5/400	44/9272	0.113636363636364	2.63409090909091	2.30691333172557	0.0398019805826475	0.763345127602917	0.761624365284495
GO:0003899	GO:0003899	DNA-directed 5'-3' RNA polymerase activity	3/400	20/9272		0.15	3.477	0.0526886401794249	0.799737187918662	0.797934389200429
GO:0034062	GO:0034062	5'-3' RNA polymerase activity	3/400	20/9272		0.15	3.477	0.0526886401794249	0.799737187918662	0.797934389200429
GO:0097747	GO:0097747	RNA polymerase activity	3/400	20/9272		0.15	3.477	0.0526886401794249	0.799737187918662	0.797934389200429
GO:0002020	GO:0002020	protease binding	6/400	63/9272	0.0952380952380952	2.20761904761905	2.04209788197927	0.0534586654027199	0.799737187918662	0.797934389200429
GO:0016765	GO:0016765	transferase activity, transferring alkyl or aryl (other than methyl) groups	5/400	48/9272	0.104166666666667	2.41458333333333	2.08627727786522	0.0546717003497153	0.799737187918662	0.797934389200429
GO:0001056	GO:0001056	RNA polymerase III activity	2/400	10/9272		0.2	4.636	0.0664286281512751	0.799737187918662	0.797934389200429
GO:0004030	GO:0004030	aldehyde dehydrogenase [NAD(P)+] activity	2/400	10/9272		0.2	4.636	0.0664286281512751	0.799737187918662	0.797934389200429
GO:0004056	GO:0004056	estrogen response element binding	2/400	10/9272		0.2	4.636	0.0664286281512751	0.799737187918662	0.797934389200429
GO:0099528	GO:0099528	G protein-coupled neurotransmitter receptor activity	2/400	10/9272		0.2	4.636	0.0664286281512751	0.799737187918662	0.797934389200429
GO:0140142	GO:0140142	neurocytoplasmic carrier activity	3/400	22/9272	0.136363636363636	3.16090909090909	2.1545645233229	0.0668522570914839	0.799737187918662	0.797934389200429
GO:0140640	GO:0140640	catalytic activity, acting on a nucleic acid	21/400	344/9272	0.061046511627907	1.41505813953488	1.66568772453337	0.068226890809918	0.799737187918662	0.797934389200429
GO:0004386	GO:0004386	helicase activity	7/400	84/9272	0.0833333333333333	1.93166666666667	1.82126116388005	0.0699572095648657	0.799737187918662	0.797934389200429
GO:0051117	GO:0051117	ATPase binding	3/400	23/9272	0.130434782608696	3.02347826086956	2.0629922330037	0.074517435896405	0.799737187918662	0.797934389200429
GO:0005338	GO:0005338	nucleotide-sugar transmembrane transporter activity	2/400	11/9272	0.181818181818182	4.21454545454545	2.26500670144844	0.0789350584272511	0.799737187918662	0.797934389200429
GO:0032977	GO:0032977	membrane insertase activity	2/400	11/9272	0.181818181818182	4.21454545454545	2.26500670144844	0.0789350584272511	0.799737187918662	0.797934389200429
GO:0033549	GO:0033549	MAP kinase phosphatase activity	2/400	11/9272	0.181818181818182	4.21454545454545	2.26500670144844	0.0789350584272511	0.799737187918662	0.797934389200429
GO:1904047	GO:1904047	S-adenosyl-L-methionine binding	2/400	11/9272	0.181818181818182	4.21454545454545	2.26500670144844	0.0789350584272511	0.799737187918662	0.797934389200429
GO:0004175	GO:0004175	endopeptidase activity	13/400	196/9272	0.0663265306122449	1.53744897959184	1.61473238059335	0.0814039256172403	0.799737187918662	0.797934389200429
GO:0016462	GO:0016462	pyrophosphatase activity	25/400	432/9272	0.0578703703703704	1.34143518518519	1.54314428234237	0.0816893730674613	0.799737187918662	0.797934389200429
GO:0140223	GO:0140223	general transcription initiation factor activity	3/400	24/9272		0.125	2.8975	0.0825522800384586	0.799737187918662	0.797934389200429
GO:0008287	GO:0008287	protein kinase regulator activity	9/400	123/9272	0.0731707317073171	1.69609756097561	1.65013081160926	0.083948085542923	0.799737187918662	0.797934389200429
GO:0016818	GO:0016818	inhibase activity, acting on acid anhydrides, in phosphorus-containing anhydrides	25/400	435/9272	0.05747712643678161	1.33218390804598	1.50679201738015	0.0867882134849953	0.799737187918662	0.797934389200429
GO:0005176	GO:0005176	integrin binding	5/400	55/9272	0.0909090909090909	2.10727272727273	1.7487367715206	0.0874242757054501	0.799737187918662	0.797934389200429
GO:0016817	GO:0016817	hydrolase activity, acting on acid anhydrides	25/400	436/9272	0.0573394495412844	1.32912844036697	1.49473196642635	0.0885341783617962	0.799737187918662	0.797934389200429
GO:0042605	GO:0042605	peptide antigen binding	3/400	25/9272		0.12	2.7816	1.8932991700563	0.0909412866670114	0.799737187918662
GO:0003707	GO:0003707	nuclear steroid receptor activity	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0003925	GO:0003925	G protein activity	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0004190	GO:0004190	aspartic-type endopeptidase activity	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0030331	GO:0030331	nuclear estrogen receptor binding	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0043236	GO:0043236	laminin binding	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0046935	GO:0046935	1-phosphatidylinositol-3-kinase regulator activity	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0007001	GO:0007001	aspartic-type peptidase activity	2/400	12/9272	0.166666666666667	3.86333333333333	2.10736400815137	0.092100908841847	0.799737187918662	0.797934389200429
GO:0008017	GO:0008017	microtubule binding	9/400	126/9272	0.0714285714285714	1.65571428571429	1.57350033311618	0.0941473089419579	0.799737187918662	0.797934389200429
GO:0044183	GO:0044183	protein folding chaperone	4/400	41/9272	0.0975609756097561	2.26146341463415	1.71879757388132	0.0989735948678618	0.799737187918662	0.797934389200429
GO:0003777	GO:0003777	microtubule motor activity	3/400	26/9272	0.115384615384615	2.67461538461538	1.81554628765525	0.0996862898271597	0.799737187918662	0.797934389200429
GO:0004601	GO:0004601	peroxidase activity	3/400	26/9272	0.115384615384615	2.67461538461538	1.81554628765525	0.0996862898271597	0.799737187918662	0.797934389200429
GO:0014057	GO:0014057	ATP-dependent activity	18/400	303/9272	0.0594050405940594	1.3770297029703	1.41679621450457	0.10497768236615	0.799737187918662	0.797934389200429

GO:0016493	GO:0016493	C-C chemokine receptor activity	2/400	22/9272	0.0909090909090909	2.10727272727273	1.10402166720266	0.245000256890349	0.900261473516303	0.898232069038123
GO:0019706	GO:0019706	protein-cysteine S-palmitoyltransferase activity	2/400	22/9272	0.0909090909090909	2.10727272727273	1.10402166720266	0.245000256890349	0.900261473516303	0.898232069038123
GO:0019707	GO:0019707	protein-cysteine S-acyltransferase activity	2/400	22/9272	0.0909090909090909	2.10727272727273	1.10402166720266	0.245000256890349	0.900261473516303	0.898232069038123
GO:0019957	GO:0019957	C-C chemokine binding	2/400	22/9272	0.0909090909090909	2.10727272727273	1.10402166720266	0.245000256890349	0.900261473516303	0.898232069038123
GO:0042887	GO:0042887	amide transmembrane transporter activity	2/400	22/9272	0.0909090909090909	2.10727272727273	1.10402166720266	0.245000256890349	0.900261473516303	0.898232069038123
