

Supptbl29_QuickGO_Infectionmarkers				GO IDs (by protein)							
GO IDs (by annotation)				GO IDs (by protein)							
Code	Name	Percentage	Count	Code	Name	Percentage	Count				
GO:0015671	oxygen transport	9.09	10	GO:0015671	oxygen transport	28.57	4				
GO:0055114	oxidation-reduction process	5.45	6	GO:0006810	transport	28.57	4				
GO:0006810	transport	5.45	6	GO:0055114	oxidation-reduction process	21.43	3				
GO:0006955	immune response	3.64	4	GO:0019752	carboxylic acid metabolic process	21.43	3				
GO:0006412	translation	3.64	4	GO:0006955	immune response	21.43	3				
GO:0032729	positive regulation of interferon-gamma production	2.73	3	GO:0005975	carbohydrate metabolic process	21.43	3				
GO:0019752	carboxylic acid metabolic process	2.73	3	GO:0019882	antigen processing and presentation	14.29	2				
GO:0006954	inflammatory response	2.73	3	GO:0090036	regulation of protein kinase C signaling	7.14	1				
GO:0005975	carbohydrate metabolic process	2.73	3	GO:0071407	cellular response to organic cyclic compound	7.14	1				
GO:0070328	triglyceride homeostasis	1.82	2	GO:0070328	triglyceride homeostasis	7.14	1				
GO:0051016	barbed-end actin filament capping	1.82	2	GO:0051897	positive regulation of protein kinase B signaling	7.14	1				
GO:0045630	positive regulation of T-helper 2 cell differentiation	1.82	2	GO:0051291	protein heterooligomerization	7.14	1				
GO:0042632	cholesterol homeostasis	1.82	2	GO:0051142	positive regulation of NK T cell proliferation	7.14	1				
GO:0042095	interferon-gamma biosynthetic process	1.82	2	GO:0051016	barbed-end actin filament capping	7.14	1				

GO:0019882	antigen processing and presentation	1.82	2	GO:0050729	positive regulation of inflammatory response	7.14		1	
GO:0010744	positive regulation of macrophage derived foam cell differentiation	1.82	2	GO:0048747	muscle fiber development	7.14		1	
GO:0090036	regulation of protein kinase C signaling	0.91	1	GO:0048661	positive regulation of smooth muscle cell proliferation	7.14		1	
GO:0071407	cellular response to organic cyclic compound	0.91	1	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	7.14		1	
GO:0051897	positive regulation of protein kinase B signaling	0.91	1	GO:0045727	positive regulation of translation	7.14		1	
GO:0051291	protein heterooligomerization	0.91	1	GO:0045662	negative regulation of myoblast differentiation	7.14		1	
GO:0051142	positive regulation of NK T cell proliferation	0.91	1	GO:0045630	positive regulation of T-helper 2 cell differentiation	7.14		1	
GO:0050729	positive regulation of inflammatory response	0.91	1	GO:0042632	cholesterol homeostasis	7.14		1	
GO:0048747	muscle fiber development	0.91	1	GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	7.14		1	
GO:0048661	positive regulation of smooth muscle cell proliferation	0.91	1	GO:0042346	positive regulation of NF-kappaB import into nucleus	7.14		1	

GO:0045944	positive regulation of transcription from RNA polymerase II promoter	0.91	1	GO:0042254	ribosome biogenesis	7.14	1	
GO:0045727	positive regulation of translation	0.91	1	GO:0042253	granulocyte macrophage colony-stimulating factor biosynthetic process	7.14	1	
GO:0045662	negative regulation of myoblast differentiation	0.91	1	GO:0042231	interleukin-13 biosynthetic process	7.14	1	
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	0.91	1	GO:0042104	positive regulation of activated T cell proliferation	7.14	1	
GO:0042346	positive regulation of NF-kappaB import into nucleus	0.91	1	GO:0042095	interferon-gamma biosynthetic process	7.14	1	
GO:0042254	ribosome biogenesis	0.91	1	GO:0042094	interleukin-2 biosynthetic process	7.14	1	
GO:0042253	granulocyte macrophage colony-stimulating factor biosynthetic process	0.91	1	GO:0042092	type 2 immune response	7.14	1	
GO:0042231	interleukin-13 biosynthetic process	0.91	1	GO:0042088	T-helper 1 type immune response	7.14	1	
GO:0042104	positive regulation of activated T cell proliferation	0.91	1	GO:0042033	chemokine biosynthetic process	7.14	1	
GO:0042094	interleukin-2 biosynthetic process	0.91	1	GO:0035655	interleukin-18-mediated signaling pathway	7.14	1	
GO:0042092	type 2 immune response	0.91	1	GO:0034105	positive regulation of tissue remodeling	7.14	1	

GO:0042088	T-helper 1 type immune response	0.91	1	GO:0032819	positive regulation of natural killer cell proliferation	7.14		1		
GO:0042033	chemokine biosynthetic process	0.91	1	GO:0032740	positive regulation of interleukin-17 production	7.14		1		
GO:0035655	interleukin-18-mediated signaling pathway	0.91	1	GO:0032729	positive regulation of interferon-gamma production	7.14		1		
GO:0034105	positive regulation of tissue remodeling	0.91	1	GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	7.14		1		
GO:0032819	positive regulation of natural killer cell proliferation	0.91	1	GO:0032148	activation of protein kinase B activity	7.14		1		
GO:0032740	positive regulation of interleukin-17 production	0.91	1	GO:0031663	lipopolysaccharide-mediated signaling pathway	7.14		1		
GO:0032725	positive regulation of granulocyte macrophage colony-stimulating factor production	0.91	1	GO:0031175	neuron projection development	7.14		1		
GO:0032148	activation of protein kinase B activity	0.91	1	GO:0031115	negative regulation of microtubule polymerization	7.14		1		
GO:0031663	lipopolysaccharide-mediated signaling pathway	0.91	1	GO:0030431	sleep	7.14		1		

GO:0031175	neuron projection development	0.91	1	GO:0030155	regulation of cell adhesion	7.14		1		
GO:0031115	negative regulation of microtubule polymerization	0.91	1	GO:0030101	natural killer cell activation	7.14		1		
GO:0030431	sleep	0.91	1	GO:0030036	actin cytoskeleton organization	7.14		1		
GO:0030155	regulation of cell adhesion	0.91	1	GO:0030032	lamellipodium assembly	7.14		1		
GO:0030101	natural killer cell activation	0.91	1	GO:0030030	cell projection organization	7.14		1		
GO:0030036	actin cytoskeleton organization	0.91	1	GO:0019083	viral transcription	7.14		1		
GO:0030032	lamellipodium assembly	0.91	1	GO:0014070	response to organic cyclic compound	7.14		1		
GO:0030030	cell projection organization	0.91	1	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	7.14		1		
GO:0019083	viral transcription	0.91	1	GO:0010744	positive regulation of macrophage derived foam cell differentiation	7.14		1		
GO:0014070	response to organic cyclic compound	0.91	1	GO:0010628	positive regulation of gene expression	7.14		1		
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	0.91	1	GO:0008284	positive regulation of cell proliferation	7.14		1		
GO:0010628	positive regulation of gene expression	0.91	1	GO:0007596	blood coagulation	7.14		1		

Supptbl30_RNAseq_SigGenes_CVvsMock															
Gene	baseMean	log2FoldChange	IfcSE	stat	pvalue	padj	Hsap_EntryID	Hsap_GeneSymbol	Hsap_GeneName	Hsap_ProteinID	GalGal_EntryID	GalGal_GeneSymbol	GalGal_GeneName	GalGal_ProteinID	
CIRC	1973.70451	9.188293	0.46	10.609	3E-26	5.3E-24	#NV	#NV	#NV	#NV	#NV	#NV	#NV	#NV	
ENSG00000077782	165.417566	3.040421	0.63	4.4639	8E-06	0.00088	2260	FGFR1	fibroblast growth factor receptor 1	#NV	#NV	#NV	#NV	#NV	
ENSG00000100314	50.1338946	-1.7092	0.66	-4.064	5E-05	0.00499	164633	CABP7	calcium binding protein 7	ENSP00000216144	#NV	#NV	#NV	#NV	
ENSG00000100678	307.299392	2.991145	0.66	6.1733	7E-10	8.5E-08	6547	SLC8A3	solute carrier family 8 member A3	#NV	#NV	#NV	#NV	#NV	
ENSG00000113140	501.156999	4.058727	0.56	6.3549	2E-10	2.7E-08	6678	SPARC	secreted protein acidic and cysteine rich	#NV	#NV	#NV	#NV	#NV	
ENSG00000123572	1797.00782	-2.60513	0.38	-4.438	9E-06	0.00098	203447	NRK	Nik related kinase	#NV	#NV	#NV	#NV	#NV	
ENSG00000124145	124.897356	2.908933	0.58	3.9952	6E-05	0.00657	6385	SDC4	syndecan 4	ENSP00000361818	#NV	#NV	#NV	#NV	
ENSG00000125910	222.87833	-3.09378	0.54	-4.027	6E-05	0.00579	8698	S1PR4	sphingosine-1-phosphate receptor 4	ENSP00000246115	#NV	#NV	#NV	#NV	
ENSG00000126803	3202.78286	3.571942	0.32	8.1288	4E-16	6.1E-14	3306	HSPA2	heat shock protein family A (Hsp70) member 2	ENSP00000378199	#NV	#NV	#NV	#NV	
ENSG00000131711	104.38603	2.131659	0.67	3.8886	0.0001	0.00989	4131	MAP1B	microtubule associated protein 1B	#NV	#NV	#NV	#NV	#NV	
ENSG00000135114	739.542589	2.957902	0.42	4.9846	6E-07	7.2E-05	8638	OASL	2'-5'-oligoadenylate synthetase like	#NV	#NV	#NV	#NV	#NV	
ENSG00000142627	189.006852	3.092017	0.54	4.3168	2E-05	0.00167	1969	EPHA2	EPH receptor A2	#NV	#NV	#NV	#NV	#NV	
ENSG00000149451	1448.3078	-2.29579	0.29	-4.693	3E-06	0.00031	80332	ADAM33	ADAM metallopeptidase domain 33	#NV	#NV	#NV	#NV	#NV	
ENSG00000151929	235.20746	5.197788	0.54	7.6658	2E-14	2.4E-12	9531	BAG3	BCL2 associated athanogene 3	ENSP00000358081	#NV	#NV	#NV	#NV	
ENSG00000153246	105.433531	-3.47876	0.66	-5.029	5E-07	5.7E-05	22925	PLA2R1	phospholipase A2 receptor 1	#NV	#NV	#NV	#NV	#NV	
ENSG00000177469	63.0329423	2.765872	0.67	4.1937	3E-05	0.00287	284119	CAVIN1	caveolae associated protein 1	#NV	#NV	#NV	#NV	#NV	
ENSG00000181649	349.942477	4.053217	0.59	6.1283	9E-10	1.1E-07	7262	PHLDA2	pleckstrin homology like domain family A member 2	ENSP00000319231	#NV	#NV	#NV	#NV	
ENSG00000185745	231.985501	3.134733	0.63	4.6158	4E-06	0.00044	3434	IFIT1	interferon induced protein with tetratricopeptide repeats 1	ENSP00000360869	#NV	#NV	#NV	#NV	
ENSG00000186431	237.095436	6.033883	0.57	7.6504	2E-14	2.7E-12	2204	FCAR	Fc fragment of IgA receptor	ENSP00000477977	#NV	#NV	#NV	#NV	
ENSG00000262664	60.064329	1.938699	0.67	4.389	1E-05	0.00122	124641	OVCA2	OVCA2, serine hydrolase domain containing	ENSP00000461388	#NV	#NV	#NV	#NV	

UL22	6844.90673	10.57959	0.41	12.111	9E-34	3.2E-31	#NV	#NV		#NV						
UL23	378.236366	7.028752	0.53	8.5098	2E-17	2.5E-15	#NV	#NV		#NV						
UL24	1430.76793	8.586834	0.49	10.112	5E-24	8.9E-22	#NV	#NV		#NV						
UL25	1750.22667	9.438999	0.45	10.769	5E-27	1E-24	#NV	#NV		#NV						
UL26	9584.66027	11.14421	0.43	12.53	5E-36	2.6E-33	#NV	#NV		#NV						
UL26.5	18644.6839	7.814648	0.55	12.77	2E-37	1.5E-34	#NV	#NV		#NV						
UL27	13075.3135	11.47772	0.42	12.16	5E-34	1.9E-31	#NV	#NV		#NV						
UL28	2126.79419	9.234869	0.46	10.668	1E-26	3E-24	#NV	#NV		#NV						
UL29	12124.4661	11.61968	0.41	12.943	3E-38	1.8E-35	#NV	#NV		#NV						
UL3	7710.25426	10.86793	0.43	12.262	1E-34	5.8E-32	#NV	#NV		#NV						
UL3.5	1879.16249	8.923131	0.47	9.7403	2E-22	3.4E-20	#NV	#NV		#NV						
UL30	4677.35748	1.900415	0.67	6.2169	5E-10	6.5E-08	#NV	#NV		#NV						
UL31	10849.1074	10.95248	0.42	15.741	8E-56	1.5E-52	#NV	#NV		#NV						
UL32	827.34748	7.393804	0.53	9.1045	9E-20	1.3E-17	#NV	#NV		#NV						
UL33	7796.95753	10.90218	0.41	14.316	2E-46	2.4E-43	#NV	#NV		#NV						
UL34	4612.57135	10.23549	0.44	11.65	2E-31	6.8E-29	#NV	#NV		#NV						
UL35	6622.58307	10.50734	0.43	11.255	2E-29	5.4E-27	#NV	#NV		#NV						
UL36	8672.47024	10.89386	0.39	15.865	1E-56	3.1E-53	#NV	#NV		#NV						
UL37	1173.11147	8.488278	0.48	9.9498	3E-23	4.3E-21	#NV	#NV		#NV						
UL38	4424.20685	10.13972	0.44	11.547	8E-31	2.2E-28	#NV	#NV		#NV						
UL39	11127.2157	11.59032	0.4	12.883	6E-38	3.7E-35	#NV	#NV		#NV						
UL4	2574.55706	9.098209	0.46	10.609	3E-26	5.3E-24	#NV	#NV		#NV						
UL40	15146.3634	11.76528	0.4	12.379	3E-35	1.5E-32	#NV	#NV		#NV						
UL41	1356.29463	8.686202	0.47	10.125	4E-24	7.9E-22	#NV	#NV		#NV						
UL42	14595.4997	11.77021	0.42	13.123	2E-39	1.8E-36	#NV	#NV		#NV						
UL43	23166.2357	11.96219	0.41	15.741	8E-56	1.5E-52	#NV	#NV		#NV						
UL44	11986.976	11.70492	0.42	12.312	8E-35	3.3E-32	#NV	#NV		#NV						
UL45	921.092746	8.190333	0.51	9.6852	3E-22	5.7E-20	#NV	#NV		#NV						
UL46	21027.9005	11.96158	0.41	13.627	3E-42	2.8E-39	#NV	#NV		#NV						
UL47	3704.25889	10.23837	0.43	11.578	5E-31	1.6E-28	#NV	#NV		#NV						
UL48	38802.977	12.60554	0.4	18.271	1E-74	7.8E-71	#NV	#NV		#NV						
UL49	16165.8036	11.77363	0.4	15.451	7E-54	1.2E-50	#NV	#NV		#NV						
UL49.5	17307.4889	11.37162	0.39	16.622	5E-62	1.8E-58	#NV	#NV		#NV						
UL5	1198.72993	8.569147	0.46	9.9756	2E-23	3.4E-21	#NV	#NV		#NV						
UL50	776.890698	7.623173	0.5	9.1765	4E-20	6.8E-18	#NV	#NV		#NV						
UL51	6507.67035	10.72054	0.45	12.155	5E-34	1.9E-31	#NV	#NV		#NV						
UL52	3126.10668	9.817747	0.46	11.249	2E-29	5.6E-27	#NV	#NV		#NV						
UL53	2504.97521	9.459443	0.45	10.888	1E-27	3E-25	#NV	#NV		#NV						
UL54	15843.7267	11.86026	0.4	12.48	1E-35	4.4E-33	#NV	#NV		#NV						
UL55	9279.91185	11.16091	0.44	12.567	3E-36	1.7E-33	#NV	#NV		#NV						
UL56	33361.5333	4.677625	0.63	12.592	2E-36	1.3E-33	#NV	#NV		#NV						
UL6	945.847293	8.369631	0.48	9.1145	8E-20	1.2E-17	#NV	#NV		#NV						
UL7	2240.72345	9.174526	0.46	10.65	2E-26	3.6E-24	#NV	#NV		#NV						
UL8	3594.12831	10.08686	0.43	11.444	3E-30	6.6E-28	#NV	#NV		#NV						
UL9	1774.92358	8.981226	0.47	10.45	1E-25	2.8E-23	#NV	#NV		#NV						
US1	7958.33282	11.16792	0.42	12.49	8E-36	4.1E-33	#NV	#NV		#NV						