GO:0016209	GO:0016209	antioxidant activity	3/400	40/9272		0.075	1.7385	0.993836898617977	0.247698567996131	0.900261473516303
GO:0005509	GO:0005509	calcium ion binding	18/400	349/9272	0.0515759312320917	1.195530089595989	0.790593751987256	0.248871679478783	0.900261473516303	0.898232069038123
GO:0030414	GO:0030414	peptidase inhibitor activity	5/400	79/9272	0.0632911392405063	1.46708860759494	0.885251579033871	0.254320874010986	0.900261473516303	0.898232069038123
GO:0003727	GO:0003727	single-stranded RNA binding	3/400	41/9272	0.0731707317073171	1.69609756097561	0.948462543669234	0.259440013257324	0.900261473516303	0.898232069038123
GO:0001637	GO:0001637	G protein-coupled chemoattractant receptor activity	2/400	23/9272	0.0869565217391304	2.01565217391304	1.03548556803388	0.261236716032893	0.900261473516303	0.898232069038123
GO:0004364	GO:0004364	glutathione transferase activity	2/400	23/9272	0.0869565217391304	2.01565217391304	1.03548556803388	0.261236716032893	0.900261473516303	0.898232069038123
GO:0004950	GO:0004950	chemokine receptor activity	2/400	23/9272	0.0869565217391304	2.01565217391304	1.03548556803388	0.261236716032893	0.900261473516303	0.898232069038123
GO:0016893	GO:0016893	endonuclease activity, active with either ribo- or deoxyribonucleic acids and producing 5'-phosphor	2/400	23/9272	0.0869565217391304	2.01565217391304	1.03548556803388	0.261236716032893	0.900261473516303	0.898232069038123
GO:0050840	GO:0050840	extracellular matrix binding	2/400	23/9272	0.0869565217391304	2.01565217391304	1.03548556803388	0.261236716032893	0.900261473516303	0.898232069038123
GO:0016829	GO:0016829	lyase activity	7/400	121/9272	0.0578512396694215	1.34099173553719	0.801649969598801	0.267135531767493	0.900261473516303	0.898232069038123
GO:0008168	GO:0008168	methyltransferase activity	8/400	142/9272	0.0563380281690141	1.305915498296775	0.779996717900616	0.26976269395892	0.900261473516303	0.898232069038123
GO:0009092	GO:0009092	cytoskeletal protein binding	21/400	420/9272		0.05	1.159	0.70082052341155	0.271735959619865	0.900261473516303
GO:0019205	GO:0019205	nucleobase-containing compound kinase activity	2/400	24/9272	0.0833333333333333	1.93166666666667	0.970341905687735	0.27748075566875	0.900261473516303	0.898232069038123
GO:0051539	GO:0051539	4 iron, 4 sulfur cluster binding	2/400	24/9272	0.0833333333333333	1.93166666666667	0.970341905687735	0.27748075566875	0.900261473516303	0.898232069038123
GO:0097110	GO:0097110	scaffold protein binding	2/400	24/9272	0.0833333333333333	1.93166666666667	0.970341905687735	0.27748075566875	0.900261473516303	0.898232069038123
GO:0019956	GO:0019956	chemokine binding	2/400	25/9272		0.08	1.8544	0.908266580793035	0.293701579060206	0.900261473516303
GO:0051427	GO:0051427	hormone receptor binding	2/400	25/9272		0.08	1.8544	0.908266580793035	0.293701579060206	0.900261473516303
GO:0090905	GO:0090905	ligand-gated monoatomic anion channel activity	2/400	25/9272		0.08	1.8544	0.908266580793035	0.293701579060206	0.900261473516303
GO:0016491	GO:0016491	oxidoreductase activity	22/400	449/9272	0.0489977728285078	1.13576837416481	0.626175639307816	0.297588911739493	0.900261473516303	0.898232069038123
GO:0004843	GO:0004843	cysteine-type deubiquitinase activity	2/400	64/9272		0.0625	1.44875	0.764881774788806	0.2979554866814	0.900261473516303
GO:0005254	GO:0005254	chloride channel activity	3/400	45/9272	0.0666666666666667	1.54533333333333	0.778611046276261	0.306979662912246	0.900261473516303	0.898232069038123
GO:1901681	GO:1901681	sulfur compound binding	6/400	106/9272	0.056063735849057	1.31207547169811	0.686128029604982	0.307425461893385	0.900261473516303	0.898232069038123
GO:0016417	GO:0016417	S-acyltransferase activity	2/400	26/9272	0.0769230769230769	1.78307692307692	0.84897846616125	0.309871019846293	0.900261473516303	0.898232069038123
GO:0014062	GO:0014062	ATP-dependent protein folding chaperone	2/400	26/9272	0.0769230769230769	1.78307692307692	0.84897846616125	0.309871019846293	0.900261473516303	0.898232069038123
GO:0061135	GO:0061135	endopeptidase regulator activity	5/400	86/9272	0.0581395348837209	1.34767441860465	0.687766885739955	0.313138989443308	0.900261473516303	0.898232069038123
GO:0042393	GO:0042393	histone binding	7/400	128/9272		0.0546875	1.26765625	0.647439911323074	0.315133378772238	0.900261473516303
GO:0003724	GO:0003724	RNA helicase activity	3/400	46/9272	0.0652173913043478	1.51173913043478	0.738759939676926	0.318941123656264	0.900261473516303	0.898232069038123
GO:0008186	GO:0008186	ATP-dependent activity, acting on RNA	3/400	46/9272	0.0652173913043478	1.51173913043478	0.738759939676926	0.318941123656264	0.900261473516303	0.898232069038123
GO:1990841	GO:1990841	promoter-specific chromatin binding	2/400	27/9272	0.0740740740740741	1.71703703703704	0.79223227771557	0.325996373356818	0.900261473516303	0.898232069038123
GO:0016791	GO:0016791	phosphatase activity	9/400	174/9272	0.0517241379310345	1.19896651724138	0.562551118847391	0.336666751583474	0.900261473516303	0.898232069038123
GO:0015108	GO:0015108	chloride transmembrane transporter activity	4/400	68/9272	0.0588232941176471	1.36352941176471	0.638834298033612	0.373425114190728	0.900261473516303	0.898232069038123
GO:0014296	GO:0014296	general transcription initiation factor binding	2/400	28/9272	0.0714285714285714	1.65571428571429	0.737812845998984	0.341955237527494	0.900261473516303	0.898232069038123
GO:0019209	GO:0019209	kinase activator activity	4/400	69/9272	0.0579714474927536	1.343376811594203	0.608566368338006	0.347338158809361	0.900261473516303	0.898232069038123
GO:0004602	GO:0004602	glutathione peroxidase activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0004675	GO:0004675	transmembrane receptor protein serine/threonine kinase activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0005112	GO:0005112	Notch binding	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0005372	GO:0005372	water transmembrane transporter activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0008195	GO:0008195	phosphatidate phosphatase activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0008252	GO:0008252	nucleotidase activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0016594	GO:0016594	glycine binding	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0016849	GO:0016849	phosphorus-oxygen lyase activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0022851	GO:0022851	GABA-gated chloride ion channel activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0042813	GO:0042813	Wnt receptor activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0043014	GO:0043014	alpha-tubulin binding	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0005015	GO:0005015	nucleoside monophosphate kinase activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0051959	GO:0051959	dynein light intermediate chain binding	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0071889	GO:0071889	14-3-3 protein binding	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:00140311	GO:00140311	protein sequestering activity	1/400	10/9272		0.1	2.318	0.885412281099774	0.356740801625184	0.900261473516303