Supptbl31_RNAseq_SigGenes_RB1BvsMock															
Gene	baseMean	log2FoldChange	IfcSE	stat	pvalue	padj	Hsap_EntryID	Hsap_GeneSymbol	Hsap_GeneName	Hsap_ProteinID	GalGal_EntrezID	GalGal_GeneSymbol	GalGal_GeneNameID	GalGal_ProteinID	
CIRC	1973.70451	9.042976	0.48	10.4	1.6E-25	0	#NV	#NV	#NV	#NV	#NV	#NV	#NV	#NV	
ENSG00000007171	164.901662	-2.920972	0.64	-4	6.3E-05	0	4843	NOS2	nitric oxide synthase 2	#NV	#NV	#NV	#NV	#NV	
ENSG00000007866	53.4949579	3.085491	0.66	3.78	0.00016	0.01	7005	TEAD3	TEA domain transcription factor 3	#NV	#NV	#NV	#NV	#NV	
ENSG00000026297	111.143459	-2.921674	0.64	-4.33	1.5E-05	0	8635	RNASET2	ribonuclease T2	#NV	#NV	#NV	#NV	#NV	
ENSG0000044446	138.47382	-2.672537	0.64	-4.02	5.8E-05	0	5256	PHKA2	phosphorylase kinase regulatory subunit alpha 2	#NV	#NV	#NV	#NV	#NV	
ENSG0000050767	101.120774	-2.638667	0.66	-4.7	2.6E-06	0	91522	COL23A1	collagen type XXIII alpha 1 chain	#NV	#NV	#NV	#NV	#NV	
ENSG0000054690	43.6707204	2.540296	0.64	4.09	4.4E-05	0	57475	PLEKHH1	pleckstrin homology, MyTH4 and FERM domain containing H1	#NV	#NV	#NV	#NV	#NV	
ENSG0000056972	174.162729	-3.42648	0.63	-5.07	4E-07	0	10758	TRAF3IP2	TRAF3 interacting protein 2	#NV	#NV	#NV	#NV	#NV	
ENSG0000057468	141.031289	-3.38014	0.64	-4.84	1.3E-06	0	4438	MSH4	mutS homolog 4	ENSP00000263	#NV	#NV	#NV	#NV	
ENSG0000057704	142.909603	-2.646941	0.65	-4.07	4.6E-05	0	57458	TMCC3	transmembrane and coiled-coil domain family 3	#NV	#NV	#NV	#NV	#NV	
ENSG0000077782	165.417566	3.696642	0.65	5.07	4E-07	0	2260	FGFR1	fibroblast growth factor receptor 1	#NV	#NV	#NV	#NV	#NV	
ENSG0000088826	36.7456588	2.297629	0.63	3.83	0.00013	0.01	54498	SMOX	spermine oxidase	#NV	#NV	#NV	#NV	#NV	
ENSG0000100505	77.2514361	3.868401	0.67	5.14	2.8E-07	0	114088	TRIM9	tripartite motif containing 9	#NV	#NV	#NV	#NV	#NV	
ENSG0000100522	462.641021	2.647344	0.44	3.99	6.5E-05	0	64841	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	ENSP00000216	#NV	#NV	#NV	#NV	
ENSG0000100678	307.299392	2.911645	0.67	5.64	1.7E-08	0	6547	SLC8A3	solute carrier family 8 member A3	#NV	#NV	#NV	#NV	#NV	

ENSG00000101966	60.0069431	-2.066053	0.67	-4.06	5E-05	0.331	XIAP	X-linked inhibitor of apoptosis	#NV	#NV	#NV	#NV	#NV
ENSG00000106211	212.432533	3.387645	0.66	4.62	3.9E-06	0.3315	HSPB1	heat shock protein family B (small) member 1	ENSP00000248	#NV	#NV	#NV	#NV
ENSG00000110328	65.1503203	2.030671	0.65	3.88	0.0001	0.01	GALNT18	polypeptide N-acetylgalactosaminyltransferase 18	ENSP00000227	#NV	#NV	#NV	#NV
ENSG00000111731	285.093983	-2.884808	0.55	-3.99	6.5E-05	0.9847	C2CD5	C2 calcium dependent domain containing 5	#NV	#NV	#NV	#NV	#NV
ENSG00000112679	78.6405177	-1.999089	0.67	-4.19	2.8E-05	0.56940	DUSP22	dual specificity phosphatase 22	#NV	#NV	#NV	#NV	#NV
ENSG00000113140	501.156999	5.197888	0.59	7.67	1.7E-14	0.6678	SPARC	secreted protein acidic and cysteine rich	#NV	#NV	#NV	#NV	#NV
ENSG00000114541	103.904781	-2.286641	0.67	-4.48	7.3E-06	0.23150	FRMD4B	FERM domain containing 4B	#NV	#NV	#NV	#NV	#NV
ENSG00000116704	91.0416216	-2.579768	0.65	-3.91	9.3E-05	0.01	SLC35D1	solute carrier family 35 member D1	ENSP00000235	#NV	#NV	#NV	#NV
ENSG00000116793	91.3233239	-2.840513	0.66	-4.74	2.1E-06	0.10745	PHTF1	putative homeodomain transcription factor 1	#NV	#NV	#NV	#NV	#NV
ENSG00000119403	153.378777	-2.561175	0.64	-3.74	0.00018	0.01	PHF19	PHD finger protein 19	#NV	#NV	#NV	#NV	#NV
ENSG00000119661	164.494517	3.466986	0.62	4.46	8.2E-06	0.83544	DNAL1	dynein axonemal light chain 1	#NV	#NV	#NV	#NV	#NV
ENSG00000124145	124.897356	3.687245	0.61	4.91	9.3E-07	0.6385	SDC4	syndecan 4	ENSP00000361	#NV	#NV	#NV	#NV
ENSG00000124762	305.4201	3.125415	0.54	4.28	1.8E-05	0.1026	CDKN1A	cyclin dependent kinase inhibitor 1A	#NV	#NV	#NV	#NV	#NV
ENSG00000125355	108.449905	-2.635609	0.65	-3.8	0.00015	0.01	TMEM255A	transmembrane protein 255A	#NV	#NV	#NV	#NV	#NV
ENSG00000125910	222.87833	-5.294117	0.6	-6.26	4E-10	0.8698	S1PR4	sphingosine-1-phosphate receptor 4	ENSP00000246	#NV	#NV	#NV	#NV

ENSG00000126803	3202.78286	3.975574	0.36	8.51	1.8E-17	0	3306	HSPA2	heat shock protein family A (Hsp70) member 2	ENSP00000378	#NV	#NV	#NV	#NV
ENSG00000128218	110.589245	-3.874355	0.65	-5.27	1.4E-07	0	29802	VPREB3	V-set pre-B cell surrogate light chain 3	ENSP00000381	#NV	#NV	#NV	#NV
ENSG00000131711	104.38603	3.161405	0.67	4.76	1.9E-06	0	4131	MAP1B	microtubule associated protein 1B	#NV	#NV	#NV	#NV	#NV
ENSG00000132205	78.5113274	4.193952	0.67	4.71	2.5E-06	0	84034	EMILIN2	elastin microfibril interfacser 2	#NV	#NV	#NV	#NV	#NV
ENSG00000132334	105.380873	-3.497117	0.64	-4.33	1.5E-05	0	5791	PTPRE	protein tyrosine phosphatase, receptor type E	#NV	#NV	#NV	#NV	#NV
ENSG00000132429	70.5497653	-2.589012	0.66	-4.44	9.1E-06	0	64208	POPD3	popeye domain containing 3	ENSP00000254	#NV	#NV	#NV	#NV
ENSG00000132677	104.627393	-3.727051	0.64	-4.42	9.9E-06	0	57127	RHBG	Rh family B glycoprotein (gene/pseudogene)	#NV	#NV	#NV	#NV	#NV
ENSG00000133466	82.895501	-1.824241	0.67	-4.1	4.1E-05	0	114904	C1QTNF6	C1q and TNF related 6	#NV	#NV	#NV	#NV	#NV
ENSG00000134369	247.219381	3.628964	0.61	4.8	1.6E-06	0	89796	NAV1	neuron navigator 1	#NV	#NV	#NV	#NV	#NV
ENSG00000135114	739.542589	3.589435	0.45	5.95	2.7E-09	0	8638	OASL	2'-5'-oligoadenylate synthetase like	#NV	#NV	#NV	#NV	#NV
ENSG00000135272	48.4858647	-2.265677	0.67	-4.02	5.8E-05	0	29969	MDFIC	MyoD family inhibitor domain containing	#NV	#NV	#NV	#NV	#NV
ENSG00000136048	49.1326403	-1.956571	0.67	-3.87	0.00011	0.01	55332	DRAM1	DNA damage regulated autophagy modulator 1	#NV	#NV	#NV	#NV	#NV
ENSG00000136068	1393.67158	-3.15948	0.5	-4.74	2.2E-06	0	2317	FLNB	filamin B	#NV	#NV	#NV	#NV	#NV
ENSG00000139223	91.0681008	-2.158046	0.65	-4.07	4.7E-05	0	23519	ANP32D	acidic nuclear phosphoprotein 32 family member D	ENSP00000266	#NV	#NV	#NV	#NV
ENSG00000141524	293.812611	-4.187388	0.6	-6.08	1.2E-09	0	11322	TMC6	transmembrane channel like 6	#NV	#NV	#NV	#NV	#NV

ENSG00000142089	1752.70422	2.957639	0.39	5.24	1.6E-07	0	10410	IFITM3	interferon induced transmembrane protein 3	#NV	#NV	#NV	#NV	#NV
ENSG00000143061	93.439765	2.195248	0.66	3.75	0.00018	0.01	3321	IGSF3	immunoglobulin superfamily member 3	#NV	#NV	#NV	#NV	#NV
ENSG00000143369	117.122072	3.000985	0.66	3.75	0.00018	0.01	1893	ECM1	extracellular matrix protein 1	#NV	#NV	#NV	#NV	#NV
ENSG00000144182	136.668275	-2.831068	0.63	-4.3	1.7E-05	0	51601	LIPT1	lipoyltransferase 1	#NV	#NV	#NV	#NV	#NV
ENSG00000144597	146.340386	-3.459449	0.62	-4.99	5.9E-07	0	85403	EAF1	ELL associated factor 1	#NV	#NV	#NV	#NV	#NV
ENSG00000144935	85.1292054	-3.337954	0.65	-4.43	9.6E-06	0	7220	TRPC1	transient receptor potential cation channel subfamily C member 1	#NV	#NV	#NV	#NV	#NV
ENSG00000149451	1448.3078	-2.198492	0.32	-3.94	8.1E-05	0	80332	ADAM33	ADAM metallopeptidase domain 33	#NV	#NV	#NV	#NV	#NV
ENSG00000151929	235.20746	5.284914	0.57	7.47	8E-14	0	9531	BAG3	BCL2 associated athanogene 3	ENSP00000358	#NV	#NV	#NV	#NV
ENSG00000154096	303.990886	3.412833	0.65	4.22	2.4E-05	0	7070	THY1	Thy-1 cell surface antigen	#NV	#NV	#NV	#NV	#NV
ENSG00000155545	81.7184432	-2.290727	0.66	-4.26	2E-05	0	166968	MIER3	MIER family member 3	#NV	#NV	#NV	#NV	#NV
ENSG00000155719	149.703367	-4.267412	0.62	-5.62	1.9E-08	0	146183	OTOA	otoancorin	#NV	#NV	#NV	#NV	#NV
ENSG00000158006	151.334784	-4.221513	0.61	-5.37	7.7E-08	0	5051	PAFAH2	platelet activating factor acetylhydrolase 2	#NV	#NV	#NV	#NV	#NV
ENSG00000158406	277.0671	3.097404	0.64	3.92	8.7E-05	0.01	8365	HIST1H4	histone cluster 1 H4 family member h	ENSP00000489	#NV	#NV	#NV	#NV
ENSG00000162738	56.5053628	-2.372122	0.67	-4.18	2.9E-05	0	57216	VANGL2	VANGL planar cell polarity protein 2	ENSP00000357	#NV	#NV	#NV	#NV
ENSG00000162976	54.8948948	-2.185775	0.67	-4.01	6.1E-05	0	130814	PQLC3	PQ loop repeat containing 3	#NV	#NV	#NV	#NV	#NV
ENSG00000163545	41.6161057	2.442169	0.63	3.89	9.9E-05	0.01	81788	NUAK2	NUAK family kinase 2	ENSP00000356	#NV	#NV	#NV	#NV
ENSG00000164111	280.009165	3.197122	0.59	4.18	2.9E-05	0	308	ANXA5	annexin A5	#NV	#NV	#NV	#NV	#NV