GO:0010005	GO:0010005	deubiquitinase activity	4/400	70/9272	0.0571428571428571	1.32457142857143	0.578762937461125	0.357258554773103	0.900261473516303	0.898232069038123
GO:0014909	GO:0014909	palmitoyltransferase activity	2/400	29/9272	0.068965172413793	1.59862068965517	0.685530473502713	0.357825362904943	0.900261473516303	0.898232069038123
GO:0016667	GO:0016667	oxidoreductase activity, acting on a sulfur group of donors	2/400	29/9272	0.068965172413793	1.59862068965517	0.685530473502713	0.357825362904943	0.900261473516303	0.898232069038123
GO:0016922	GO:0016922	nuclear receptor binding	3/400	50/9272		0.06	1.3908	0.588314453220935	0.36672926639525	0.900261473516303
GO:0003746	GO:0003746	translation elongation factor activity	2/400	30/9272	0.0666666666666667	1.54533333333333	0.635217142068811	0.373554511256369	0.900261473516303	0.898232069038123
GO:0005544	GO:0005544	calcium-dependent phospholipid binding	2/400	30/9272	0.0666666666666667	1.54533333333333	0.635217142068811	0.373554511256369	0.900261473516303	0.898232069038123
GO:0016763	GO:0016763	pentosyltransferase activity	2/400	30/9272	0.0666666666666667	1.54533333333333	0.635217142068811	0.373554511256369	0.900261473516303	0.898232069038123
GO:0032813	GO:0032813	tumor necrosis factor receptor superfamily binding	2/400	30/9272	0.0666666666666667	1.54533333333333	0.635217142068811	0.373554511256369	0.900261473516303	0.898232069038123
GO:0005090	GO:0005090	ATPase regulator activity	2/400	30/9272	0.0666666666666667	1.54533333333333	0.635217142068811	0.373554511256369	0.900261473516303	0.898232069038123
GO:0016705	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	6/400	115/9272	0.0521739130434783	1.20939130434783	0.479748333659316	0.376952219051115	0.900261473516303	0.898232069038123
GO:0003697	GO:0003697	single-stranded DNA binding	3/400	51/9272	0.0588232941176471	1.36352941176471	0.582736507864914	0.378607560171543	0.900261473516303	0.898232069038123
GO:0001091	GO:0001091	RNA polymerase II general transcription initiation factor binding	1/400	11/9272	0.0909090909090909	2.10727272727273	0.780197444107525	0.384521375944978	0.900261473516303	0.898232069038123
GO:0004550	GO:0004550	nucleoside diphosphate kinase activity	1/400	11/9272	0.0909090909090909	2.10727272727273	0.780197444107525	0.384521375944978	0.900261473516303	0.898232069038123
GO:0004953	GO:0004953	isocanoid receptor activity	1/400	11/9272	0.0909090909090909	2.10727272727273	0.780197444107525	0.384521375944978	0.900261473516303	0.898232069038123
GO:0005217	GO:0005217									

GO:0005416	GO:0005416	amino acid:monatomic cation symporter activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0008266	GO:0008266	poly(U) RNA binding	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0015035	GO:0015035	protein-disulfide reductase activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0015144	GO:0015144	carbohydrate transmembrane transporter activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0015377	GO:0015377	chloride:monatomic cation symporter activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0016411	GO:0016411	acylglycerol O-acyltransferase activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0016799	GO:0016799	hydrolase activity, hydrolyzing N-glycosyl compounds	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0017080	GO:0017080	sodium channel regulator activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0030371	GO:0030371	translation repressor activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0071617	GO:0071617	lysophospholipid acyltransferase activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:1990380	GO:1990380	K48-linked deubiquitinase activity	1/400	14/9272	0.0714285714285714	1.65571428571429	0.521317849137772	0.460885293170323	0.900261473516303	0.898232069038123
GO:0016747	GO:0016747	acyltransferase activity, transferring groups other than amino-acyl groups	7/400	14/9272	0.0469798657718121	1.0889932885906	0.232522011912099	0.464089791087297	0.900261473516303	0.898232069038123
GO:0016796	GO:0016796	exonuclease activity, active with either rbo- or deoxyribonucleic acids and producing 5'-phosphom	2/400	36/9272	0.0555555555555556	1.287777777777778	0.36732379496608	0.464112948357564	0.900261473516303	0.898232069038123
GO:0019003	GO:0019003	GDP binding	2/400	36/9272	0.0555555555555556	1.287777777777778	0.36732379496608	0.464112948357564	0.900261473516303	0.898232069038123
GO:0044389	GO:0044389	ubiquitin-like protein ligase binding	7/400	151/9272	0.0463576158940397	1.07456953642384	0.196160341375716	0.478117657520702	0.900261473516303	0.898232069038123
GO:0008289	GO:0008289	lipid binding	17/400	381/9272	0.0446194225721785	1.0342782152231	0.145073438126926	0.479041973122833	0.900261473516303	0.898232069038123
GO:0008201	GO:0008201	heparin binding	3/400	60/9272		0.05	1.159	0.262348330297274	0.900261473516303	0.898232069038123
GO:0051087	GO:0051087	protein-folding chaperone binding	3/400	60/9272		0.05	1.159	0.262348330297274	0.900261473516303	0.898232069038123
GO:0001530	GO:0001530	lipopolysaccharide binding	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0004890	GO:0004890	GABA-A receptor activity	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0015296	GO:0015296	monatomic anion:monatomic cation symporter activity	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0038187	GO:0038187	pattern recognition receptor activity	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0043325	GO:0043325	phosphatidylinositol-3,4-bisphosphate binding	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0045125	GO:0045125	bioactive lipid receptor activity	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0140272	GO:0140272	exocytic protein binding	1/400	15/9272	0.0666666666666667	1.545333333333333	0.448802287604944	0.484178216342917	0.900261473516303	0.898232069038123
GO:0005126	GO:0005126	cytokine receptor binding	7/400	153/9272	0.0457516339869281	1.06052287561699	0.160278099098745	0.492047785035226	0.900261473516303	0.898232069038123
GO:0005262	GO:0005262	calcium channel activity	2/400	38/9272	0.0526315789473684		1.22	0.288537366509412	0.900261473516303	0.898232069038123
GO:0008013	GO:0008013	beta-catenin binding	2/400	38/9272	0.0526315789473684		1.22	0.288537366509412	0.900261473516303	0.898232069038123
GO:0017018	GO:0017018	myosin phosphatase activity	2/400	38/9272	0.0526315789473684		1.22	0.288537366509412	0.900261473516303	0.898232069038123
GO:0045182	GO:0045182	translation regulator activity	5/400	108/9272	0.0462962962962963	1.07314814814815	0.162351084079482	0.501212459835603	0.900261473516303	0.898232069038123
GO:0047722	GO:0047722	protein serine/threonine phosphatase activity	3/400	62/9272	0.0483870967741935	1.12161290322581	0.20399078504082	0.504366126490023	0.900261473516303	0.898232069038123
GO:0030594	GO:0030594	neurotransmitter receptor activity	3/400	62/9272	0.0483870967741935	1.12161290322581	0.20399078504082	0.504366126490023	0.900261473516303	0.898232069038123
GO:0008080	GO:0008080	N-acetyltransferase activity	2/400	39/9272	0.0512820512820513	1.18871794871795	0.250759048169104	0.506435179852338	0.900261473516303	0.898232069038123
GO:0008374	GO:0008374	O-acetyltransferase activity	2/400	39/9272	0.0512820512820513	1.18871794871795	0.250759048169104	0.506435179852338	0.900261473516303	0.898232069038123
GO:0001223	GO:0001223	transcription coactivator binding	1/400	14/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0005231	GO:0005231	excitatory extracellular ligand-gated monoatomic ion channel activity	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0008187	GO:0008187	poly-pyrimidine tract binding	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0008649	GO:0008649	rRNA methyltransferase activity	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0016645	GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0016702	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporat	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0016917	GO:0016917	GABA receptor activity	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0036002	GO:0036002	pre-mRNA binding	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0061631	GO:0061631	ubiquitin conjugating enzyme activity	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0140102	GO:0140102	catalytic activity, acting on a rRNA	1/400	16/9272		0.0625	1.44875	0.38144796260156	0.900261473516303	0.898232069038123
GO:0008509	GO:0008509	monatomic anion transmembrane transporter activity	4/400	86/9272	0.0465116279069767	1.07813953488372	0.154575032514131	0.511877851900397	0.900261473516303	0.898232069038123
GO:0008234	GO:0008234	cysteine-type peptidase activity	5/400	110/9272	0.0454545454545455	1.05363636363636	0.120155331225936	0.51757959970904	0.900261473516303	0.898232069038123
GO:0046873	GO:0046873	metal ion transmembrane transporter activity	10/400	227/9272	0.0440528634361234	1.02114537444934	0.068486747683904	0.5193555067750789	0.900261473516303	0.898232069038123
GO:0016811	GO:0016811	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	2/400	40/9272		0.05	1.159	0.213974362778684	0.900261473516303	0.898232069038123
GO:0098960	GO:0098960	postsynaptic neurotransmitter receptor activity	2/400	40/9272		0.05	1.159	0.213974362778684	0.900261473516303	0.898232069038123
GO:0003713	GO:0003713	transcription coactivator activity	5/400	111/9272	0.0450450450450405	1.04414414414414	0.099344920988196	0.525678254310764	0.900261473516303	0.898232069038123
GO:0004721	GO:0004721	phosphoprotein phosphatase activity	5/400	111/9272	0.0450450450450405	1.04414414414414	0.099344920988196	0.525678254310764	0.900261473516303	0.898232069038123
GO:0140097	GO:0140097	catalytic activity, acting on DNA	5/400	111/9272	0.0450450450450405	1.04414414414414	0.099344920988196	0.525678254310764	0.900261473516303	0.898232069038123
GO:0008171	GO:0008171	O-methyltransferase activity	1/400	17/9272	0.0588232941176471	1.36352941176471	0.318535853572241	0.527795282263834	0.900261473516303	0.898232069038123
GO:0008378	GO:0008378	galactosyltransferase activity	1/400	17/9272	0.0588232941176471	1.36352941176471	0.318535853572241	0.527795282263834	0.900261473516303	0.898232069038123
GO:0016701	GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen	1/400	17/9272	0.0588232941176471	1.36352941176471	0.318535853572241	0.527795282263834	0.900261473516303	0.898232069038123
GO:0017025	GO:0017025	TBP-class protein binding	1/400	17/9272	0.0588232941176471	1.36352941176471	0.318535853572241	0.527795282263834	0.900261473516303	0.898232069038123
GO:0031624	GO:0031624	ubiquitin conjugating enzyme binding	1/400	17/9272	0.0588232941176471	1.36352941176471	0.318535853572241	0.527795282263834	0.900261473516303	0.898232069038123
GO:0034237	GO:0034237	protein kinase A regulatory subunit binding	1/400	17/9272	0.0588232941176471	1.36352941176471	0.318535853572241	0.527795282263834	0.900261473516303	0.898232069038123
GO:0016798	GO:0016798	hydrolase activity, acting on glycosyl bonds	3/400	65/9272	0.0461538461538462	1.06984615384615	0.119983802836964	0.536411082053942	0.900261473516303	0.898232069038123
GO:0030295	GO:0030295	protein kinase activator activity	3/400	65/9272	0.0461538461538462	1.06984615384615	0.119983802836964	0.536411082053942	0.900261473516303	0.898232069038123
GO:0001221	GO:0001221	transcription coregulator binding	2/400	42/9272	0.0476190476190476	1.10380952380952	0.143167194027656	0.546525906432545	0.900261473516303	0.898232069038123
GO:0004521	GO:0004521	RNA endonuclease activity	2/400	42/9272	0.0476190476190476	1.10380952380952	0.143167194027656	0.546525906432545	0.900261473516303	0.898232069038123
GO:0005230	GO:0005230	extracellular ligand-gated monoatomic ion channel activity	2/400	42/9272	0.0476190476190476	1.10380952380952	0.143167194027656	0.546525906432545	0.900261473516303	0.898232069038123
GO:0001671	GO:0001671	ATPase activator activity	1/400	18/9272	0.0555555555555556	1.287777777777778	0.25948441536728	0.548203914040654	0.900261473516303	0.898232069038123
GO:0004402	GO:0004402	histone acetyltransferase activity	1/400	18/9272	0.0555555555555556	1.287777777777778	0.25948441536728	0.548203914040654	0.900261473516303	0.898232069038123

GO:0031072	GO:0031072	heat shock protein binding	2/400	51/9272	0.0392156862745098	0.909019607843137	-0.13833319290696	0.652708671267667	0.909068805295225	0.907019546986709
GO:0099529	GO:0099529	neurotransmitter receptor activity involved in regulation of postsynaptic membrane potential	1/400	24/9272	0.9658333333333333	0.035584989283688	0.653446105854668	0.909068805295225	0.907019546986709	
GO:0016755	GO:0016755	aminoacyltransferase activity	11/400	277/9272	0.0397111913357401	0.920505415162455	-0.28520646507041	0.655186797982498	0.9091351169239344	0.907085761384718
GO:0050839	GO:0050839	cell adhesion molecule binding	5/400	129/9272	0.0387596899224806	0.898449612403101	-0.24661222427442	0.659495352653499	0.910655402085586	0.908602567208789
GO:0005496	GO:0005496	steroid binding	2/400	52/9272	0.0384615384615385	0.891538461538465	-0.16653077043588	0.663199481822709	0.910655402085586	0.908602567208789
GO:0004812	GO:0004812	aminoacyl-tRNA ligase activity	1/400	25/9272	0.04	0.9272	-0.07738975547955	0.668435461137771	0.910655402085586	0.908602567208789
GO:0015175	GO:0015175	neutral L-amino acid transmembrane transporter activity	1/400	25/9272	0.04	0.9272	-0.07738975547955	0.668435461137771	0.910655402085586	0.908602567208789