ENSG00000166123	63.88266	-2.508223	0.67	-4.33	1.5E-05	0.84706	GPT2	glutamic--pyruvic transaminase 2	#NV	#NV	#NV	#NV	#NV
ENSG00000166575	96.6483879	-2.247743	0.67	-4.44	9E-06	0.65084	TMEM135	transmembrane protein 135	#NV	#NV	#NV	#NV	#NV
ENSG00000168785	71.3575128	-2.62495	0.67	-4.46	8.1E-06	0.10098	TSPAN5	tetraspanin 5	ENSP00000421	#NV	#NV	#NV	#NV
ENSG00000170989	53.3609111	-2.031732	0.66	-3.77	0.00016	0.011901	S1PR1	sphingosine-1-phosphate receptor 1	ENSP00000305	#NV	#NV	#NV	#NV
ENSG00000171097	89.192642	-2.717145	0.65	-4.04	5.3E-05	0.883	KYAT1	kynurenine aminotransferase 1	#NV	#NV	#NV	#NV	#NV
ENSG00000171476	198.003302	-3.028297	0.6	-4.3	1.7E-05	0.84525	HOPX	HOP homeobox	#NV	#NV	#NV	#NV	#NV
ENSG00000173083	103.82873	-2.505611	0.67	-4.63	3.7E-06	0.10855	HPSE	heparanase	#NV	#NV	#NV	#NV	#NV
ENSG00000176533	98.1910363	-1.566912	0.67	-4.07	4.7E-05	0.2788	GNG7	G protein subunit gamma 7	#NV	#NV	#NV	#NV	#NV
ENSG00000179604	262.194768	3.502608	0.65	4.68	2.9E-06	0.23580	CDC42E_P4	CDC42 effector protein 4	ENSP00000338	#NV	#NV	#NV	#NV
ENSG00000181396	53.0326334	-1.761936	0.67	-3.8	0.00015	0.0179701	OGFOD3	2-oxoglutarate and iron dependent oxygenase domain containing 3	#NV	#NV	#NV	#NV	#NV
ENSG00000181649	349.942477	3.954771	0.62	5.58	2.3E-08	0.7262	PHLDA2	pleckstrin homology like domain family A member 2	ENSP00000319	#NV	#NV	#NV	#NV
ENSG00000181704	67.5025313	-2.181401	0.66	-4.05	5.2E-05	0.286451	YIPF6	Yip1 domain family member 6	#NV	#NV	#NV	#NV	#NV
ENSG00000182158	110.124275	-3.209258	0.63	-4.59	4.3E-06	0.64764	CREB3L2	cAMP responsive element binding protein 3 like 2	#NV	#NV	#NV	#NV	#NV
ENSG00000182866	50.4280559	-1.76933	0.67	-3.75	0.00017	0.013932	LCK	LCK proto-oncogene, Src family tyrosine kinase	#NV	#NV	#NV	#NV	#NV
ENSG00000185022	340.385033	3.024028	0.49	4.42	9.9E-06	0.23764	MAFF	MAF bZIP transcription factor F	#NV	#NV	#NV	#NV	#NV

ENSG00000185477	145.886809	-3.122728	0.64	-4.58	4.7E-06	0	285513	GPRIN3	GPRIN family member 3	ENSP00000476	#NV	#NV	#NV	#NV
ENSG00000185551	90.3154662	2.755272	0.67	3.98	6.8E-05	0	7026	NR2F2	nuclear receptor subfamily 2 group F member 2	#NV	#NV	#NV	#NV	#NV
ENSG00000185745	231.985501	3.527457	0.65	4.86	1.2E-06	0	3434	IFIT1	interferon induced protein with tetratricopeptide repeats 1	ENSP00000360	#NV	#NV	#NV	#NV
ENSG00000186431	237.095436	5.468722	0.59	7.06	1.7E-12	0	2204	FCAR	Fc fragment of IgA receptor	ENSP00000477	#NV	#NV	#NV	#NV
ENSG00000196372	60.7865864	-1.937963	0.67	-3.85	0.00012	0.01	79754	ASB13	ankyrin repeat and SOCS box containing 13	#NV	#NV	#NV	#NV	#NV
ENSG00000198018	162.250614	-3.199438	0.6	-4.64	3.5E-06	0	57089	ENTPD7	ectonucleoside triphosphate diphosphohydrolase 7	ENSP00000359	#NV	#NV	#NV	#NV
ENSG00000198554	253.303454	-2.768514	0.63	-3.94	8E-05	0	11169	WDHD1	WD repeat and HMG-box DNA binding protein 1	#NV	#NV	#NV	#NV	#NV
ENSG00000262664	60.064329	1.863359	0.66	4.14	3.5E-05	0	124641	OVCA2	OVCA2, serine hydrolase domain containing	ENSP00000461	#NV	#NV	#NV	#NV
ENSGALG0000007526	133.900645	-2.175421	0.67	-3.91	9.3E-05	0.01	#NV	#NV	#NV	422305	ES1ML2	ES1 protein homolog	ENSGALP0000012159	
ENSGALG0000014978	1047.50829	-2.659331	0.45	-4.03	5.5E-05	0	#NV	#NV	#NV	427211	IQGAP2	IQ motif containing	ENSGALP0000046997	
ENSGALG0000015059	378.047387	-4.298061	0.56	-6.57	5E-11	0	#NV	#NV	#NV	418339	FAAHL	fatty acid amid	ENSGALP0000051106	
ENSGALG0000015398	1393.94452	-2.309085	0.36	-3.82	0.00013	0.01	#NV	#NV	#NV	418426	BTLA	B and T lymphocyte	ENSGALP0000063786	
ENSGALG0000023818	2880.45608	6.650882	0.46	12.5	1.3E-35	0	#NV	#NV	#NV	428310	HSPB9	heat shock protein	ENSGALP0000063630	
ENSGALG0000028567	113.99874	2.706849	0.67	3.88	0.00011	0.01	#NV	#NV	#NV	396215	MYL9	myosin, light chain	ENSGALP0000041913	
ENSGALG0000038019	241.865329	5.5531	0.59	7.43	1.1E-13	0	#NV	#NV	#NV	#NV	#NV	#NV	#NV	
ENSGALG0000040995	622.330384	2.666428	0.64	4.71	2.4E-06	0	#NV	#NV	#NV	#NV	#NV	#NV	#NV	
ENSGALG0000041683	167.511059	4.405097	0.64	5.95	2.7E-09	0	#NV	#NV	#NV	#NV	#NV	#NV	#NV	
ENSGALG0000045136	102.277387	-1.308479	0.67	-3.78	0.00015	0.01	#NV	#NV	#NV	#NV	#NV	#NV	#NV	
ENSGALG0000045632	356.119917	3.722856	0.63	5.15	2.6E-07	0	#NV	#NV	#NV	#NV	#NV	#NV	#NV	

Supptbl32_RNAseq_SigGenes_CVvsRB1B																
Gene	log2FoldC								Hsap_Eentr	Hsap_GeneS	Hsap_GeneNa	GalGalGeneSy			GalGalGeneN	
	baseMean	change	IfcSE	stat	pvalue	padj	ezID	ymbol				GalGalEntrezID	mbol	ame	GalGalProteinID	
ENSG00000007866	53.49495789	-3.204624	0.66	-4.59	4.4E-06	0.002	7005	TEAD3	TEA domain transcription factor 3	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000050767	101.1207739	2.22495	0.66	4.379	1.2E-05	0.004	91522	COL23A1	collagen type XXIII alpha 1 chain mutS homolog	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000057468	141.0312891	2.645438	0.64	4.148	3.4E-05	0.009	4438	MSH4	4	ENSP0000263187	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000078124	66.22107756	2.707282	0.67	4.449	8.6E-06	0.003	55331	ACER3	alkaline ceramidase 3	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000102595	232.4666465	2.881901	0.65	4.337	1.4E-05	0.005	55757	UGGT2	UDP-glucose glycoprotein glucosyltransf erase 2 coiled-coil serine rich	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000107771	62.60784017	2.093067	0.67	4.104	4.1E-05	0.01	54462	CCSER2	protein 2	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000115457	41.36365758	-1.131074	0.53	-7.11	1.2E-12	5E-09	3485	IGFBP2	insulin like growth factor binding protein 2 elastin	ENSP0000401698	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000132205	78.51132742	-4.37076	0.67	-5.52	3.4E-08	3E-05	84034	EMILIN2	microfibril interfacer 2 glutamate-ammonia ligase	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000135821	38.5290406	-1.334967	0.54	-7.43	1.1E-13	6E-10	2752	GLUL	THUMP domain	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000138050	128.5629627	3.040722	0.61	4.165	3.1E-05	0.008	80745	THUMPD2	containing 2	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000141524	293.8126115	3.810319	0.6	5.682	1.3E-08	2E-05	11322	TMC6	transmembrane channel like 6	#NV	#NV	#NV	#NV	#NV	#NV	#NV
ENSG00000144182	136.6682751	3.039133	0.63	4.545	5.5E-06	0.002	51601	LIPT1	lipoyltransferase 1	#NV	#NV	#NV	#NV	#NV	#NV	#NV

ENSG00000144597	146.340386	2.783934	0.62	4.164	3.1E-05	0.008	85403	EAF1	ELL associated factor 1	#NV	#NV	#NV	#NV	
ENSG00000154856	631.7928113	-3.142342	0.66	-4.79	1.7E-06	8E-04	147495	APCDD1	APC down-regulated 1	#NV	#NV	#NV	#NV	
ENSG00000155545	81.71844316	2.526737	0.66	4.448	8.7E-06	0.003	166968	MIER3	MIER family member 3	#NV	#NV	#NV	#NV	
ENSG00000155719	149.7033674	3.267542	0.62	4.869	1.1E-06	6E-04	146183	OTOA	otoancorin platelet activating factor acetylhydrolase 2	#NV	#NV	#NV	#NV	
ENSG00000158006	151.3347841	2.991423	0.61	4.199	2.7E-05	0.008	5051	PAFAH2	ubiquitin specific peptidase 49	#NV	#NV	#NV	#NV	
ENSG00000164663	102.0078206	3.361214	0.64	4.231	2.3E-05	0.007	25862	USP49	transmembrane protein 135	#NV	#NV	#NV	#NV	
ENSG00000166575	96.64838791	2.269349	0.67	4.457	8.3E-06	0.003	65084	TMEM135	tubulin tyrosine ligase like 11	#NV	#NV	#NV	#NV	
ENSG00000175764	171.923911	3.497284	0.58	4.88	1.1E-06	6E-04	158135	TTLL11	G protein subunit gamma 7	#NV	#NV	#NV	#NV	
ENSG00000176533	98.19103634	1.637762	0.67	4.131	3.6E-05	0.009	2788	GNG7	Yip1 domain family	#NV	#NV	#NV	#NV	
ENSG00000181704	67.50253129	2.686551	0.66	4.442	8.9E-06	0.003	286451	YIPF6	member 6	#NV	#NV	#NV	#NV	
ENSG00000182158	110.1242754	2.835819	0.63	4.202	2.7E-05	0.008	64764	CREB3L2	cAMP responsive element binding protein 3 like 2	#NV	#NV	#NV	#NV	
ENSG00000184381	161.6470181	3.141849	0.55	4.422	9.8E-06	0.004	8398	PLA2G6	phospholipase A2 group VI	#NV	#NV	#NV	#NV	
ENSG00000186130	80.61139854	2.316138	0.67	4.397	1.1E-05	0.004	10773	ZBTB6	zinc finger and BTB domain containing 6	ENSP00000362763	#NV	#NV	#NV	#NV
ENSG00000189283	54.2859888	-2.43064	0.65	-4.33	1.5E-05	0.005	2272	FHIT	fragile histidine triad	ENSP00000417557	#NV	#NV	#NV	#NV

Supptbl33_RNAseq_QuickGO_CVI988vsmock

GO IDs (by annotation)				GO IDs (by protein)			
Code	Name	Percentage	Count	Code	Name	Percentage	Count
	fibroblast growth factor receptor signaling pathway	4.26	16	GO:0008543	fibroblast growth factor receptor signaling pathway	4.76	1
GO:0008543	positive regulation of cell proliferation	2.66	10	GO:0008284	positive regulation of cell proliferation	4.76	1
GO:0008284	termination of RNA polymerase I transcription	1.33	5	GO:0006363	termination of RNA polymerase I transcription	4.76	1
GO:0006363	response to virus peptidyl-tyrosine phosphorylation protein	1.33	5	GO:0009615	response to virus peptidyl-tyrosine phosphorylation	9.52	2
GO:0018108	phosphorylation receptor-mediated endocytosis	1.33	5	GO:0006468	protein phosphorylation receptor-mediated endocytosis	9.52	2
GO:0006468	GO:0006898	1.06	4	GO:0006898	GO:0007165	19.05	4
GO:0006898	signal transduction G-protein coupled receptor signaling pathway	1.06	4	GO:0007165	signal transduction G-protein coupled receptor signaling pathway	19.05	4
GO:0007165	GO:0007186	1.06	4	GO:0007186	GO:0009408	4.76	1
GO:0007186	response to heat	1.06	4	GO:0009408	response to cold	4.76	1
GO:0009408	GO:0009409	1.06	4	GO:0009409	negative regulation of viral genome replication defense response to virus	9.52	2
GO:0045071	transcription initiation from RNA polymerase I promoter	1.06	4	GO:0045071	transcription initiation from RNA polymerase I promoter	9.52	2
GO:0051607	GO:0006361	1.06	4	GO:0006361	GO:0006508	4.76	1
GO:0051607	immune response proteolysis	1.06	4	GO:0006508	GO:0006955	4.76	1
	GO:0006955			GO:0006955	GO:0007283	14.29	3
	GO:0007283			GO:0007283	GO:0016310	4.76	1
	GO:0016310			GO:0016310	GO:0016477	14.29	3
	GO:0016477			GO:0016477	cell migration ephrin receptor	14.29	3
	GO:0048013			GO:0048013	GO:0000165	4.76	1
	GO:0000165			GO:0000165	GO:0001525	4.76	1
	GO:0001525			GO:0001525	GO:0001657	9.52	2
	GO:0001657			GO:0001657	GO:0002376	9.52	2
	GO:0002376			GO:0002376	GO:0006351	9.52	2
	GO:0006351			GO:0006351	GO:0006355	9.52	2
	GO:0006355			GO:0006355	GO:0006811	4.76	1
	GO:0006811			GO:0006811			

GO:0006814	sodium ion transport	0.53	2 GO:0006814	sodium ion transport	4.76	1
GO:0006816	calcium ion transport	0.53	2 GO:0006816	calcium ion transport	4.76	1
	mitochondrial calcium ion transmembrane transport			mitochondrial calcium ion transmembrane transport	4.76	1
GO:0006851	cellular calcium ion homeostasis	0.53	2 GO:0006851	cellular calcium ion homeostasis	4.76	1
GO:0006874	apoptotic process	0.53	2 GO:0006874	apoptotic process	9.52	2
GO:0006915	male meiotic nuclear division	0.53	2 GO:0006915	male meiotic nuclear division	4.76	1
GO:0007140	nuclear division	0.53	2 GO:0007140			
	spermatid			spermatid development	4.76	1
GO:0007286	development	0.53	2 GO:0007286	brain development	9.52	2
GO:0007420	brain development	0.53	2 GO:0007420	learning	4.76	1
GO:0007612	learning	0.53	2 GO:0007612	memory	4.76	1
GO:0007613	memory	0.53	2 GO:0007613	regulation of gene expression	9.52	2
GO:0010468	regulation of skeletal muscle contraction	0.53	2 GO:0010468	regulation of skeletal muscle contraction	4.76	1
GO:0014819	viral process	0.53	2 GO:0014819	viral process	9.52	2
GO:0016032	cell differentiation	0.53	2 GO:0016032	cell differentiation	9.52	2
GO:0030154	lung development	0.53	2 GO:0030154	lung development	9.52	2
GO:0030324	sodium ion transmembrane transport	0.53	2 GO:0030324	sodium ion transmembrane transport	4.76	1
GO:0035725	wound healing	0.53	2 GO:0035725	wound healing	9.52	2
GO:0042060	regulation of cell proliferation	0.53	2 GO:0042060	regulation of cell proliferation	9.52	2
GO:0042127	myelination	0.53	2 GO:0042127	myelination	4.76	1
GO:0042552	positive regulation of MAP kinase activity	0.53	2 GO:0042552	positive regulation of MAP kinase activity	4.76	1
GO:0043406	innate immune response	0.53	2 GO:0043406	innate immune response	9.52	2
GO:0045087	oligodendrocyte differentiation	0.53	2 GO:0045087	oligodendrocyte differentiation	4.76	1
GO:0048709	mitochondrial calcium ion homeostasis	0.53	2 GO:0048709	mitochondrial calcium ion homeostasis	4.76	1
GO:0051560	long-term synaptic potentiation	0.53	2 GO:0051560	long-term synaptic potentiation	4.76	1
GO:0060291	cell chemotaxis	0.53	2 GO:0060291	cell chemotaxis	4.76	1
GO:0060326	type I interferon signaling pathway	0.53	2 GO:0060326	type I interferon signaling pathway	9.52	2
GO:0060337	calcium ion transmembrane transport	0.53	2 GO:0060337	calcium ion transmembrane transport	4.76	1
GO:0070588	cellular response to type I interferon	0.53	2 GO:0070588	cellular response to type I interferon	4.76	1
GO:0071357		0.53	2 GO:0071357			

GO:0071360	cellular response to exogenous dsRNA	0.53	2	GO:0071360	cellular response to exogenous dsRNA	4.76	1
GO:0071456	cellular response to hypoxia	0.53	2	GO:0071456	cellular response to hypoxia	4.76	1
GO:0090238	positive regulation of arachidonic acid secretion	0.53	2	GO:0090238	positive regulation of arachidonic acid secretion	4.76	1
GO:0000122	negative regulation of transcription by RNA polymerase II	0.27	1	GO:0000122	negative regulation of transcription by RNA polymerase II	4.76	1
GO:0000226	microtubule cytoskeleton organization	0.27	1	GO:0000226	microtubule cytoskeleton organization	4.76	1
GO:0001501	skeletal system development	0.27	1	GO:0001501	skeletal system development	4.76	1
GO:0001503	ossification	0.27	1	GO:0001503	ossification	4.76	1
GO:0001523	retinoid metabolic process	0.27	1	GO:0001523	retinoid metabolic process	4.76	1
GO:0001578	microtubule bundle formation	0.27	1	GO:0001578	microtubule bundle formation	4.76	1
GO:0001649	osteoblast differentiation	0.27	1	GO:0001649	osteoblast differentiation	4.76	1
GO:0001701	in utero embryonic development	0.27	1	GO:0001701	in utero embryonic development	4.76	1
GO:0001759	organ induction	0.27	1	GO:0001759	organ induction	4.76	1
GO:0001764	neuron migration	0.27	1	GO:0001764	neuron migration	4.76	1
GO:0001816	cytokine production	0.27	1	GO:0001816	cytokine production	4.76	1
GO:0001843	neural tube closure	0.27	1	GO:0001843	neural tube closure	4.76	1
GO:0001890	placenta development	0.27	1	GO:0001890	placenta development	4.76	1
GO:0001934	positive regulation of protein phosphorylation	0.27	1	GO:0001934	positive regulation of protein phosphorylation	4.76	1
GO:0001937	negative regulation of endothelial cell proliferation	0.27	1	GO:0001937	negative regulation of endothelial cell proliferation	4.76	1
GO:0002053	positive regulation of mesenchymal cell proliferation	0.27	1	GO:0002053	positive regulation of mesenchymal cell proliferation	4.76	1
GO:0002062	chondrocyte differentiation	0.27	1	GO:0002062	chondrocyte differentiation	4.76	1
GO:0002244	hematopoietic progenitor cell differentiation	0.27	1	GO:0002244	hematopoietic progenitor cell differentiation	4.76	1
GO:0002446	neutrophil mediated immunity	0.27	1	GO:0002446	neutrophil mediated immunity	4.76	1

GO:0002576	platelet degranulation	0.27	1	GO:0002576	platelet degranulation	4.76	1
GO:0003376	sphingosine-1-phosphate signaling pathway	0.27	1	GO:0003376	sphingosine-1-phosphate signaling pathway	4.76	1
GO:0006024	glycosaminoglycan biosynthetic process	0.27	1	GO:0006024	glycosaminoglycan biosynthetic process	4.76	1
GO:0006027	glycosaminoglycan catabolic process	0.27	1	GO:0006027	glycosaminoglycan catabolic process	4.76	1
GO:0006353	DNA-templated transcription, termination	0.27	1	GO:0006353	DNA-templated transcription, termination	4.76	1
GO:0006457	protein folding	0.27	1	GO:0006457	protein folding	4.76	1
GO:0006897	endocytosis	0.27	1	GO:0006897	endocytosis	4.76	1
GO:0006986	response to unfolded protein	0.27	1	GO:0006986	response to unfolded protein	4.76	1
GO:0007141	male meiosis I	0.27	1	GO:0007141	male meiosis I	4.76	1
GO:0007154	cell communication	0.27	1	GO:0007154	cell communication	4.76	1
GO:0007155	cell adhesion	0.27	1	GO:0007155	cell adhesion	4.76	1
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0.27	1	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	4.76	1
GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	0.27	1	GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	4.76	1
GO:0007202	activation of phospholipase C	0.27	1	GO:0007202	activation of phospholipase C	4.76	1
GO:0007204	activity	0.27	1	GO:0007204	activity	4.76	1
GO:000725	positive regulation of cytosolic calcium ion concentration	0.27	1	GO:000725	positive regulation of cytosolic calcium ion concentration	4.76	1
GO:0007275	multicellular organism development	0.27	1	GO:0007275	multicellular organism development	4.76	1
GO:0007399	nervous system development	0.27	1	GO:0007399	nervous system development	4.76	1
GO:0007409	axonogenesis	0.27	1	GO:0007409	axonogenesis	4.76	1
GO:0007435	salivary gland morphogenesis	0.27	1	GO:0007435	salivary gland morphogenesis	4.76	1
GO:0007507	heart development	0.27	1	GO:0007507	heart development	4.76	1
GO:0007605	sensory perception of sound	0.27	1	GO:0007605	sensory perception of sound	4.76	1
GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	0.27	1	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	4.76	1

	intrinsic apoptotic signaling pathway in response to DNA damage	0.27	1 GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	4.76	1
GO:0009303	rRNA transcription NAD biosynthetic process	0.27	1 GO:0009303	rRNA transcription NAD biosynthetic process	4.76	1
GO:0009435		0.27	1 GO:0009435		4.76	1
GO:0009629	response to gravity animal organ	0.27	1 GO:0009629	response to gravity animal organ	4.76	1
GO:0009887	morphogenesis	0.27	1 GO:0009887	morphogenesis	4.76	1
GO:0009987	cellular process	0.27	1 GO:0009987	cellular process	4.76	1
GO:0010288	response to lead	0.27	1 GO:0010288	response to lead ion	4.76	1
	ion	0.27		positive regulation of phospholipase activity	4.76	1
GO:0010518	positive regulation of phospholipase activity	0.27	1 GO:0010518		4.76	1
	regulation of lamellipodium	0.27		regulation of lamellipodium assembly	4.76	1
GO:0010591	assembly	0.27	1 GO:0010591	positive regulation of endothelial cell	4.76	1
	positive regulation of endothelial cell	0.27		migration	4.76	1
GO:0010595	migration	0.27	1 GO:0010595		4.76	1
	negative regulation of gene expression	0.27	1 GO:0010629	negative regulation of gene expression	4.76	1
		0.27			4.76	1
GO:0010664	negative regulation of striated muscle cell apoptotic process	0.27	1 GO:0010664	negative regulation of striated muscle cell apoptotic process	4.76	1
		0.27			4.76	1
GO:0010762	regulation of fibroblast migration	0.27	1 GO:0010762	regulation of fibroblast migration	4.76	1
	positive regulation of phospholipase C	0.27		positive regulation of phospholipase C	4.76	1
GO:0010863	activity	0.27	1 GO:0010863	activity	4.76	1
	regulation of phosphate	0.27			4.76	1
GO:0010966	transport	0.27	1 GO:0010966	regulation of phosphate transport	4.76	1
	positive regulation of neuron	0.27			4.76	1
	projection	0.27		positive regulation of neuron projection	4.76	1
GO:0010976	development	0.27	1 GO:0010976	development	4.76	1
		0.27			4.76	1
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	0.27	1 GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	4.76	1
	dendrite	0.27			4.76	1
GO:0016358	development	0.27	1 GO:0016358	dendrite development	4.76	1
		0.27			4.76	1
GO:0016525	negative regulation of angiogenesis	0.27	1 GO:0016525	negative regulation of angiogenesis	4.76	1

GO:0019060	intracellular transport of viral protein in host cell	0.27	1	GO:0019060	intracellular transport of viral protein in host cell	4.76	1
GO:0019363	pyridine nucleotide biosynthetic process	0.27	1	GO:0019363	pyridine nucleotide biosynthetic process	4.76	1
GO:0019674	NAD metabolic process	0.27	1	GO:0019674	NAD metabolic process	4.76	1
GO:0021510	spinal cord development	0.27	1	GO:0021510	spinal cord development	4.76	1
GO:0021537	telencephalon development	0.27	1	GO:0021537	telencephalon development	4.76	1
GO:0021769	orbitofrontal cortex development	0.27	1	GO:0021769	orbitofrontal cortex development	4.76	1
GO:0021847	ventricular zone neuroblast division	0.27	1	GO:0021847	ventricular zone neuroblast division	4.76	1
GO:0022604	regulation of cell morphogenesis	0.27	1	GO:0022604	regulation of cell morphogenesis	4.76	1
GO:0030001	metal ion transport	0.27	1	GO:0030001	metal ion transport	4.76	1
GO:0030198	extracellular matrix organization	0.27	1	GO:0030198	extracellular matrix organization	4.76	1
GO:0030203	glycosaminoglycan metabolic process	0.27	1	GO:0030203	glycosaminoglycan metabolic process	4.76	1
GO:0030216	keratinocyte differentiation	0.27	1	GO:0030216	keratinocyte differentiation	4.76	1
GO:0030316	osteoclast differentiation	0.27	1	GO:0030316	osteoclast differentiation	4.76	1
GO:0030326	embryonic limb morphogenesis	0.27	1	GO:0030326	embryonic limb morphogenesis	4.76	1
GO:0030334	regulation of cell migration	0.27	1	GO:0030334	regulation of cell migration	4.76	1
GO:0030901	midbrain development	0.27	1	GO:0030901	midbrain development	4.76	1
GO:0031662	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle	0.27	1	GO:0031662	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle	4.76	1
GO:0032091	involved in G2/M transition of mitotic cell cycle	0.27	1	GO:0032091	negative regulation of protein binding	4.76	1
GO:0032387	negative regulation of intracellular transport	0.27	1	GO:0032387	negative regulation of intracellular transport	4.76	1

GO:0032496	response to lipopolysaccharide	0.27	1	GO:0032496	response to lipopolysaccharide	4.76	1
GO:0032526	response to retinoic acid	0.27	1	GO:0032526	response to retinoic acid	4.76	1
GO:0032781	positive regulation of ATPase activity	0.27	1	GO:0032781	positive regulation of ATPase activity	4.76	1
	positive regulation of neutrophil				positive regulation of neutrophil		
GO:0033031	apoptotic process	0.27	1	GO:0033031	apoptotic process	4.76	1
GO:0033591	response to L-ascorbic acid	0.27	1	GO:0033591	response to L-ascorbic acid	4.76	1
	mammary gland epithelial cell				mammary gland epithelial cell		
GO:0033598	proliferation	0.27	1	GO:0033598	proliferation	4.76	1
	regulation of cell adhesion mediated by integrin				regulation of cell adhesion mediated by integrin		
GO:0033628	response to cytokine	0.27	1	GO:0033628	response to cytokine	4.76	1
GO:0034097	cellular response to heat	0.27	1	GO:0034097	cellular response to heat	4.76	1
GO:0034605	cellular response to interferon-alpha	0.27	1	GO:0034605	cellular response to interferon-alpha	4.76	1
GO:0035457	fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	0.27	1	GO:0035457	fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	4.76	1
GO:0035607	phosphatidylinositol-3-phosphate biosynthetic process	0.27	1	GO:0035607	phosphatidylinositol-3-phosphate biosynthetic process	4.76	1
GO:0036092	Fc receptor signaling pathway	0.27	1	GO:0036092	Fc receptor signaling pathway	4.76	1
GO:0038093	protein refolding	0.27	1	GO:0038093	protein refolding	4.76	1
GO:0042026	neutrophil activation	0.27	1	GO:0042026	neutrophil activation	4.76	1
GO:0042119	negative regulation of T cell proliferation	0.27	1	GO:0042119	negative regulation of T cell proliferation	4.76	1
GO:0042130	inner ear morphogenesis	0.27	1	GO:0042130	inner ear morphogenesis	4.76	1
GO:0042472	outer ear morphogenesis	0.27	1	GO:0042472	outer ear morphogenesis	4.76	1
GO:0042473	middle ear morphogenesis	0.27	1	GO:0042473	middle ear morphogenesis	4.76	1
GO:0042474	positive regulation of transcription factor import into nucleus	0.27	1	GO:0042474	positive regulation of transcription factor import into nucleus	4.76	1
GO:0042993				GO:0042993		4.76	1