GO:0016875	GO:0016875	ligase activity, forming carbon-oxygen bonds	1/400	25/9272	0.04	0.9272	-0.07738975547955	0.668435461137771	0.910655402085586	0.908602567208789
GO:0120013	GO:0120013	lipid transfer activity	1/400	25/9272	0.04	0.9272	-0.07738975547955	0.668435461137771	0.910655402085586	0.908602567208789
GO:0170055	GO:0170055	lipid transmembrane transporter activity	1/400	25/9272	0.04	0.9272	-0.07738975547955	0.668435461137771	0.910655402085586	0.908602567208789
GO:0001227	GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	5/400	131/9272	0.0381673089312977	0.884732824427481	-0.28211551090783	0.672768573700662	0.910655402085586	0.908602567208789
GO:0050660	GO:0050660	flavin adenine dinucleotide binding	2/400	53/9272	0.0377358490566038	0.874716981132075	-0.19420962814649	0.673434257879155	0.910655402085586	0.908602567208789
GO:0140297	GO:0140297	DNA-binding transcription factor binding	8/400	207/9272	0.0386473429951691	0.895845410628016	-0.32178233296955	0.675511004216375	0.910655402085586	0.908602567208789
GO:0003779	GO:0003779	actin binding	7/400	182/9272	0.0384615384615385	0.891538461538465	-0.3137704407002	0.675659845375428	0.910655402085586	0.908602567208789
GO:0001540	GO:0001540	amyloid-beta binding	1/400	26/9272	0.0384615384615385	0.891538461538465	-0.11758935533274	0.68277803878943	0.910655402085586	0.908602567208789
GO:0016597	GO:0016597	amino acid binding	1/400	26/9272	0.0384615384615385	0.891538461538465	-0.11758935533274	0.68277803878943	0.910655402085586	0.908602567208789
GO:0016879	GO:0016879	ligase activity, forming carbon-nitrogen bonds	1/400	26/9272	0.0384615384615385	0.891538461538465	-0.11758935533274	0.68277803878943	0.910655402085586	0.908602567208789
GO:0032451	GO:0032451	demethylase activity	1/400	26/9272	0.0384615384615385	0.891538461538465	-0.11758935533274	0.68277803878943	0.910655402085586	0.908602567208789
GO:0004986	GO:0004986	cytokine receptor activity	2/400	54/9272	0.037037037037037	0.858518518518516	-0.22139134892108	0.683415500593094	0.910655402085586	0.908602567208789
GO:0022890	GO:0022890	inorganic cation transmembrane transporter activity	12/400	309/9272	0.0388349514563107	0.900194174757281	-0.3788706395806	0.68824881151274	0.914635410933511	0.912573604165749
GO:0022853	GO:0022853	active monoatomic ion transmembrane transporter activity	5/400	134/9272	0.0371343283358209	0.864925373134326	-0.33441297425228	0.682030803849479	0.914635410933511	0.912573604165749
GO:0008094	GO:0008094	ATP-dependent activity, acting on DNA	2/400	55/9272	0.0363636363636364	0.842906090909091	-0.24808620641369	0.683145995213542	0.914635410933511	0.912573604165749
GO:0020037	GO:0020037	heme binding	3/400	82/9272	0.036585658536585	0.848048780487805	-0.29345119342615	0.683432614743315	0.914635410933511	0.912573604165749
GO:0034212	GO:0034212	peptide N-acetyltransferase activity	1/400	27/9272	0.037037037037037	0.858518518518516	-0.15631855892941	0.686501679767607	0.914635410933511	0.912573604165749
GO:0001217	GO:0001217	DNA-binding transcription repressor activity	5/400	135/9272	0.037037037037037	0.858518518518516	-0.35159864294981	0.686277317956634	0.914635410933511	0.912573604165749
GO:0008047	GO:0008047	enzyme activator activity	10/400	262/9272	0.0381673089312977	0.884732824427481	-0.40186151894011	0.700018040206597	0.914635410933511	0.912573604165749
GO:0060090	GO:0060090	molecular adaptor activity	19/400	484/9272	0.0392561983471074	0.909558677685951	-0.43201819751335	0.70002821954129	0.914635410933511	0.912573604165749
GO:0008170	GO:0008170	N-methyltransferase activity	2/400	56/9272	0.0357142857142857	0.827857142857143	-0.27434326756284	0.7026287424093963	0.915804914656542	0.913740471547847
GO:0001784	GO:0001784	phosphotyrosine residue binding	1/400	28/9272	0.0357142857142857	0.827857142857143	-0.19369596501715	0.709633029480204	0.918248040556312	0.916178900508145
GO:0016278	GO:0016278	lysine N-methyltransferase activity	1/400	28/9272	0.0357142857142857	0.827857142857143	-0.19369596501715	0.709633029480204	0.918248040556312	0.916178900508145
GO:0016279	GO:0016279	protein-lysine N-methyltransferase activity	1/400	28/9272	0.0357142857142857	0.827857142857143	-0.19369596501715	0.709633029480204	0.918248040556312	0.916178900508145
GO:0004620	GO:0004620	phospholipase activity	2/400	58/9272	0.034827586206897	0.799310344827586	-0.32553478298441	0.720863920374084	0.918470650979213	0.91640019866396
GO:0051082	GO:0051082	unfolded protein binding	2/400	58/9272	0.034827586206897	0.799310344827586	-0.32553478298441	0.720863920374084	0.918470650979213	0.91640019866396
GO:0042054	GO:0042054	histone methyltransferase activity	1/400	29/9272	0.034827586206897	0.799310344827586	-0.22982646058673	0.722197589000749	0.918470650979213	0.91640019866396
GO:0046915	GO:0046915	transition metal ion transmembrane transporter activity	1/400	29/9272	0.034827586206897	0.799310344827586	-0.22982646058673	0.722197589000749	0.918470650979213	0.91640019866396
GO:0051018	GO:0051018	protein kinase A binding	1/400	29/9272	0.034827586206897	0.799310344827586	-0.22982646058673	0.722197589000749	0.918470650979213	0.91640019866396
GO:0016118	GO:0016118	organic hydroxy compound transmembrane transporter activity	1/400	29/9272	0.034827586206897	0.799310344827586	-0.22982646058673	0.722197589000749	0.918470650979213	0.91640019866396
GO:0004518	GO:0004518	nuclease activity	4/400	113/9272	0.03539830084956	0.820530973451327	-0.40755593232034	0.724740887407404	0.918470650979213	0.91640019866396
GO:0016788	GO:0016788	hydrolase activity, acting on ester bonds	17/400	443/9272	0.038374178329571	0.889525959367946	-0.50592817186016	0.727505960482581	0.918470650979213	0.91640019866396
GO:0051213	GO:0051213	dioxygenase activity	2/400	59/9272	0.0339883050847458	0.785762711864407	-0.35051213016011	0.72982336151117	0.918470650979213	0.91640019866396
GO:0004906	GO:0004906	tetrapyrrole binding	3/400	87/9272	0.034827586206897	0.799310344827586	-0.39932598732926	0.73118538069519	0.918470650979213	0.91640019866396
GO:0031492	GO:0031492	nucleosomal DNA binding	1/400	30/9272	0.0333333333333333	0.772666666666667	-0.26480323404091	0.734219764095383	0.918470650979213	0.91640019866396
GO:0008324	GO:0008324	monatomic cation transmembrane transporter activity	12/400	321/9272	0.0373831775700935	0.866542056074766	-0.51570621702887	0.736788927975843	0.918470650979213	0.91640019866396
GO:0019787	GO:0019787	ubiquitin-like protein transferase activity	10/400	272/9272	0.036764758823529	0.852205882352941	-0.52529451494185	0.7430262495158807	0.918470650979213	0.91640019866396