GO:0043009	chordate embryonic development negative regulation of apoptotic process	0.27	1 GO:0043009	chordate embryonic development negative regulation of apoptotic process	4.76	1
GO:0043066	neutrophil degranulation	0.27	1 GO:0043066	neutrophil degranulation	4.76	1
GO:0043312	positive regulation of MAPK cascade response to peptide hormone	0.27	1 GO:0043312	positive regulation of MAPK cascade response to peptide hormone	4.76	1
GO:0043434	GO:0043473	0.27	1 GO:0043434	GO:0043473	4.76	1
GO:0043473	protein kinase B signaling	0.27	1 GO:0043491	protein kinase B signaling	4.76	1
GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	0.27	1 GO:0043517	regulation of blood vessel endothelial cell migration	4.76	1
GO:0043535	cell migration	0.27	1 GO:0043535	positive regulation of blood vessel endothelial cell migration	4.76	1
GO:0043536	positive regulation of viral genome replication	0.27	1 GO:0043536	positive regulation of blood vessel endothelial cell migration	4.76	1
GO:0045070	response to ethanol	0.27	1 GO:0045070	positive regulation of viral genome replication	4.76	1
GO:0045471	regulation of cell differentiation	0.27	1 GO:0045471	response to ethanol	4.76	1
GO:0045595	positive regulation of neuron differentiation	0.27	1 GO:0045595	regulation of cell differentiation	4.76	1
GO:0045666	differentiation	0.27	1 GO:0045666	positive regulation of neuron differentiation	4.76	1
GO:0045765	regulation of angiogenesis	0.27	1 GO:0045765	regulation of angiogenesis	4.76	1
GO:0045773	positive regulation of axon extension	0.27	1 GO:0045773	positive regulation of axon extension	4.76	1
GO:0045787	positive regulation of cell cycle	0.27	1 GO:0045787	positive regulation of cell cycle	4.76	1
GO:0045860	positive regulation of protein kinase activity	0.27	1 GO:0045860	positive regulation of protein kinase activity	4.76	1
GO:0045995	regulation of embryonic development	0.27	1 GO:0045995	regulation of embryonic development	4.76	1
GO:0046058	cAMP metabolic process	0.27	1 GO:0046058	cAMP metabolic process	4.76	1
GO:0046686	response to cadmium ion	0.27	1 GO:0046686	response to cadmium ion	4.76	1

GO:0046718	viral entry into host cell	0.27	1	GO:0046718	viral entry into host cell	4.76	1
	protein autophosphorylation				protein autophosphorylation	4.76	1
GO:0046777	positive regulation of protein export from nucleus	0.27	1	GO:0046777	positive regulation of protein export from nucleus	4.76	1
GO:0046827	bone remodeling	0.27	1	GO:0046827	bone remodeling	4.76	1
GO:0046849	phosphatidylinositol phosphorylation	0.27	1	GO:0046849	phosphatidylinositol phosphorylation	4.76	1
GO:0046854	mitochondrion transport along microtubule	0.27	1	GO:0046854	mitochondrion transport along microtubule	4.76	1
GO:0047497	phosphatidylinositol-mediated signaling	0.27	1	GO:0047497	phosphatidylinositol-mediated signaling	4.76	1
GO:0048015	paraxial mesoderm development	0.27	1	GO:0048015	paraxial mesoderm development	4.76	1
GO:0048339	regulation of lateral mesodermal cell fate specification	0.27	1	GO:0048339	regulation of lateral mesodermal cell fate specification	4.76	1
GO:0048378	cell maturation	0.27	1	GO:0048378	cell maturation	4.76	1
GO:0048469	blood vessel morphogenesis	0.27	1	GO:0048469	blood vessel morphogenesis	4.76	1
GO:0048514	axon extension	0.27	1	GO:0048514	axon extension	4.76	1
GO:0048675	generation of neurons	0.27	1	GO:0048675	generation of neurons	4.76	1
GO:0048699	skeletal system morphogenesis	0.27	1	GO:0048699	skeletal system morphogenesis	4.76	1
GO:0048705	mesenchymal cell differentiation	0.27	1	GO:0048705	mesenchymal cell differentiation	4.76	1
GO:0048762	inner ear development	0.27	1	GO:0048762	inner ear development	4.76	1
GO:0048839	cell motility	0.27	1	GO:0048839	cell motility	4.76	1
GO:0048870	regulation of defense response to virus	0.27	1	GO:0048870	regulation of defense response to virus	4.76	1
GO:0050688	negative regulation of defense response to virus by host	0.27	1	GO:0050688	negative regulation of defense response to virus by host	4.76	1
GO:0050689	regulation of catalytic activity	0.27	1	GO:0050689	regulation of catalytic activity	4.76	1
GO:0050821	protein stabilization	0.27	1	GO:0050821	protein stabilization	4.76	1
GO:0050900	leukocyte migration	0.27	1	GO:0050900	leukocyte migration	4.76	1
GO:0051097	negative regulation of helicase activity	0.27	1	GO:0051097	negative regulation of helicase activity	4.76	1

GO:0051174	regulation of phosphorus metabolic process	0.27	1	GO:0051174	regulation of phosphorus metabolic process	4.76	1
GO:0051384	response to glucocorticoid	0.27	1	GO:0051384	response to glucocorticoid	4.76	1
GO:0051496	positive regulation of stress fiber assembly	0.27	1	GO:0051496	positive regulation of stress fiber assembly	4.76	1
GO:0051591	positive regulation of cAMP response to calcium ion	0.27	1	GO:0051591	positive regulation of cAMP response to calcium ion	4.76	1
GO:0051592	positive regulation of focal adhesion assembly	0.27	1	GO:0051592	positive regulation of focal adhesion assembly	4.76	1
GO:0051894	positive regulation of protein kinase B signaling	0.27	1	GO:0051894	positive regulation of protein kinase B signaling	4.76	1
GO:0051897	negative regulation of protein kinase B signaling	0.27	1	GO:0051897	negative regulation of protein kinase B signaling	4.76	1
GO:0051898	transmembrane transport	0.27	1	GO:0051898	transmembrane transport	4.76	1
GO:0055085	positive regulation of cardiac muscle cell proliferation	0.27	1	GO:0055085	positive regulation of cardiac muscle cell proliferation	4.76	1
GO:0060045	regulation of postsynaptic membrane potential	0.27	1	GO:0060045	regulation of postsynaptic membrane potential	4.76	1
GO:0060078	auditory receptor cell development	0.27	1	GO:0060078	auditory receptor cell development	4.76	1
GO:0060117	inner ear receptor cell stereocilium organization	0.27	1	GO:0060117	inner ear receptor cell stereocilium organization	4.76	1
GO:0060122	interferon-gamma-mediated signaling pathway	0.27	1	GO:0060122	interferon-gamma-mediated signaling pathway	4.76	1
GO:0060333	bone development	0.27	1	GO:0060333	bone development	4.76	1
GO:0060348	calcium ion transport into cytosol	0.27	1	GO:0060348	calcium ion transport into cytosol	4.76	1
GO:0060402	branching involved in mammary gland duct morphogenesis	0.27	1	GO:0060402	branching involved in mammary gland duct morphogenesis	4.76	1
GO:0060444	branching involved in salivary gland morphogenesis	0.27	1	GO:0060444	branching involved in salivary gland morphogenesis	4.76	1
GO:0060445	lung-associated mesenchyme development	0.27	1	GO:0060445	lung-associated mesenchyme development	4.76	1
GO:0060484		0.27	1	GO:0060484		4.76	1

	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	0.27	1	GO:0060665	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	4.76	1
GO:0060721	regulation of spongiotrophoblast cell proliferation	0.27	1	GO:0060721	regulation of spongiotrophoblast cell proliferation	4.76	1
GO:0061162	establishment of monopolar cell polarity	0.27	1	GO:0061162	establishment of monopolar cell polarity	4.76	1
GO:0070194	synaptonemal complex disassembly	0.27	1	GO:0070194	synaptonemal complex disassembly	4.76	1
GO:0070309	lens fiber cell morphogenesis	0.27	1	GO:0070309	lens fiber cell morphogenesis	4.76	1
GO:0070372	regulation of ERK1 and ERK2 cascade	0.27	1	GO:0070372	regulation of ERK1 and ERK2 cascade	4.76	1
GO:0070640	vitamin D3 metabolic process	0.27	1	GO:0070640	vitamin D3 metabolic process	4.76	1
GO:0070848	response to growth factor	0.27	1	GO:0070848	response to growth factor	4.76	1
GO:0070873	regulation of glycogen metabolic process	0.27	1	GO:0070873	regulation of glycogen metabolic process	4.76	1
GO:0071222	cellular response to lipopolysaccharide	0.27	1	GO:0071222	cellular response to lipopolysaccharide	4.76	1
GO:0071260	cellular response to mechanical stimulus	0.27	1	GO:0071260	cellular response to mechanical stimulus	4.76	1
GO:0071320	cellular response to cAMP	0.27	1	GO:0071320	cellular response to cAMP	4.76	1
GO:0071346	cellular response to interferon-gamma	0.27	1	GO:0071346	cellular response to interferon-gamma	4.76	1
GO:0071354	cellular response to interleukin-6	0.27	1	GO:0071354	cellular response to interleukin-6	4.76	1
GO:0071356	cellular response to tumor necrosis factor	0.27	1	GO:0071356	cellular response to tumor necrosis factor	4.76	1
GO:0071363	cellular response to growth factor stimulus	0.27	1	GO:0071363	cellular response to growth factor stimulus	4.76	1
GO:0072593	reactive oxygen species metabolic process	0.27	1	GO:0072593	reactive oxygen species metabolic process	4.76	1

GO:0090080	positive regulation of MAPKK cascade by fibroblast growth factor receptor signaling pathway	0.27	1 GO:0090080	positive regulation of MAPKK cascade by fibroblast growth factor receptor signaling pathway	4.76	1
GO:0090084	negative regulation of inclusion body assembly	0.27	1 GO:0090084	negative regulation of inclusion body assembly	4.76	1
GO:0090272	negative regulation of fibroblast growth factor production	0.27	1 GO:0090272	negative regulation of fibroblast growth factor production	4.76	1
GO:0090399	replicative senescence	0.27	1 GO:0090399	replicative senescence	4.76	1
GO:0090403	oxidative stress-induced premature senescence	0.27	1 GO:0090403	oxidative stress-induced premature senescence	4.76	1
GO:0090630	activation of GTPase activity	0.27	1 GO:0090630	activation of GTPase activity	4.76	1
GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	0.27	1 GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	4.76	1
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	0.27	1 GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	4.76	1
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	0.27	1 GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	4.76	1
GO:0098703	calcium ion import across plasma membrane	0.27	1 GO:0098703	calcium ion import across plasma membrane	4.76	1
GO:1900034	regulation of cellular response to heat	0.27	1 GO:1900034	regulation of cellular response to heat	4.76	1
GO:1900138	negative regulation of phospholipase A2 activity	0.27	1 GO:1900138	negative regulation of phospholipase A2 activity	4.76	1
GO:1900139	negative regulation of arachidonic acid secretion	0.27	1 GO:1900139	negative regulation of arachidonic acid secretion	4.76	1

GO:1901896	positive regulation of calcium-transporting ATPase activity	0.27	1 GO:1901896	positive regulation of calcium-transporting ATPase activity	4.76	1
GO:1903078	positive regulation of protein localization to plasma membrane	0.27	1 GO:1903078	positive regulation of protein localization to plasma membrane	4.76	1
GO:1903209	positive regulation of oxidative stress-induced cell death	0.27	1 GO:1903209	positive regulation of oxidative stress-induced cell death	4.76	1
GO:1903465	positive regulation of mitotic cell cycle DNA replication	0.27	1 GO:1903465	positive regulation of mitotic cell cycle DNA replication	4.76	1
GO:1903543	positive regulation of exosomal secretion	0.27	1 GO:1903543	positive regulation of exosomal secretion	4.76	1
GO:1903547	regulation of growth hormone activity	0.27	1 GO:1903547	regulation of growth hormone activity	4.76	1
GO:1903553	positive regulation of extracellular exosome assembly	0.27	1 GO:1903553	positive regulation of extracellular exosome assembly	4.76	1
GO:1903779	regulation of cardiac conduction	0.27	1 GO:1903779	regulation of cardiac conduction	4.76	1
GO:1905564	positive regulation of vascular endothelial cell proliferation	0.27	1 GO:1905564	positive regulation of vascular endothelial cell proliferation	4.76	1
GO:1990034	calcium ion export across plasma membrane	0.27	1 GO:1990034	calcium ion export across plasma membrane	4.76	1
GO:2000147	positive regulation of cell motility	0.27	1 GO:2000147	positive regulation of cell motility	4.76	1
GO:2000546	positive regulation of endothelial cell chemotaxis to fibroblast growth factor	0.27	1 GO:2000546	positive regulation of endothelial cell chemotaxis to fibroblast growth factor	4.76	1
GO:2000830	positive regulation of parathyroid hormone secretion	0.27	1 GO:2000830	positive regulation of parathyroid hormone secretion	4.76	1
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	0.27	1 GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	4.76	1

Supptbl34_RNAseq_QuickGO_RB1Bvsmock				GO IDs (by protein)				
GO IDs (by annotation)				GO IDs (by protein)				
Code	Name	Percentage	Count	Code	Name	Percentage	Count	
GO:0006355	regulation of transcription, DNA-templated	1.40	16	GO:0006355	regulation of transcription, DNA-templated	13.10	11	
GO:0008543	fibroblast growth factor receptor signaling pathway	1.40	16	GO:0008543	fibroblast growth factor receptor signaling pathway	1.19	1	
GO:0006351	transcription, DNA-templated	0.96	11	GO:0006351	transcription, DNA-templated	13.10	11	
GO:0008284	positive regulation of cell proliferation	0.96	11	GO:0008284	positive regulation of cell proliferation	2.38	2	
GO:0001843	neural tube closure	0.87	10	GO:0001843	neural tube closure	2.38	2	
GO:0007186	G-protein coupled receptor signaling pathway	0.87	10	GO:0007186	G-protein coupled receptor signaling pathway	3.57	3	
GO:0006468	protein phosphorylation	0.79	9	GO:0006468	protein phosphorylation	4.76	4	
GO:0007165	signal transduction	0.79	9	GO:0007165	signal transduction	10.71	9	
GO:0009615	response to virus	0.79	9	GO:0009615	response to virus	4.76	4	
GO:0055114	oxidation-reduction process	0.79	9	GO:0055114	oxidation-reduction process	7.14	6	
GO:0043066	negative regulation of apoptotic process	0.70	8	GO:0043066	negative regulation of apoptotic process	8.33	7	
GO:0006334	nucleosome assembly	0.61	7	GO:0006334	nucleosome assembly	2.38	2	
GO:0007275	multicellular organism development	0.61	7	GO:0007275	multicellular organism development	7.14	6	
GO:0042127	regulation of cell proliferation	0.61	7	GO:0042127	regulation of cell proliferation	7.14	6	
GO:0051607	defense response to virus	0.61	7	GO:0051607	defense response to virus	3.57	3	
GO:0090179	planar cell polarity pathway involved in neural tube closure	0.61	7	GO:0090179	planar cell polarity pathway involved in neural tube closure	1.19	1	
GO:0006357	regulation of transcription by RNA polymerase II	0.52	6	GO:0006357	regulation of transcription by RNA polymerase II	5.95	5	
GO:0006915	apoptotic process	0.52	6	GO:0006915	apoptotic process	7.14	6	
GO:0007050	cell cycle arrest	0.52	6	GO:0007050	cell cycle arrest	1.19	1	
GO:0015696	ammonium transport	0.52	6	GO:0015696	ammonium transport	1.19	1	
GO:0045071	negative regulation of viral genome replication	0.52	6	GO:0045071	negative regulation of viral genome replication	3.57	3	

GO:0045944	positive regulation of transcription by RNA polymerase II	0.52	6	GO:0045944	positive regulation of transcription by RNA polymerase II	4.76	4
GO:0046208	spermine catabolic process	0.52	6	GO:0046208	spermine catabolic process	4.76	4
GO:0090103	cochlea morphogenesis	0.52	6	GO:0090103	cochlea morphogenesis	1.19	1
GO:0001525	angiogenesis	0.44	5	GO:0001525	angiogenesis	4.76	4
GO:0006469	negative regulation of protein kinase activity	0.44	5	GO:0006469	negative regulation of protein kinase activity	2.38	2
GO:0006470	protein dephosphorylation	0.44	5	GO:0006470	protein dephosphorylation	3.57	3
GO:0006811	ion transport	0.44	5	GO:0006811	ion transport	3.57	3
GO:0006955	immune response	0.44	5	GO:0006955	immune response	5.95	5
GO:0006974	cellular response to DNA damage stimulus	0.44	5	GO:0006974	cellular response to DNA damage stimulus	3.57	3
GO:0007155	cell adhesion	0.44	5	GO:0007155	cell adhesion	4.76	4
GO:0008285	negative regulation of cell proliferation	0.44	5	GO:0008285	negative regulation of cell proliferation	1.19	1
GO:0009409	response to cold	0.44	5	GO:0009409	response to cold	2.38	2
GO:0016477	cell migration	0.44	5	GO:0016477	cell migration	4.76	4
GO:0042060	wound healing	0.44	5	GO:0042060	wound healing	4.76	4
GO:0045893	positive regulation of transcription, DNA-templated	0.44	5	GO:0045893	positive regulation of transcription, DNA-templated	3.57	3
GO:0050870	positive regulation of T cell activation	0.44	5	GO:0050870	positive regulation of T cell activation	2.38	2
GO:0070588	calcium ion transmembrane transport	0.44	5	GO:0070588	calcium ion transmembrane transport	2.38	2
GO:0000122	negative regulation of transcription by RNA polymerase II	0.35	4	GO:0000122	negative regulation of transcription by RNA polymerase II	3.57	3
GO:0006629	lipid metabolic process	0.35	4	GO:0006629	lipid metabolic process	3.57	3
GO:0006809	nitric oxide biosynthetic process	0.35	4	GO:0006809	nitric oxide biosynthetic process	1.19	1
GO:0006816	calcium ion transport	0.35	4	GO:0006816	calcium ion transport	2.38	2
GO:0006986	response to unfolded protein	0.35	4	GO:0006986	response to unfolded protein	3.57	3
GO:0007283	spermatogenesis	0.35	4	GO:0007283	spermatogenesis	2.38	2
GO:0009408	response to heat	0.35	4	GO:0009408	response to heat	1.19	1
GO:0010629	negative regulation of gene expression	0.35	4	GO:0010629	negative regulation of gene expression	3.57	3

GO:0016567	protein ubiquitination	0.35	4	GO:0016567	protein ubiquitination	3.57	3
GO:0030036	actin cytoskeleton organization	0.35	4	GO:0030036	actin cytoskeleton organization	2.38	2
GO:0030154	cell differentiation	0.35	4	GO:0030154	cell differentiation	3.57	3
GO:0035556	intracellular signal transduction	0.35	4	GO:0035556	intracellular signal transduction	4.76	4
GO:0043312	neutrophil degranulation	0.35	4	GO:0043312	neutrophil degranulation	4.76	4
GO:0043547	positive regulation of GTPase activity	0.35	4	GO:0043547	positive regulation of GTPase activity	3.57	3
GO:0045087	innate immune response	0.35	4	GO:0045087	innate immune response	4.76	4
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	0.35	4	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	2.38	2
GO:0051894	positive regulation of focal adhesion assembly	0.35	4	GO:0051894	positive regulation of focal adhesion assembly	2.38	2
GO:0051897	positive regulation of protein kinase B signaling	0.35	4	GO:0051897	positive regulation of protein kinase B signaling	3.57	3
GO:0060122	inner ear receptor cell stereocilium organization	0.35	4	GO:0060122	inner ear receptor cell stereocilium organization	2.38	2
GO:0071346	cellular response to interferon-gamma	0.35	4	GO:0071346	cellular response to interferon-gamma	4.76	4
GO:0001701	in utero embryonic development	0.26	3	GO:0001701	in utero embryonic development	3.57	3
GO:0001736	establishment of planar polarity	0.26	3	GO:0001736	establishment of planar polarity	1.19	1
GO:0001764	neuron migration	0.26	3	GO:0001764	neuron migration	3.57	3
GO:0002062	chondrocyte differentiation	0.26	3	GO:0002062	chondrocyte differentiation	2.38	2
GO:0002376	immune system process	0.26	3	GO:0002376	immune system process	3.57	3
GO:0002576	platelet degranulation	0.26	3	GO:0002576	platelet degranulation	3.57	3
GO:0003376	sphingosine-1-phosphate signaling pathway	0.26	3	GO:0003376	sphingosine-1-phosphate signaling pathway	2.38	2
GO:0005977	glycogen metabolic process	0.26	3	GO:0005977	glycogen metabolic process	1.19	1
GO:0006048	UDP-N-acetylglucosamine biosynthetic process	0.26	3	GO:0006048	UDP-N-acetylglucosamine biosynthetic process	1.19	1

GO:0006464	cellular protein modification process	0.26	3	GO:0006464	cellular protein modification process	2.38	2
GO:0006508	proteolysis	0.26	3	GO:0006508	proteolysis	1.19	1
GO:0006935	chemotaxis	0.26	3	GO:0006935	chemotaxis	1.19	1
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	0.26	3	GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	1.19	1
GO:0007010	cytoskeleton organization	0.26	3	GO:0007010	cytoskeleton organization	1.19	1
GO:0007160	cell-matrix adhesion	0.26	3	GO:0007160	cell-matrix adhesion	2.38	2
GO:0007229	integrin-mediated signaling pathway	0.26	3	GO:0007229	integrin-mediated signaling pathway	1.19	1
GO:0007266	Rho protein signal transduction	0.26	3	GO:0007266	Rho protein signal transduction	2.38	2
GO:0007420	brain development	0.26	3	GO:0007420	brain development	3.57	3
GO:0007596	blood coagulation	0.26	3	GO:0007596	blood coagulation	3.57	3
GO:0007605	sensory perception of sound	0.26	3	GO:0007605	sensory perception of sound	2.38	2
GO:0016032	viral process	0.26	3	GO:0016032	viral process	3.57	3
GO:0016310	phosphorylation	0.26	3	GO:0016310	phosphorylation	3.57	3
GO:0018108	peptidyl-tyrosine phosphorylation	0.26	3	GO:0018108	peptidyl-tyrosine phosphorylation	2.38	2
GO:0019221	cytokine-mediated signaling pathway	0.26	3	GO:0019221	cytokine-mediated signaling pathway	3.57	3
GO:0022007	convergent extension involved in neural plate elongation	0.26	3	GO:0022007	convergent extension involved in neural plate elongation	1.19	1
GO:0030336	negative regulation of cell migration	0.26	3	GO:0030336	negative regulation of cell migration	1.19	1
GO:0030500	regulation of bone mineralization	0.26	3	GO:0030500	regulation of bone mineralization	2.38	2
GO:0035329	hippo signaling	0.26	3	GO:0035329	hippo signaling	1.19	1
GO:0035335	peptidyl-tyrosine dephosphorylation	0.26	3	GO:0035335	peptidyl-tyrosine dephosphorylation	2.38	2
GO:0042493	response to drug	0.26	3	GO:0042493	response to drug	2.38	2
GO:0042742	defense response to bacterium	0.26	3	GO:0042742	defense response to bacterium	1.19	1
GO:0045892	negative regulation of transcription, DNA-templated	0.26	3	GO:0045892	negative regulation of transcription, DNA-templated	2.38	2
GO:0046597	negative regulation of viral entry into host cell	0.26	3	GO:0046597	negative regulation of viral entry into host cell	1.19	1

GO:0050771	negative regulation of axonogenesis	0.26	3	GO:0050771	negative regulation of axonogenesis	1.19	1
GO:0050852	T cell receptor signaling pathway	0.26	3	GO:0050852	T cell receptor signaling pathway	2.38	2
GO:0050900	leukocyte migration	0.26	3	GO:0050900	leukocyte migration	3.57	3
GO:0051592	response to calcium ion	0.26	3	GO:0051592	response to calcium ion	2.38	2
GO:0060071	Wnt signaling pathway, planar cell polarity pathway	0.26	3	GO:0060071	Wnt signaling pathway, planar cell polarity pathway	1.19	1
GO:0060337	type I interferon signaling pathway	0.26	3	GO:0060337	type I interferon signaling pathway	3.57	3
GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	0.17	2	GO:0000079	regulation of cyclin-dependent protein serine/threonine kinase activity	1.19	1
GO:0000082	G1/S transition of mitotic cell cycle	0.17	2	GO:0000082	G1/S transition of mitotic cell cycle	1.19	1
GO:0000165	MAPK cascade	0.17	2	GO:0000165	MAPK cascade	1.19	1
GO:0000183	chromatin silencing at rDNA	0.17	2	GO:0000183	chromatin silencing at rDNA	1.19	1
GO:0001503	ossification	0.17	2	GO:0001503	ossification	2.38	2
GO:0001578	microtubule bundle formation	0.17	2	GO:0001578	microtubule bundle formation	2.38	2
GO:0001657	ureteric bud development	0.17	2	GO:0001657	ureteric bud development	2.38	2
GO:0001937	negative regulation of endothelial cell proliferation	0.17	2	GO:0001937	negative regulation of endothelial cell proliferation	2.38	2
GO:0001952	regulation of cell-matrix adhesion	0.17	2	GO:0001952	regulation of cell-matrix adhesion	1.19	1
GO:0001955	blood vessel maturation	0.17	2	GO:0001955	blood vessel maturation	1.19	1
GO:0002693	positive regulation of cellular extravasation	0.17	2	GO:0002693	positive regulation of cellular extravasation	1.19	1
GO:0003245	cardiac muscle tissue growth involved in heart morphogenesis	0.17	2	GO:0003245	cardiac muscle tissue growth involved in heart morphogenesis	1.19	1
GO:0005975	carbohydrate metabolic process	0.17	2	GO:0005975	carbohydrate metabolic process	1.19	1
GO:0006027	glycosaminoglycan catabolic process	0.17	2	GO:0006027	glycosaminoglycan catabolic process	2.38	2
GO:0006281	DNA repair	0.17	2	GO:0006281	DNA repair	1.19	1
GO:0006298	mismatch repair	0.17	2	GO:0006298	mismatch repair	1.19	1

GO:0006366	transcription by RNA polymerase II	0.17	2	GO:0006366	transcription by RNA polymerase II	2.38	2
GO:0006367	transcription initiation from RNA polymerase II promoter	0.17	2	GO:0006367	transcription initiation from RNA polymerase II promoter	2.38	2
GO:0006401	RNA catabolic process	0.17	2	GO:0006401	RNA catabolic process	1.19	1
GO:0006527	arginine catabolic process	0.17	2	GO:0006527	arginine catabolic process	1.19	1
GO:0006575	cellular modified amino acid metabolic process	0.17	2	GO:0006575	cellular modified amino acid metabolic process	1.19	1
GO:0006801	superoxide metabolic process	0.17	2	GO:0006801	superoxide metabolic process	1.19	1
GO:0006814	sodium ion transport	0.17	2	GO:0006814	sodium ion transport	1.19	1
GO:0006851	mitochondrial calcium ion transmembrane transport	0.17	2	GO:0006851	mitochondrial calcium ion transmembrane transport	1.19	1
GO:0006874	cellular calcium ion homeostasis	0.17	2	GO:0006874	cellular calcium ion homeostasis	1.19	1
GO:0006882	cellular zinc ion homeostasis	0.17	2	GO:0006882	cellular zinc ion homeostasis	1.19	1
GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	0.17	2	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	1.19	1
GO:0007031	peroxisome organization	0.17	2	GO:0007031	peroxisome organization	1.19	1
GO:0007140	male meiotic nuclear division	0.17	2	GO:0007140	male meiotic nuclear division	1.19	1
GO:0007179	transforming growth factor beta receptor signaling pathway	0.17	2	GO:0007179	transforming growth factor beta receptor signaling pathway	1.19	1
GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	0.17	2	GO:0007193	adenylate cyclase-inhibiting G-protein coupled receptor signaling pathway	1.19	1
GO:0007267	cell-cell signaling	0.17	2	GO:0007267	cell-cell signaling	1.19	1
GO:0007286	spermatid development	0.17	2	GO:0007286	spermatid development	1.19	1
GO:0007346	regulation of mitotic cell cycle	0.17	2	GO:0007346	regulation of mitotic cell cycle	1.19	1
GO:0007399	nervous system development	0.17	2	GO:0007399	nervous system development	2.38	2

GO:0007519	skeletal muscle tissue development	0.17		2	GO:0007519	skeletal muscle tissue development	2.38	2
GO:0007612	learning	0.17		2	GO:0007612	learning	1.19	1
GO:0007613	memory	0.17		2	GO:0007613	memory	1.19	1
GO:0008150	biological_process	0.17		2	GO:0008150	biological_process	2.38	2
GO:0008360	regulation of cell shape	0.17		2	GO:0008360	regulation of cell shape	1.19	1
GO:0008652	cellular amino acid biosynthetic process	0.17		2	GO:0008652	cellular amino acid biosynthetic process	2.38	2
GO:0009058	biosynthetic process	0.17		2	GO:0009058	biosynthetic process	2.38	2
GO:0009249	protein lipoylation	0.17		2	GO:0009249	protein lipoylation	1.19	1
GO:0009952	anterior/posterior pattern specification	0.17		2	GO:0009952	anterior/posterior pattern specification	2.38	2
GO:0010033	response to organic substance	0.17		2	GO:0010033	response to organic substance	2.38	2
GO:0010466	negative regulation of peptidase activity	0.17		2	GO:0010466	negative regulation of peptidase activity	2.38	2
GO:0010468	regulation of gene expression	0.17		2	GO:0010468	regulation of gene expression	2.38	2
GO:0010506	regulation of autophagy	0.17		2	GO:0010506	regulation of autophagy	2.38	2
GO:0010828	positive regulation of glucose transport	0.17		2	GO:0010828	positive regulation of glucose transport	1.19	1
GO:0014819	regulation of skeletal muscle contraction	0.17		2	GO:0014819	regulation of skeletal muscle contraction	1.19	1
GO:0016042	lipid catabolic process	0.17		2	GO:0016042	lipid catabolic process	1.19	1
GO:0016233	telomere capping	0.17		2	GO:0016233	telomere capping	1.19	1
GO:0016311	dephosphorylation	0.17		2	GO:0016311	dephosphorylation	2.38	2
GO:0016569	covalent chromatin modification	0.17		2	GO:0016569	covalent chromatin modification	2.38	2
GO:0018119	peptidyl-cysteine S-nitrosylation	0.17		2	GO:0018119	peptidyl-cysteine S-nitrosylation	1.19	1
GO:0019226	transmission of nerve impulse	0.17		2	GO:0019226	transmission of nerve impulse	2.38	2
GO:0030032	lamellipodium assembly	0.17		2	GO:0030032	lamellipodium assembly	1.19	1
GO:0030111	regulation of Wnt signalling pathway	0.17		2	GO:0030111	regulation of Wnt signalling pathway	2.38	2
GO:0030217	T cell differentiation	0.17		2	GO:0030217	T cell differentiation	1.19	1
GO:0030324	lung development	0.17		2	GO:0030324	lung development	2.38	2
GO:0030334	regulation of cell migration	0.17		2	GO:0030334	regulation of cell migration	2.38	2