GO:0001098	GO:0001098	basal transcription machinery binding	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0001099	GO:0001099	basal RNA polymerase II transcription machinery binding	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0004008	GO:0004008	3'-5' exonuclease activity	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0016630	GO:0016630	carbon-carbon lyase activity	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0019829	GO:0019829	ATPase-coupled monoatomic cation transmembrane transporter activity	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0030145	GO:0030145	manganese ion binding	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0031593	GO:0031593	polyubiquitin modification-dependent protein binding	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0043539	GO:0043539	protein serine/threonine kinase activator activity	1/400	31/9272	0.032258064516129	0.747741935483871	-0.29870943517787	0.745722912154444	0.918470650979213	0.91640019866396
GO:0008135	GO:0008135	translation factor activity, RNA binding	3/400	90/9272	0.0333333333333333	0.772666666666667	-0.46014875368328	0.75202880412901	0.920021004557038	0.917947057374365
GO:0005216	GO:0005216	monatomic ion channel activity	8/400	223/9272	0.0358744394618834	0.831569506726457	-0.54057427881883	0.752613708642756	0.920021004557038	0.917947057374365
GO:0008227	GO:0008227	G protein-coupled amine receptor activity	1/400	32/9272	0.03125	0.724375	-0.33161955325249	0.756729387118001	0.920021004557038	0.917947057374365
GO:0001449	GO:0001449	SNARE binding	2/400	63/9272	0.0317460317460317	0.735873015873016	-0.44664176430251	0.762360679314444	0.920021004557038	0.917947057374365
GO:0015075	GO:0015075	monatomic ion transmembrane transporter activity	15/400	404/9272	0.0371287128712871	0.860643564356436	-0.60811734356058	0.763364128551345	0.920021004557038	0.917947057374365
GO:0005096	GO:0005096	GTPase activator activity	4/400	120/9272	0.0333333333333333	0.772666666666667	-0.53220415014125	0.767012764532923	0.920021004557038	0.917947057374365
GO:0009055	GO:0009055	electron transfer activity	1/400	39/9272	0.0303030303030303	0.702424242424242	-0.36360056878681	0.7672605682480858	0.920021004557038	0.917947057374365
GO:0004519	GO:0004519	endoruclease activity	2/400	64/9272	0.03125	0.724375	-0.46979507337307	0.769898767479155	0.920021004557038	0.917947057374365
GO:0008083	GO:0008083	growth factor activity	3/400	93/9272	0.032258064516129	0.747741935483871	-0.51912431159541	0.771557434462933	0.920021004557038	0.917947057374365
GO:0004674	GO:0004674	protein serine/threonine kinase activity	9/400	254/9272	0.0354330708661417	0.821338582677165	-0.61302055560789	0.773764193772786	0.920021004557038	0.917947057374365
GO:0008514	GO:0008514	organic anion transmembrane transporter activity	5/400	149/9272	0.033557469798658	0.777852348993286	-0.5804284994648	0.776538460978218	0.920021004557038	0.91794705737436

GO:0005085	GO:0005085	guanyl-nucleotide exchange factor activity	2/400	104/9272	0.01982307692307692	0.445769230769231	-1.20684784649309	0.942981052842138	0.98398563821149	0.981767498460254
GO:0030527	GO:0030527	structural constituent of chromatin	1/400	65/9272	0.0153846153846154	0.356615384615385	-1.10522524989099	0.943673377428152	0.98398563821149	0.981767498460254
GO:0004930	GO:0004930	G protein-coupled receptor activity	9/400	326/9272	0.0276073619631902	0.639938650306748	-1.40524930073762	0.946794535373033	0.984682491061017	0.982462781436945
GO:0031267	GO:0031267	small GTPase binding	2/400	107/9272	0.0186915887850467	0.433271028037385	-1.25194021107933	0.948921370233784	0.984682491061017	0.982462781436945
GO:0000287	GO:0000287	magnesium ion binding	2/400	108/9272	0.0185185185185185	0.429259259259255	-1.2667494712227	0.950767065462375	0.984682491061017	0.982462781436945
GO:0008528	GO:0008528	G protein-coupled peptide receptor activity	1/400	69/9272	0.0144927536231884	0.335942028985507	-1.1755696035939	0.952843640905888	0.984682491061017	0.982462781436945
GO:0004672	GO:0004672	protein kinase activity	10/400	361/9272	0.0277008310249307	0.642105263157895	-1.47274721620826	0.953510047209923	0.984682491061017	0.982462781436945
GO:0001653	GO:0001653	peptide receptor activity	1/400	73/9272	0.0136986301369863	0.317534246575342	-1.24295241742275	0.960524056710618	0.986298870929711	0.984075517599183
GO:0016758	GO:0016758	hexosyltransferase activity	2/400	114/9272	0.0175438596491228	0.406666666666667	-1.35342244125116	0.960573800433116	0.986298870929711	0.984075517599183
GO:0015399	GO:0015399	primary active transmembrane transporter activity	1/400	74/9272	0.0135135135135135	0.313243243243243	-1.25937369519935	0.962240568650584	0.986298870929711	0.984075517599183
GO:0005267	GO:0005267	potassium channel activity	1/400	76/9272	0.0131578947368421	0.305	-1.29173860480208	0.965453490553978	0.986298870929711	0.984075517599183
GO:0001664	GO:0001664	protein-coupled receptor binding	3/400	155/9272	0.0193548387096774	0.448645161290325	-1.46978422427084	0.966370226515	0.986298870929711	0.984075517599183
GO:0031490	GO:0031490	chromatin DNA binding	1/400	77/9272	0.012987012987013	0.301038961038961	-1.30769054505557	0.966956166040973	0.986298870929711	0.984075517599183
GO:0051020	GO:0051020	GTPase binding	2/400	121/9272	0.0165289256198347	0.383140495867765	-1.45019761829507	0.96965572867057	0.986298870929711	0.984075517599183
GO:1901981	GO:1901981	phosphatidylinositol phosphate binding	1/400	79/9272	0.0126582278481013	0.293417721518987	-1.33915293066858	0.969768722254912	0.986298870929711	0.984075517599183
GO:0008194	GO:0008194	UDP-glycosyltransferase activity	1/400	84/9272	0.0119047619047619	0.275952380962381	-1.41539672204427	0.975798957704261	0.990555841752718	0.988322892192754
GO:0005244	GO:0005244	voltage-gated monoatomic ion channel activity	1/400	91/9272	0.010989010989011	0.254725274725275	-1.51696169751269	0.98227964980543	0.992290901906269	0.990054041106127
GO:0016874	GO:0016874	ligase activity	3/400	174/9272	0.0172413793103448	0.399655172413793	-1.69740294265738	0.982404227890649	0.992290901906269	0.990054041106127
GO:0022832	GO:0022832	voltage-gated channel activity	1/400	92/9272	0.0108695652173913	0.25195652173913	-1.53102377080344	0.98305169425351	0.992290901906269	0.990054041106127
GO:0048018	GO:0048018	receptor ligand activity	6/400	298/9272	0.0201342281879195	0.466711409395973	-1.96682635113703	0.990354995138649	0.994218459230647	0.991977253255708
GO:0030546	GO:0030546	signaling receptor activator activity	6/400	299/9272	0.020068889632107	0.465150501672241	-1.99609346449077	0.99063737824299	0.994218459230647	0.991977253255708
GO:0003729	GO:0003729	mRNA binding	3/400	194/9272	0.0154639175257732	0.358453608247425	-1.9174160665042	0.991291679155742	0.994218459230647	0.991977253255708
GO:0016773	GO:0016773	phosphotransferase activity, alcohol group as acceptor	10/400	436/9272	0.0229357798165138	0.531651376146786	-2.12699838009938	0.992411703078541	0.994218459230647	0.991977253255708
GO:0030545	GO:0030545	signaling receptor regulator activity	6/400	315/9272	0.019047619047619	0.44152380952381	-2.14121941199603	0.994218459230647	0.994218459230647	0.991977253255708