GO:0030522	intracellular receptor signaling pathway	0.17	2	GO:0030522	intracellular receptor signaling pathway	1.19	1
GO:0031295	T cell costimulation	0.17	2	GO:0031295	T cell costimulation	1.19	1
GO:0031340	positive regulation of vesicle fusion	0.17	2	GO:0031340	positive regulation of vesicle fusion	1.19	1
GO:0031532	actin cytoskeleton reorganization	0.17	2	GO:0031532	actin cytoskeleton reorganization	1.19	1
GO:0032496	response to lipopolysaccharide	0.17	2	GO:0032496	response to lipopolysaccharide	2.38	2
GO:0032731	positive regulation of interleukin-1 beta production	0.17	2	GO:0032731	positive regulation of interleukin-1 beta production	1.19	1
GO:0032869	cellular response to insulin stimulus	0.17	2	GO:0032869	cellular response to insulin stimulus	1.19	1
GO:0033690	positive regulation of osteoblast proliferation	0.17	2	GO:0033690	positive regulation of osteoblast proliferation	1.19	1
GO:0034116	positive regulation of heterotypic cell-cell adhesion	0.17	2	GO:0034116	positive regulation of heterotypic cell-cell adhesion	1.19	1
GO:0034198	cellular response to amino acid starvation	0.17	2	GO:0034198	cellular response to amino acid starvation	1.19	1
GO:0034605	cellular response to heat	0.17	2	GO:0034605	cellular response to heat	2.38	2
GO:0035544	negative regulation of SNARE complex assembly	0.17	2	GO:0035544	negative regulation of SNARE complex assembly	1.19	1
GO:0035725	sodium ion transmembrane transport	0.17	2	GO:0035725	sodium ion transmembrane transport	1.19	1
GO:0038028	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	0.17	2	GO:0038028	insulin receptor signaling pathway via phosphatidylinositol 3-kinase	1.19	1
GO:0042149	cellular response to glucose starvation	0.17	2	GO:0042149	cellular response to glucose starvation	1.19	1
GO:0042535	positive regulation of tumor necrosis factor biosynthetic process	0.17	2	GO:0042535	positive regulation of tumor necrosis factor biosynthetic process	1.19	1
GO:0042552	myelination	0.17	2	GO:0042552	myelination	1.19	1
GO:0043113	receptor clustering	0.17	2	GO:0043113	receptor clustering	1.19	1

GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	0.17	2	GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	1.19	1
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	0.17	2	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	2.38	2
GO:0043406	positive regulation of MAP kinase activity	0.17	2	GO:0043406	positive regulation of MAP kinase activity	1.19	1
GO:0043536	positive regulation of blood vessel endothelial cell migration	0.17	2	GO:0043536	positive regulation of blood vessel endothelial cell migration	2.38	2
GO:0045124	regulation of bone resorption	0.17	2	GO:0045124	regulation of bone resorption	1.19	1
GO:0045176	apical protein localization	0.17	2	GO:0045176	apical protein localization	1.19	1
GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	0.17	2	GO:0045736	negative regulation of cyclin-dependent protein serine/threonine kinase activity	2.38	2
GO:0045766	positive regulation of angiogenesis	0.17	2	GO:0045766	positive regulation of angiogenesis	2.38	2
GO:0045814	negative regulation of gene expression, epigenetic	0.17	2	GO:0045814	negative regulation of gene expression, epigenetic	2.38	2
GO:0045860	positive regulation of protein kinase activity	0.17	2	GO:0045860	positive regulation of protein kinase activity	2.38	2
GO:0046330	positive regulation of JNK cascade	0.17	2	GO:0046330	positive regulation of JNK cascade	1.19	1
GO:0046627	negative regulation of insulin receptor signaling pathway	0.17	2	GO:0046627	negative regulation of insulin receptor signaling pathway	1.19	1
GO:0046777	protein autophosphorylation	0.17	2	GO:0046777	protein autophosphorylation	2.38	2
GO:0046854	phosphatidylinositol phosphorylation	0.17	2	GO:0046854	phosphatidylinositol phosphorylation	2.38	2
GO:0048041	focal adhesion assembly	0.17	2	GO:0048041	focal adhesion assembly	1.19	1
GO:0048514	blood vessel morphogenesis	0.17	2	GO:0048514	blood vessel morphogenesis	2.38	2
GO:0048709	oligodendrocyte differentiation	0.17	2	GO:0048709	oligodendrocyte differentiation	1.19	1
GO:0050690	regulation of defense response to virus by virus	0.17	2	GO:0050690	regulation of defense response to virus by virus	1.19	1

GO:0050821	protein stabilization	0.17	2	GO:0050821	protein stabilization	2.38	2
GO:0050860	negative regulation of T cell receptor signaling pathway	0.17	2	GO:0050860	negative regulation of T cell receptor signaling pathway	2.38	2
GO:0051216	cartilage development	0.17	2	GO:0051216	cartilage development	1.19	1
GO:0051321	meiotic cell cycle	0.17	2	GO:0051321	meiotic cell cycle	1.19	1
GO:0051384	response to glucocorticoid	0.17	2	GO:0051384	response to glucocorticoid	2.38	2
GO:0051560	mitochondrial calcium ion homeostasis	0.17	2	GO:0051560	mitochondrial calcium ion homeostasis	1.19	1
GO:0051604	protein maturation	0.17	2	GO:0051604	protein maturation	1.19	1
GO:0055085	transmembrane transport	0.17	2	GO:0055085	transmembrane transport	2.38	2
GO:0060055	angiogenesis involved in wound healing	0.17	2	GO:0060055	angiogenesis involved in wound healing	1.19	1
GO:0060291	long-term synaptic potentiation	0.17	2	GO:0060291	long-term synaptic potentiation	1.19	1
GO:0061077	chaperone-mediated protein folding	0.17	2	GO:0061077	chaperone-mediated protein folding	1.19	1
GO:0061099	negative regulation of protein tyrosine kinase activity	0.17	2	GO:0061099	negative regulation of protein tyrosine kinase activity	1.19	1
GO:0061384	heart trabecula morphogenesis	0.17	2	GO:0061384	heart trabecula morphogenesis	1.19	1
GO:0070189	kynurenine metabolic process	0.17	2	GO:0070189	kynurenine metabolic process	1.19	1
GO:0070571	negative regulation of neuron projection regeneration	0.17	2	GO:0070571	negative regulation of neuron projection regeneration	1.19	1
GO:0071222	cellular response to lipopolysaccharide	0.17	2	GO:0071222	cellular response to lipopolysaccharide	2.38	2
GO:0071357	cellular response to type I interferon	0.17	2	GO:0071357	cellular response to type I interferon	1.19	1
GO:0071360	cellular response to exogenous dsRNA	0.17	2	GO:0071360	cellular response to exogenous dsRNA	1.19	1
GO:0071456	cellular response to hypoxia	0.17	2	GO:0071456	cellular response to hypoxia	1.19	1
GO:0071479	cellular response to ionizing radiation	0.17	2	GO:0071479	cellular response to ionizing radiation	1.19	1
GO:0071493	cellular response to UV-B	0.17	2	GO:0071493	cellular response to UV-B	1.19	1

GO:0071901	negative regulation of protein serine/threonine kinase activity	0.17	2	GO:0071901	negative regulation of protein serine/threonine kinase activity	1.19	1
GO:0072488	ammonium transmembrane transport	0.17	2	GO:0072488	ammonium transmembrane transport	1.19	1
GO:0072659	protein localization to plasma membrane	0.17	2	GO:0072659	protein localization to plasma membrane	2.38	2
GO:0072678	T cell migration	0.17	2	GO:0072678	T cell migration	1.19	1
GO:0090162	establishment of epithelial cell polarity	0.17	2	GO:0090162	establishment of epithelial cell polarity	2.38	2
GO:0090305	nucleic acid phosphodiester bond hydrolysis	0.17	2	GO:0090305	nucleic acid phosphodiester bond hydrolysis	1.19	1
GO:0098609	cell-cell adhesion	0.17	2	GO:0098609	cell-cell adhesion	1.19	1
GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	0.17	2	GO:1902176	negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	1.19	1
GO:1903779	regulation of cardiac conduction	0.17	2	GO:1903779	regulation of cardiac conduction	2.38	2
GO:2000379	positive regulation of reactive oxygen species metabolic process	0.17	2	GO:2000379	positive regulation of reactive oxygen species metabolic process	1.19	1
GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	0.17	2	GO:2001244	positive regulation of intrinsic apoptotic signaling pathway	1.19	1
GO:0000086	G2/M transition of mitotic cell cycle	0.09	1	GO:0000086	G2/M transition of mitotic cell cycle	1.19	1
GO:0000188	inactivation of MAPK activity	0.09	1	GO:0000188	inactivation of MAPK activity	1.19	1
GO:0000226	microtubule cytoskeleton organization	0.09	1	GO:0000226	microtubule cytoskeleton organization	1.19	1
GO:0001501	skeletal system development	0.09	1	GO:0001501	skeletal system development	1.19	1
GO:0001523	retinoid metabolic process	0.09	1	GO:0001523	retinoid metabolic process	1.19	1
GO:0001541	ovarian follicle development	0.09	1	GO:0001541	ovarian follicle development	1.19	1
GO:0001569	branching involved in blood vessel morphogenesis	0.09	1	GO:0001569	branching involved in blood vessel morphogenesis	1.19	1
GO:0001666	response to hypoxia	0.09	1	GO:0001666	response to hypoxia	1.19	1

GO:0001759	organ induction	0.09	1	GO:0001759	organ induction	1.19	1
GO:0001783	B cell apoptotic process	0.09	1	GO:0001783	B cell apoptotic process	1.19	1
GO:0001829	trophectodermal cell differentiation	0.09	1	GO:0001829	trophectodermal cell differentiation	1.19	1
GO:0001889	liver development	0.09	1	GO:0001889	liver development	1.19	1
GO:0001890	placenta development	0.09	1	GO:0001890	placenta development	1.19	1
GO:0001893	maternal placenta development	0.09	1	GO:0001893	maternal placenta development	1.19	1
GO:0001895	retina homeostasis	0.09	1	GO:0001895	retina homeostasis	1.19	1
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	0.09	1	GO:0001912	positive regulation of leukocyte mediated cytotoxicity	1.19	1
GO:0001932	regulation of protein phosphorylation	0.09	1	GO:0001932	regulation of protein phosphorylation	1.19	1
GO:0001934	positive regulation of protein phosphorylation	0.09	1	GO:0001934	positive regulation of protein phosphorylation	1.19	1
GO:0001938	positive regulation of endothelial cell proliferation	0.09	1	GO:0001938	positive regulation of endothelial cell proliferation	1.19	1
GO:0001942	hair follicle development	0.09	1	GO:0001942	hair follicle development	1.19	1
GO:0001945	lymph vessel development	0.09	1	GO:0001945	lymph vessel development	1.19	1
GO:0001947	heart looping	0.09	1	GO:0001947	heart looping	1.19	1
GO:0001960	negative regulation of cytokine-mediated signaling pathway	0.09	1	GO:0001960	negative regulation of cytokine-mediated signaling pathway	1.19	1
GO:0002053	positive regulation of mesenchymal cell proliferation	0.09	1	GO:0002053	positive regulation of mesenchymal cell proliferation	1.19	1
GO:0002227	innate immune response in mucosa	0.09	1	GO:0002227	innate immune response in mucosa	1.19	1
GO:0002230	positive regulation of defense response to virus by host	0.09	1	GO:0002230	positive regulation of defense response to virus by host	1.19	1
GO:0002244	hematopoietic progenitor cell differentiation	0.09	1	GO:0002244	hematopoietic progenitor cell differentiation	1.19	1
GO:0002377	immunoglobulin production	0.09	1	GO:0002377	immunoglobulin production	1.19	1
GO:0002446	neutrophil mediated immunity	0.09	1	GO:0002446	neutrophil mediated immunity	1.19	1

GO:0002710	negative regulation of T cell mediated immunity	0.09	1	GO:0002710	negative regulation of T cell mediated immunity	1.19	1
GO:0002828	regulation of type 2 immune response	0.09	1	GO:0002828	regulation of type 2 immune response	1.19	1
GO:0003084	positive regulation of systemic arterial blood pressure	0.09	1	GO:0003084	positive regulation of systemic arterial blood pressure	1.19	1
GO:0003148	outflow tract septum morphogenesis	0.09	1	GO:0003148	outflow tract septum morphogenesis	1.19	1
GO:0003149	membranous septum morphogenesis	0.09	1	GO:0003149	membranous septum morphogenesis	1.19	1
GO:0003150	muscular septum morphogenesis	0.09	1	GO:0003150	muscular septum morphogenesis	1.19	1
GO:0003334	keratinocyte development	0.09	1	GO:0003334	keratinocyte development	1.19	1
GO:0003347	epicardial cell to mesenchymal cell transition	0.09	1	GO:0003347	epicardial cell to mesenchymal cell transition	1.19	1
GO:0003382	epithelial cell morphogenesis	0.09	1	GO:0003382	epithelial cell morphogenesis	1.19	1
GO:0003402	planar cell polarity pathway involved in axis elongation	0.09	1	GO:0003402	planar cell polarity pathway involved in axis elongation	1.19	1
GO:0005980	glycogen catabolic process	0.09	1	GO:0005980	glycogen catabolic process	1.19	1
GO:0006024	glycosaminoglycan biosynthetic process	0.09	1	GO:0006024	glycosaminoglycan biosynthetic process	1.19	1
GO:0006029	proteoglycan metabolic process	0.09	1	GO:0006029	proteoglycan metabolic process	1.19	1
GO:0006041	glucosamine metabolic process	0.09	1	GO:0006041	glucosamine metabolic process	1.19	1
GO:0006044	N-acetylglucosamine metabolic process	0.09	1	GO:0006044	N-acetylglucosamine metabolic process	1.19	1
GO:0006065	UDP-glucuronate biosynthetic process	0.09	1	GO:0006065	UDP-glucuronate biosynthetic process	1.19	1
GO:0006091	generation of precursor metabolites and energy	0.09	1	GO:0006091	generation of precursor metabolites and energy	1.19	1
GO:0006103	2-oxoglutarate metabolic process	0.09	1	GO:0006103	2-oxoglutarate metabolic process	1.19	1