geneID	Count
LOC107000401/LOC713991/MRPL11/MRPL23/MRPL27/MRPL32/MRPL43/MRPL57/MRPS11/MRPS14/MRPS18C/MRPS21/MRPS23/MRPS25/MRPS34/RPL39L/RPS27L	17
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AKR1C1/HSD17B10/HSD17B13/HSD17B3/LOC711440	5
CIB1/HSPB1/PKIA/PKIB/PKIG	5
CST6/CSTA/CSTB/WFDC2	4
AKR1C1/HSD17B10/HSD17B3/LOC711440	4
CIB1/GSKIP/HSPB1/PKIA/PKIB/PKIG	6
AKR1C1/ALDH1A1/ALDH1L2/ALDH3A1/LOC711440	5
AIFM3/CISD1/CISD3/ISCA2	4
APOC1/ATP5F1/BST2/CIB1/CST6/CSTA/CSTB/FKBP1B/GSKIP/HSPB1/LEF1/MRLN/NFKBIA/PKIA/PKIB/PKIG/SLT2/WFDC2	18
CIB1/GSKIP/HSPB1/PKIA/PKIB/PKIG	6
AKR1C1/HSD17B10/LOC711440	3
AIFM3/CISD1/CISD3/GLRX5/ISCA2/RSAD2	6
AIFM3/CISD1/CISD3/GLRX5/ISCA2/RSAD2	6
AKR1C1/DECR2/DUS1L/LOC711440/TM7SF2	5
APOC1/FABP4/FABP5/LOC711440/PTGDS	5
AKR1C1/ALDH1A1/ALDH1L2/ALDH3A1/LOC711440	5
APOC1/BST2/CIB1/CST6/CSTA/CSTB/GSKIP/HSPB1/MRLN/PKIA/PKIB/PKIG/SLT2/WFDC2	14
IPO4/KPNA2/NFKBIA	3
ST3GAL6/ST6GALNAC5/ST8SIA1	3
BCL10/CIB1/CISH/CKS1B/EREG/GSKIP/HSPB1/LOC713991/PKIA/PKIB/PKIG/SOCS2	12
APOC1/FABP4/FABP5/PTGDS	4
IPO4/KPNA2/SNUPN	3
DTWD2/DUS1L/FARSA/POP5/POP7/PTRHD1/TRMT61A	7
ADH5/AKR1C1/LOC711440	3
DUSP14/DUSP23/DUSP4	3
ATOX1/EMC6/EMC9/IPO4/KPNA2/SNUPN	6
APTX/DDX60/DHX58/EIF2AK2/OAS1	5
POLR1D/POLR2V/POLR2K	3
POLR1D/POLR2V/POLR2K	3
POLR1D/POLR2V/POLR2K	3
BCL10/CSTA/ECM1/FN1/ITGA3/TNFAIP3	6
DTWD2/GSTA3/GSTP1/RABGGTA/SRM	5
POLR1D/POLR2K	2
ALDH1A1/ALDH1L2	2
ESR1/ESR2	2
GABRB1/HRH4	2
IPO4/KPNA2/SNUPN	3
APTX/CHD7/DDX4/DHX34/DHX58/DTWD2/DUS1L/EMG1/FARSA/FIH1/MCM3/N6AMT1/POLR1D/POLR2V/POLR2K/POP5/POP7/PTRHD1/RUVBL2/TREX1/TRMT61A	21
CHD7/DDX4/DHX34/DHX58/FIH1/MCM3/RUVBL2	7
ATP1B1/ATP5F1/ESR1	3
SLC35B4/SLC35E3	2
EMC6/EMC9	2
DUSP14/DUSP4	2
BMT2/N6AMT1	2
ADAM28/CAPN3/CFB/CTSD/GZMH/LOC106992406/NRIP2/PSMB5/PSMB9/SEC11C/TMPRSS2/TPP1/USP27X	13
ABCF2/AGAP1/APTX/ARF5/CHD7/DHX34/ENPP5/GNA11/GNA15/HRAS/HSPA1A/KIF23/MCM3/MX1/MX2/NUDT1/ORC1/PLPP1/PSMC2/PSMC3/RAB27B/RAB5C/REM2/RGS16/RUVBL2	25
GTF3C6/SNAPC2/SNAPC5	3
CIB1/CKS1B/EREG/GSKIP/HSPB1/LOC713991/PKIA/PKIB/PKIG	9
ABCF2/AGAP1/APTX/ARF5/CHD7/DHX34/ENPP5/GNA11/GNA15/HRAS/HSPA1A/KIF23/MCM3/MX1/MX2/NUDT1/ORC1/PLPP1/PSMC2/PSMC3/RAB27B/RAB5C/REM2/RGS16/RUVBL2	25
FN1/GPNMB/ISG15/ITGA3/SYK	5
ABCF2/AGAP1/APTX/ARF5/CHD7/DHX34/ENPP5/GNA11/GNA15/HRAS/HSPA1A/KIF23/MCM3/MX1/MX2/NUDT1/ORC1/PLPP1/PSMC2/PSMC3/RAB27B/RAB5C/REM2/RGS16/RUVBL2	25
LOC106996676/LOC723473/MAMU-AG	3
ESR1/ESR2	2
GNA11/RAB27B	2
CTSD/NRIP2	2
ESR1/LEF1	2
NID1/SLT2	2
CISH/SOCS2	2
CTSD/NRIP2	2
CCDC181/KIF11/KIF13A/KIF23/LOC697790/MX1/MX2/SKA3/SPAG6	9
HSPA1A/HSPB1/HSPD1/HSPE1	4
KIF11/KIF13A/KIF23	3
PRDX5/PRDX6/PTGS2	3
ABCF2/ATP1B1/CHD7/DDX4/DHX34/DHX58/HSPA1A/HSPD1/FIH1/KIF11/KIF13A/KIF23/MCM3/ORC1/PSMC2/PSMC3/RUVBL2/TP53	18
HSPB1/PLEK	2
APTX/TREX1	2
GNA11/GNA15	2
DNAH12/DYNLRB2	2
NFKBIA/XAF1	2
CCDC181/EHFC1/KIF11/KIF13A/KIF23/LOC697790/MX1/MX2/SKA3/SPAG6/TPPPP3	11
FKBP10/FKBP1B/FKBP9	3
EBP/PTGDS/PTGES2	3
IPO4/KPNA2/NFKBIA	3
PRDX5/PRDX6/PTGS2	3
APTX/TREX1	2
AKR1C1/L/LOC711440	2
ADH5/AKR1C1/LOC711440	3
BRIX1/EMG1/MRPL11/MRPS18C	4
ADAM28/AM21/CAPN3/CFB/CTSD/GZMH/LOC106992406/NRIP2/PSMB5/PSMB9/PSMC2/PSMC3/SEC11C/SENP3/TMPRSS2/TNFAIP3/TPP1/USP18/USP27X	19
AKR1C1/LOC711440	2
LEF1/NFKBIA	2
ADH5/AKR1C1/HSD17B10/HSD17B13/HSD17B3/LOC711440	6
FKBP10/FKBP1B/FKBP9	3
RAB27B/SHROOM4/SPATA6L	3
DDX4/DHX58/DTWD2/DUS1L/EMG1/FARSA/FIH1/POLR1D/POLR2V/POLR2K/POP5/POP7/PTRHD1/TRMT61A	14
BST2/CST6/CSTA/CSTB/FN1/RPS27L/WFDC2	7
APOC1/FABP4/FABP5/GLRA1/LOC711440/PTGDS	6
AGR2/EREG	2
SCN11A/SCN4A	2
AKR1C1/LOC711440	2
APOBEC3B/GNPD2	2
CIB1/HRAS	2
CFB/GZMH/LOC106992406/SEC11C/TMPRSS2/TPP1	6
ADH5/AKR1C1/HSD17B10/HSD17B13/HSD17B3/LOC711440	6
AKR1C1/LOC711440	2
EMC6/EMC9	2
LOC106996676/LOC723473/MAMU-AG	3
ATOX1/FS/TP53	3
EBP/FKBP10/FKBP1B/FKBP9/GNPD2/PTGDS/PTGES2	7
ABCF2/AGAP1/ARF5/CHD7/DHX34/GNA11/GNA15/HRAS/HSPA1A/KIF23/MCM3/MX1/MX2/ORC1/PSMC2/PSMC3/RAB27B/RAB5C/REM2/RGS16/RUVBL2	21
CAPN3/FN1/HMGCL/LOC107000401/LOC693939/LOC713991/MRPL11/MRPL23/MRPL27/MRPL32/MRPL43/MRPL57/MRPS11/MRPS14/MRPS18C/MRPS21/MRPS23/MRPS25/MRPS34	22
ARMT1/BMT2/DPH5/EMG1/GATM/METTL21A/N6AMT1/PEMT/TRMT61A	9
ABCF2/CHD7/DHX34/HSPA1A/KIF23/MCM3/ORC1/PSMC2/PSMC3/RUVBL2	10
PRDX8/PROCA1	2
APOC1/FABP4/FABP5/GLRA1/LOC711440/PTGDS	6
GLRX/TXN2	2
SNAPC2/SNAPC5	2
CMPK2/NME4	2
POP5/POP7	2
FARSA/HSD17B10/IFIT5	3
ATP1B1/SCN11A/SCN4A/SLC41A3/SLC6A9	5
AKR1C1/LOC711440	2
BCL10/NFKBIA	2
APBA1/IPO4/KPNA2/LOC106996676/LOC723473/MAMU-AG/NFKBIA	7
CFB/GZMH/LOC106992406/SEC11C/TMPRSS2/TPP1	6
CFB/GZMH/LOC106992406/SEC11C/TMPRSS2/TPP1	6
ESR1/LEF1	2
FN1/RPS27L	2
DUSP14/DUSP23/DUSP4/EYA1	4
KIF11/KIF13A/KIF23	3
BST2/CST6/CSTA/CSTB/WFDC2	5
APTX/TREX1	2
SIVA1/TNFSF13	2
FKBP1B/REM2	2
DDR1/NID1	2

CCR4/CX3CR1	2
GLUL/ZDHHC12	2
GLUL/ZDHHC12	2
CCR4/CX3CR1	2
AQP3/SLC15A2	2
PRDX5/PRDX6/PTGS2	3
AIF1/CAPN3/CETN2/CIB1/CLEC4A/EFHC1/ESYT3/FKBP10/FKBP9/JAG1/NID1/PCDH17/PCDH7/PCDHB2/PRF1/PRRG4/S100P/SLT2	18
BST2/CST6/CSTA/CSTB/WFDC2	5
DDX80/DHX58/IFT5	3
CCR4/CX3CR1	2
GSTA3/GSTP1	2
CCR4/CX3CR1	2
POP5/POP7	2
NID1/SLT2	2
CD38/CENPV/DDT/HMGCL/PCBD1/PTGES2/UROS	7
ARM11/BMT2/DPH5/EMG1/METTL21A/N6AMT1/PEMT/TRMT61A	8
AIF1/CAPN3/CCDC181/EFHC1/FHL3/FSCN1/KIF11/KIF13A/KIF23/LOC697790/MX1/MX2/NEBL/PFN2/PPP1R9A/RAB27B/SHROOM4/SKA3/SPAG6/SPX1A6L/TPPP3	21
CMPK2/NME4	2
ISCA2/RSAD2	2
NLGN3/SYK	2
CCR4/CX3CR1	2
FABP4/SOCS2	2
GABRB1/GLRA1	2
ADH5/AIFM3/AKR1C1/ALDH1A1/ALDH1L2/ALDH3A1/CYP27A1/DECRR2/DUS1L/GLRX/HSOD17B10/HSOD17B13/HSOD17B3/LOC711440/PCBD1/PRDX5/PRDX6/PTGS2/RDH14/RIOX1/TMT5F	22
SENP3/TNFAIP3/USP18/USP27X	4
CLCN5/GABRB1/GLRA1	3
BMT2/FN1/GLRA1/N6AMT1/SLT2/TWSG1	6
GLUL/ZDHHC12	2
HSPA1A/HSPD1	2
BST2/CST6/CSTA/CSTB/WFDC2	5
CHD7/CKS1B/LEF1/LOC702864/SCML1/TSPYL5/ZNHIT1	7
DDX4/DHX58/IFIH1	3
DDX4/DHX58/IFIH1	3
CHD7/TP53	2
APTX/ARM11/CTDNEP1/DUSP14/DUSP23/DUSP4/EYA1/NT5C/PLPP1	9
CLCN5/GABRB1/GLRA1/SLC12A5	4
BCL10/ESR1	2
BCL10/CKS1B/EREG/LOC713991	4
PRDX6	1
BMMPR1B	1
JAG1	1
AQP3	1
PLPP1	1
NT5C	1
GLRA1	1
CD38	1
GABRB1	1
NID1	1
EFHC1	1
CMPK2	1
DNAH12	1
ESR1	1
NFKBIA	1
SENP3/TNFAIP3/USP18/USP27X	4
GLUL/ZDHHC12	2
GLRX/TXN2	2
ESR1/LEF1/LRIF1	3
ELOC/TSPM	2
CPNE2/ESYT3	2
PNP/RXYLT1	2
SIVA1/TNFSF13	2
ATP1B1/ATPSIF1	2
AKR1C1/CYP27A1/LOC711440/PCBD1/PTGS2/RIOX1	6
APTX/MCM3/TP53	3
ESR1	1
NME4	1
LTBR	1
BNIP1	1
FKBP1B	1
HRH4	1
FKBP1B	1
ALDH1L2	1
EREG	1
SYK	1
ATRAID	1
PRRG4	1
CKS1B	1
PGLYRP3	1
PRELID1	1
FKBP1B	1
AKR1C1/CYP27A1/LOC711440/PCBD1	4
BNIP1/STX4	2
SLC35B4/SLC35E3	2
SLC35B4/SLC35E3	2
AGAP1/ARF5/GNA11/GNA15/HRAS/MX1/MX2/RAB27B/RAB5C/REM2/RGS16	11
BCL10/HSPA1A/ISG15/LOC697790/NFKBIA/PML/PRDX6	7
ADH5/APOBEC3B/CHURC1/DHX58/ENPP5/ESR1/ESR2/GLRA1/IFIH1/LOC716637/MT1E/PGLYRP3/PML/POLR21/POLR2K/RABGGTA/TMEM163/TNFAIP3/XAF1/ZCCHC3/ZNF593	21
AIF1/FSCN1/NEBL/PPP1R9A/SHROOM4	5
APTX/CHD7/ESR1/FOXA1/HMGN3/KAT2A/LEF1/MEIS1/ORC1/PLAC8/SCML1/TP53/TSPYL5/ZNHIT1	14
ARM11/DPH5/N6AMT1	3
KAT2A/PAFAH1B3/SAT2	3
P2RY14	1
GDI1	1
GLRA1	1
SLC6A9	1
P2RY14	1
ISG15	1
RAB27B	1
PLPP1	1
RPS27L	1
ESYT3	1
TNFAIP3	1
ISG15	1
DPH5/EMG1/N6AMT1/PEMT/TRMT61A	5
CLCN5/GABRB1/GLRA1	3
SLC12A5/SLC15A2/SLC6A9	3
B4GALT3/PIGQ/PNP/POFUT2/RXYLT1/ST3GAL6/ST6GALNAC5/ST8SIA1	8
OAS1/POLR1D/POLR21/POLR2K	4
APOBEC3B/GNPD2/HINT2/PGLYRP3	4
SENP3/TNFAIP3/USP18/USP27X	4
BCL10/ESR1/HSPB1/LEF1/LRIF1/NFKBIA/TBX20	7
GABRB1/GLRA1	2
GABRB1/GLRA1	2
BMMPR1B/PML	2
SIVA1	1
CAPN3	1
APTX	1
KAT2A	1
ATP1B1	1
APOBEC3B	1
SHANK1	1
AGPAT1	1
ATP1B1	1
KAT2A/KPNA2/LEF1	3
SLC35B4/SLC35E3	2
AKR1C1/LOC711440	2
LIPA/PGAP1/PRDX6/PROCA1/PTRH1	5
RABGGTA	1
MAP3K21	1

SLC6A9	1
IFT5	1
TXN2	1
AQP3	1
SLC12A5	1
AGPAT1	1
CD38	1
GLRX	1
SAMD4A	1
AGPAT1	1
USP27X	1
AGPAT1/GLUL/KAT2A/PAFAH1B3/PRDX6/SAT2/ZDHHC12	7
APTX/TREX1	2
HRAS/RAB27B	2
BCL10/HSPA1A/ISG15/LOC697790/NFKBIA/PML/PRDX6	7
AMPH/APOC1/ATP5MC3/CPNE2/ESR1/ESR2/ESYT3/FABP4/FABP5/JAG1/LOC697790/PSD3/PSMB4/PTGDS/SNX10/STXBP6/TPP1	17
FN1/SLIT2/TWSG1	3
HSPD1/HSPH1/STUB1	3
PSMB4	1
GABRB1	1
SLC12A5	1
PGLYRP3	1
PLEK	1
LPAR1	1
SIVA1	1
ECM1/LOC100430627/OSM/SIVA1/SOCS2/SYK/TNFSF13	7
BNIP1/TRPC5	2
ESR1/LEF1	2
DUSP14/DUSP4	2
EIF2AK2/ELOC/RPS27L/SAMD4A/TSFM	5
CTDNEP1/DUSP14/DUSP4	3
GABRB1/GLRA1/HRH4	3
KAT2A/SAT2	2
AGPAT1/PRDX6	2
ESR1	1
GLRA1	1
IFT5	1
EMG1	1
ALDH1L2	1
PTGS2	1
GABRB1	1
RBPMS	1
CDC34	1
EMG1	1
CLCN5/GABRB1/GLRA1/SLC12A5	4
CAPN3/SENP3/TNFAIP3/USP18/USP27X	5
ATP1B1/BNIP1/SCN11A/SCN4A/SLC12A5/SLC39A1/SLC41A3/SLC6A9/TMEM38A/TRPC5	10
HINT2/PGLYRP3	2
GLRA1/HRH4	2
BCL10/IRF4/KAT2A/MAK/RBPMS	5
CTDNEP1/DUSP14/DUSP23/DUSP4/EYA1	5
APTX/CHD7/N6AMT1/RUVBL2/TREX1	5
ARMT1	1
B4GALT3	1
PTGS2	1
ESR1	1
LOC716637	1
GSKIP	1
CD38/GLA/MOGS	3
CKS1B/EREG/LOC713991	3
ESR1/LEF1	2
POPS/POP7	2
GABRB1/GLRA1	2
ATP1B1	1
KAT2A	1
HRH4	1
TRMT61A	1
NID1	1
GAR1	1
CDC34	1
CHD7	1
RIOX1	1
CLCN5/GABRB1/GLRA1/SLC12A5	4
FKBP1B/GLRX/REM2	3
PCBD1/UROS	2
FN1/PGLYRP3/SLIT2/TWSG1	4
COR4/CX3CR1/TWSG1	3
CAPN3/USP27X	2
EMG1/TRMT61A	2
AQP3/BCL2A1/BNIP1/CLCN5/GABRB1/GLRA1/PRF1/SCN11A/SCN4A/TMEM38A/TRPC5	11
AQP3/BCL2A1/BNIP1/CLCN5/GABRB1/GLRA1/PRF1/SCN11A/SCN4A/TMEM38A/TRPC5	11
SLC25A1/SLC35E3/SLC41A3	3
FKBP1B/GLRX/REM2	3
CIB1/FKBP1B	2
AQP3/ATP1B1/ATP5MC3/BNIP1/CLCN5/GABRB1/GLRA1/SCN11A/SCN4A/SLC12A5/SLC15A2/SLC39A1/SLC41A3/SLC6A9/TMEM38A/TRPC5	16
AGAP1/ARF5/GNA11/GNA15/HRAS/MX1/MX2/RAB27B/RAB5C/REM2/SRPRB	11
SLC6A9	1
SHANK1	1
RIOX1	1
OAS1	1
RIOX1	1
SLC12A5/SLC15A2/SLC6A9	3
LIPA/PRDX6/PROCA1	3
FKBP1B/GLRX/REM2	3
ESR1/ESR2	2
APTXYK	2
ESR1/ESR2	2
DTX3L/HERC5/LOC716637/NEURL4/PML/RNF181/SH3RF2/STUB1	8
AGPAT1/CDC34/DTX3L/F13A1/GLUL/HERC5/KAT2A/LOC716637/NEURL4/PAFAH1B3/PML/PRDX6/RNF181/SAT2/SH3RF2/STUB1/TNFAIP3/ZDHHC12	18
SLC39A1	1
EIF4EBP3	1
LOC100430627	1
KAT2A	1
EIF2AK2/ELOC/RPS27L/TSFM	4
APTXYK	2
GLA/MOGS	2
BNIP1/TRPC5	2
BMPR1B/DDR1	2
SYK	1
PRELID1	1
TMED1	1
LOC716637	1
CKS1B/PML/TNFAIP3	3
AGR2/ECM1/EREG	3
COR4/CX3CR1/LTB4R	3
AMPH/CPNE2/ESYT3/JAG1/LOC697790/PSD3/SNX10/STXBP6/TPP1	9
HMGN3/ZNHIT1	2
AGAP1/ARF5/GNA11/GNA15/HRAS/MX1/MX2/RAB27B/RAB5C/REM2/SRPRB	11
AGAP1/ARF5/GNA11/GNA15/HRAS/MX1/MX2/RAB27B/RAB5C/REM2/SRPRB	11
SLC12A5/SLC15A2/SLC25A1/SLC35E3/SLC41A3/SLC6A9	6
FN1	1
PRF1	1
SLC41A3	1
GLRA1	1
APTXYK/ARMT1/CTDNEP1/DUSP14/DUSP23/DUSP4/EYA1/NT5C/PLPP1	9
DTX3L/HERC5/LOC716637/NEURL4/PML/RNF181/SH3RF2/STUB1	8
CDC34/DTX3L/HERC5/LOC716637/NEURL4/PML/RNF181/SH3RF2/STUB1/TNFAIP3	10
KAT2A/SAT2	2
PCBD1/UROS	2

HSPA1A/TOMM34	2
GLRA1	1
CDC34/DTX3L/F13A1/HERC5/LOC716637/NEURL4/PML/RNF181/SH3RF2/STUB1/TNFAIP3	11
FN1/GPNMB/ISG15/ITGA3/SYK	5
ESR1/ESR2	2
FARSA	1
SLC6A9	1
FARSA	1
PRELID1	1
FABP4	1
BATF3/FOXP2/LEF1/SATB1/ZNF471	5
AIFM3/DUS1L	2
BCL10/ESR1/HSPB1/KAT2A/LEF1/LRIF1/NFKBIA/TBX20	8
AIF1/FHL3/FSCN1/NEBL/PFN2/PPP1RBA/SHROOM4	7
APBA1	1
GLRA1	1
GLUL	1
RIOX1	1
CCR4/CX3CR1	2
ATP1B1/ATP5MC3/BNIP1/SCN11A/SCN4A/SLC12A5/SLC15A2/SLC39A1/SLC41A3/SLC6A9/TMEM38A/TRPC5	12
ATP1B1/SLC12A5/SLC15A2/SLC41A3/SLC6A9	5
CHD7/RUVBL2	2
CYC1/CYP27A1/PTGS2	3
KAT2A	1
BATF3/FOXP2/LEF1/SATB1/ZNF471	5
AGAP1/ARHGAP21/BCL10/CKS1B/EREG/FN1/GDI1/LOC713991/RPS27L/SRGAP1	10
ATP1B1/BCL10/BNIP1/CAPN3/CIB1/ELOC/FHL3/FSCN1/HRAS/IRF4/JAG1/KAT2A/MAK/PML/RBPMS/SAV1/SHANK1/STX4/USP18	19
NGAMT1/PEMT	2
SYK	1
NGAMT1	1
NGAMT1	1
PRDX6/PROCA1	2
HSPB1/HSPB1	2
NGAMT1	1
SLC39A1	1
GSKIP	1
AQP3	1
APTXX/POP5/POP7/TREX1	4
APTXX/ARMT1/CTDNEP1/DUSP14/DUSP23/DUSP4/EYA1/LIPA/NT5C/PGAP1/PLPP1/POP5/POP7/PRDX6/PROCA1/PTRHD1/TREX1	17
PTGS2/RIOX1	2
CYC1/CYP27A1/PTGS2	3
HMGH3	1
ATP1B1/ATP5MC3/BNIP1/SCN11A/SCN4A/SLC12A5/SLC15A2/SLC39A1/SLC41A3/SLC6A9/TMEM38A/TRPC5	12
CDC34/DTX3L/HERC5/LOC716637/NEURL4/PML/RNF181/SH3RF2/STUB1/TNFAIP3	10
ESR1	1
ESR1	1
TREX1	1
HMGCL	1
ATP1B1	1
HMGCL	1
TNFAIP3	1
CKS1B	1
EIF2AK2/ELOC/TSFM	3
BNIP1/CLCN5/GABRB1/GLRA1/SCN11A/SCN4A/TMEM38A/TRPC5	8
HRH4	1
STX4/STXBP1	2
ATP1B1/ATP5MC3/BNIP1/CLCN5/GABRB1/GLRA1/SCN11A/SCN4A/SLC12A5/SLC15A2/SLC39A1/SLC41A3/SLC6A9/TMEM38A/TRPC5	15
AGAP1/ARHGAP21/GDI1/SRGAP1	4
CYC1	1
POP5/POP7	2
EREG/NRG2/OSM	3
BMPR1B/CSNK1E/DMPK/EIF2AK2/MAK/MAP3K21/RPS9KL1/STK33/SYK	9
FABP4/SLC25A1/SLC35B4/SLC35E3/SLC6A9	5
LOC100430627	1
CKS1B/TNFAIP3	2
BCL2A1/FOXP2/GLA/HSPB1/PLEK/PML/RBPMS/SLIT2/ZHX3	9
AGAP1/ARHGAP21/FGD2/GDI1/GPSM3/PSD3/SLIT2/SRGAP1	8
AGAP1/ARHGAP21/FGD2/GDI1/GPSM3/PSD3/SLIT2/SRGAP1	8
BNIP1/GABRB1/GLRA1	3
BNIP1/GABRB1/GLRA1	3
STXBP6	1
CKS1B	1
RIOX1	1
CLEC4A	1
S100P	1
ATP1B1/SLC12A5/TMEM38A	3
APBA1/FKBP10/FKBP1B	3
APTXX	1
STXBP1	1
SYK	1
FABP4/PRELID1	2
BNIP1/SCN11A/SCN4A/TMEM38A/TRPC5	5
CYP27A1/SCA2/RIOX1	3
KAT2A/NGAMT1/RIOX1	3
DDR1	1
SLC6A9	1
SH3RF2/SYK	2
POP5/POP7	2
FABP4/SLC25A1/SLC6A9	3
BCL10/ESR1/HSPB1/KAT2A/LEF1/LRIF1/NFKBIA/TBX20	8
ATP1B1/BCL10/CKS1B/ESR1/GSKIP/HSPB1/JTB/KIF11/PLEK/SYK	10
FABP4	1
SLC6A9	1
SLC6A9	1
FABP4/SLC25A1/SLC6A9	3
ATP1B1/BCL10/BNIP1/CIB1/ELOC/FHL3/FSCN1/HRAS/IRF4/KAT2A/MAK/PML/RBPMS/SHANK1/STX4	15
ATP1B1/BCL10/CKS1B/ESR1/GSKIP/HSPB1/JTB/KIF11/PLEK/SYK/TNFAIP3	11
MAP3K21	1
DDR1/SYK	2
LOC100430627	1
TRPC5	1
ATP1B1/SLC12A5/SLC15A2/SLC25A1/SLC35E3/SLC41A3/SLC6A9	7
SHANK1	1
STXBP6	1
BCL2A1/ITGA3/LOC69939/PGLYRP3/ZHX3	5
ADAM28	1
WFDC2	1
LOC713991/SPCS1	2
RBPMS	1
ATP1B1	1
ESR1/IRF4/LEF1/MEIS1/TBX20/ZNF48	6
TPP1	1
SPCS1	1
ESR1/IRF4/LEF1/MEIS1/TBX20/ZNF48	6
ATP5MC3/SLC15A2	2
SH3RF2	1
PML/TNFAIP3	2
ADAM28/AMZ1	2
SLC6A9	1
BNIP1	1
EIF2AK2	1
BCL10/FHL3/IRF4/KAT2A/MAK/RBPMS	6
BCL10/BCL2A1/FOXA1/LEF1/PRRG4/RAB27B/SYK	7
BNIP1/CLCN5/GABRB1/GLRA1	4
LOC100430627/OSM/TNFSF13	3
ESYT3/SNX10/STXBP6	3
BCL2A1/EPAS1/FOXP2/GLA/HSPB1/ITGA3/LOC693939/PGLYRP3/PLEK/PML/POLR1D/RBPMS/RILPL1/SLIT2/ZHX3	15
TWSG1	1
CLEC4A/FAM3A/KLRF1	3

FGD2/PSD3	2
LOC68939	1
ADGRF5/AGTRAP/CCR4/CX3CR1/GABRB1/HRH4/LPAR1/LTB4R/P2RY14	9
CIB1/IPO4	2
CIB1/HMGCL	2
AGTRAP	1
BMPR1B/CSNK1E/DDR1/DMPK/EIF2AK2/MAK/MAP3K21/RPS6KL1/STK33/SYK	10
AGTRAP	1
B4GALT3/POFUT2	2
ATP1B1	1
TMEM38A	1
GNA11/GNA15/LOC100430627	3
HMGH3	1
CIB1/PO4	2
STXBP6	1
RXYLT1	1
CLCN5	1
FARSA/GLUL/RNF181	3
CLCN5	1
EREG/LOC100430627/NRG2/OSM/TAF11/TNFSF13	6
EREG/LOC100430627/NRG2/OSM/TAF11/TNFSF13	6
DDX4/ESRP1/RBPMS	3
BMPR1B/CSNK1E/DDR1/DMPK/EIF2AK2/MAK/MAP3K21/RPS6KL1/STK33/SYK	10
EREG/LOC100430627/NRG2/OSM/TAF11/TNFSF13	6