GO:0006303	double-strand break repair via nonhomologous end joining	0.09	1	GO:0006303	double-strand break repair via nonhomologous end joining	1.19	1
GO:0006325	chromatin organization	0.09	1	GO:0006325	chromatin organization	1.19	1
GO:0006335	DNA replication-dependent nucleosome assembly	0.09	1	GO:0006335	DNA replication-dependent nucleosome assembly	1.19	1
GO:0006336	DNA replication-independent nucleosome assembly	0.09	1	GO:0006336	DNA replication-independent nucleosome assembly	1.19	1
GO:0006352	DNA-templated transcription, initiation	0.09	1	GO:0006352	DNA-templated transcription, initiation	1.19	1
GO:0006396	RNA processing	0.09	1	GO:0006396	RNA processing	1.19	1
GO:0006446	regulation of translational initiation	0.09	1	GO:0006446	regulation of translational initiation	1.19	1
GO:0006457	protein folding	0.09	1	GO:0006457	protein folding	1.19	1
GO:0006486	protein glycosylation	0.09	1	GO:0006486	protein glycosylation	1.19	1
GO:0006488	dolichol-linked oligosaccharide biosynthetic process	0.09	1	GO:0006488	dolichol-linked oligosaccharide biosynthetic process	1.19	1
GO:0006493	protein O-linked glycosylation	0.09	1	GO:0006493	protein O-linked glycosylation	1.19	1
GO:0006501	C-terminal protein lipidation	0.09	1	GO:0006501	C-terminal protein lipidation	1.19	1
GO:0006559	L-phenylalanine catabolic process	0.09	1	GO:0006559	L-phenylalanine catabolic process	1.19	1
GO:0006569	tryptophan catabolic process	0.09	1	GO:0006569	tryptophan catabolic process	1.19	1
GO:0006596	polyamine biosynthetic process	0.09	1	GO:0006596	polyamine biosynthetic process	1.19	1
GO:0006598	polyamine catabolic process	0.09	1	GO:0006598	polyamine catabolic process	1.19	1
GO:0006828	manganese ion transport	0.09	1	GO:0006828	manganese ion transport	1.19	1
GO:0006888	ER to Golgi vesicle-mediated transport	0.09	1	GO:0006888	ER to Golgi vesicle-mediated transport	1.19	1
GO:0006898	receptor-mediated endocytosis	0.09	1	GO:0006898	receptor-mediated endocytosis	1.19	1
GO:0006906	vesicle fusion	0.09	1	GO:0006906	vesicle fusion	1.19	1
GO:0006913	nucleocytoplasmic transport	0.09	1	GO:0006913	nucleocytoplasmic transport	1.19	1
GO:0006914	autophagy	0.09	1	GO:0006914	autophagy	1.19	1
GO:0006954	inflammatory response	0.09	1	GO:0006954	inflammatory response	1.19	1

GO:0006959	humoral immune response	0.09	1	GO:0006959	humoral immune response	1.19	1
GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	0.09	1	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	1.19	1
GO:0007016	cytoskeletal anchoring at plasma membrane	0.09	1	GO:0007016	cytoskeletal anchoring at plasma membrane	1.19	1
GO:0007049	cell cycle	0.09	1	GO:0007049	cell cycle	1.19	1
GO:0007129	synapsis	0.09	1	GO:0007129	synapsis	1.19	1
GO:0007131	reciprocal meiotic recombination	0.09	1	GO:0007131	reciprocal meiotic recombination	1.19	1
GO:0007141	male meiosis I	0.09	1	GO:0007141	male meiosis I	1.19	1
GO:0007154	cell communication	0.09	1	GO:0007154	cell communication	1.19	1
GO:0007166	cell surface receptor signaling pathway	0.09	1	GO:0007166	cell surface receptor signaling pathway	1.19	1
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	0.09	1	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	1.19	1
GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	0.09	1	GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	1.19	1
GO:0007202	activation of phospholipase C activity	0.09	1	GO:0007202	activation of phospholipase C activity	1.19	1
GO:0007204	positive regulation of cytosolic calcium ion concentration	0.09	1	GO:0007204	positive regulation of cytosolic calcium ion concentration	1.19	1
GO:0007257	activation of JUN kinase activity	0.09	1	GO:0007257	activation of JUN kinase activity	1.19	1
GO:0007263	nitric oxide mediated signal transduction	0.09	1	GO:0007263	nitric oxide mediated signal transduction	1.19	1
GO:0007265	Ras protein signal transduction	0.09	1	GO:0007265	Ras protein signal transduction	1.19	1
GO:0007292	female gamete generation	0.09	1	GO:0007292	female gamete generation	1.19	1
GO:0007409	axonogenesis	0.09	1	GO:0007409	axonogenesis	1.19	1
GO:0007435	salivary gland morphogenesis	0.09	1	GO:0007435	salivary gland morphogenesis	1.19	1
GO:0007507	heart development	0.09	1	GO:0007507	heart development	1.19	1
GO:0007517	muscle organ development	0.09	1	GO:0007517	muscle organ development	1.19	1

GO:0007565	female pregnancy	0.09	1	GO:0007565	female pregnancy	1.19	1
GO:0007567	parturition	0.09	1	GO:0007567	parturition	1.19	1
GO:0007599	hemostasis	0.09	1	GO:0007599	hemostasis	1.19	1
GO:0007623	circadian rhythm	0.09	1	GO:0007623	circadian rhythm	1.19	1
GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	0.09	1	GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	1.19	1
GO:0008283	cell proliferation	0.09	1	GO:0008283	cell proliferation	1.19	1
GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	0.09	1	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	1.19	1
GO:0008643	carbohydrate transport	0.09	1	GO:0008643	carbohydrate transport	1.19	1
GO:0009411	response to UV	0.09	1	GO:0009411	response to UV	1.19	1
GO:0009566	fertilization	0.09	1	GO:0009566	fertilization	1.19	1
GO:0009607	response to biotic stimulus	0.09	1	GO:0009607	response to biotic stimulus	1.19	1
GO:0009617	response to bacterium	0.09	1	GO:0009617	response to bacterium	1.19	1
GO:0009629	response to gravity	0.09	1	GO:0009629	response to gravity	1.19	1
GO:0009636	response to toxic substance	0.09	1	GO:0009636	response to toxic substance	1.19	1
GO:0009887	animal organ morphogenesis	0.09	1	GO:0009887	animal organ morphogenesis	1.19	1
GO:0009956	radial pattern formation	0.09	1	GO:0009956	radial pattern formation	1.19	1
GO:0009987	cellular process	0.09	1	GO:0009987	cellular process	1.19	1
GO:0010165	response to X-ray	0.09	1	GO:0010165	response to X-ray	1.19	1
GO:0010243	response to organonitrogen compound	0.09	1	GO:0010243	response to organonitrogen compound	1.19	1
GO:0010288	response to lead ion	0.09	1	GO:0010288	response to lead ion	1.19	1
GO:0010518	positive regulation of phospholipase activity	0.09	1	GO:0010518	positive regulation of phospholipase activity	1.19	1
GO:0010575	positive regulation of vascular endothelial growth factor production	0.09	1	GO:0010575	positive regulation of vascular endothelial growth factor production	1.19	1
GO:0010595	positive regulation of endothelial cell migration	0.09	1	GO:0010595	positive regulation of endothelial cell migration	1.19	1
GO:0010596	negative regulation of endothelial cell migration	0.09	1	GO:0010596	negative regulation of endothelial cell migration	1.19	1

GO:0010664	negative regulation of striated muscle cell apoptotic process	0.09	1	GO:0010664	negative regulation of striated muscle cell apoptotic process	1.19	1
GO:0010762	regulation of fibroblast migration	0.09	1	GO:0010762	regulation of fibroblast migration	1.19	1
GO:0010863	positive regulation of phospholipase C activity	0.09	1	GO:0010863	positive regulation of phospholipase C activity	1.19	1
GO:0010942	positive regulation of cell death	0.09	1	GO:0010942	positive regulation of cell death	1.19	1
GO:0010966	regulation of phosphate transport	0.09	1	GO:0010966	regulation of phosphate transport	1.19	1
GO:0010976	positive regulation of neuron projection development	0.09	1	GO:0010976	positive regulation of neuron projection development	1.19	1
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	0.09	1	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	1.19	1
GO:0014070	response to organic cyclic compound	0.09	1	GO:0014070	response to organic cyclic compound	1.19	1
GO:0015012	heparan sulfate proteoglycan biosynthetic process	0.09	1	GO:0015012	heparan sulfate proteoglycan biosynthetic process	1.19	1
GO:0015031	protein transport	0.09	1	GO:0015031	protein transport	1.19	1
GO:0015695	organic cation transport	0.09	1	GO:0015695	organic cation transport	1.19	1
GO:0015787	UDP-glucuronic acid transmembrane transport	0.09	1	GO:0015787	UDP-glucuronic acid transmembrane transport	1.19	1
GO:0016055	Wnt signaling pathway	0.09	1	GO:0016055	Wnt signaling pathway	1.19	1
GO:0016079	synaptic vesicle exocytosis	0.09	1	GO:0016079	synaptic vesicle exocytosis	1.19	1
GO:0016358	dendrite development	0.09	1	GO:0016358	dendrite development	1.19	1
GO:0016525	negative regulation of angiogenesis	0.09	1	GO:0016525	negative regulation of angiogenesis	1.19	1
GO:0016575	histone deacetylation	0.09	1	GO:0016575	histone deacetylation	1.19	1
GO:0019060	intracellular transport of viral protein in host cell	0.09	1	GO:0019060	intracellular transport of viral protein in host cell	1.19	1

GO:0021510	spinal cord development	0.09	1	GO:0021510	spinal cord development	1.19	1
GO:0021537	telencephalon development	0.09	1	GO:0021537	telencephalon development	1.19	1
GO:0021769	orbitofrontal cortex development	0.09	1	GO:0021769	orbitofrontal cortex development	1.19	1
GO:0021847	ventricular zone neuroblast division	0.09	1	GO:0021847	ventricular zone neuroblast division	1.19	1
GO:0022604	regulation of cell morphogenesis	0.09	1	GO:0022604	regulation of cell morphogenesis	1.19	1
GO:0030001	metal ion transport	0.09	1	GO:0030001	metal ion transport	1.19	1
GO:0030097	hemopoiesis	0.09	1	GO:0030097	hemopoiesis	1.19	1
GO:0030155	regulation of cell adhesion	0.09	1	GO:0030155	regulation of cell adhesion	1.19	1
GO:0030168	platelet activation	0.09	1	GO:0030168	platelet activation	1.19	1
GO:0030182	neuron differentiation	0.09	1	GO:0030182	neuron differentiation	1.19	1
GO:0030194	positive regulation of blood coagulation	0.09	1	GO:0030194	positive regulation of blood coagulation	1.19	1
GO:0030198	extracellular matrix organization	0.09	1	GO:0030198	extracellular matrix organization	1.19	1
GO:0030200	heparan sulfate proteoglycan catabolic process	0.09	1	GO:0030200	heparan sulfate proteoglycan catabolic process	1.19	1
GO:0030203	glycosaminoglycan metabolic process	0.09	1	GO:0030203	glycosaminoglycan metabolic process	1.19	1
GO:0030206	chondroitin sulfate biosynthetic process	0.09	1	GO:0030206	chondroitin sulfate biosynthetic process	1.19	1
GO:0030308	negative regulation of cell growth	0.09	1	GO:0030308	negative regulation of cell growth	1.19	1
GO:0030326	embryonic limb morphogenesis	0.09	1	GO:0030326	embryonic limb morphogenesis	1.19	1
GO:0030335	positive regulation of cell migration	0.09	1	GO:0030335	positive regulation of cell migration	1.19	1
GO:0030502	negative regulation of bone mineralization	0.09	1	GO:0030502	negative regulation of bone mineralization	1.19	1
GO:0030510	regulation of BMP signaling pathway	0.09	1	GO:0030510	regulation of BMP signaling pathway	1.19	1
GO:0030595	leukocyte chemotaxis	0.09	1	GO:0030595	leukocyte chemotaxis	1.19	1
GO:0030838	positive regulation of actin filament polymerization	0.09	1	GO:0030838	positive regulation of actin filament polymerization	1.19	1
GO:0030890	positive regulation of B cell proliferation	0.09	1	GO:0030890	positive regulation of B cell proliferation	1.19	1

GO:0030900	forebrain development	0.09	1	GO:0030900	forebrain development	1.19	1
GO:0030901	midbrain development	0.09	1	GO:0030901	midbrain development	1.19	1
GO:0030968	endoplasmic reticulum unfolded protein response	0.09	1	GO:0030968	endoplasmic reticulum unfolded protein response	1.19	1
GO:0031100	animal organ regeneration	0.09	1	GO:0031100	animal organ regeneration	1.19	1
GO:0031214	biomineral tissue development	0.09	1	GO:0031214	biomineral tissue development	1.19	1
GO:0031274	positive regulation of pseudopodium assembly	0.09	1	GO:0031274	positive regulation of pseudopodium assembly	1.19	1
GO:0031284	positive regulation of guanylate cyclase activity	0.09	1	GO:0031284	positive regulation of guanylate cyclase activity	1.19	1
GO:0031398	positive regulation of protein ubiquitination	0.09	1	GO:0031398	positive regulation of protein ubiquitination	1.19	1
GO:0031662	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle	0.09	1	GO:0031662	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle	1.19	1
GO:0031668	cellular response to extracellular stimulus	0.09	1	GO:0031668	cellular response to extracellular stimulus	1.19	1
GO:0032091	negative regulation of protein binding	0.09	1	GO:0032091	negative regulation of protein binding	1.19	1
GO:0032094	response to food	0.09	1	GO:0032094	response to food	1.19	1
GO:0032200	telomere organization	0.09	1	GO:0032200	telomere organization	1.19	1
GO:0032310	prostaglandin secretion	0.09	1	GO:0032310	prostaglandin secretion	1.19	1
GO:0032355	response to estradiol	0.09	1	GO:0032355	response to estradiol	1.19	1
GO:0032387	negative regulation of intracellular transport	0.09	1	GO:0032387	negative regulation of intracellular transport	1.19	1
GO:0032526	response to retinoic acid	0.09	1	GO:0032526	response to retinoic acid	1.19	1
GO:0032781	positive regulation of ATPase activity	0.09	1	GO:0032781	positive regulation of ATPase activity	1.19	1
GO:0032808	lacrimal gland development	0.09	1	GO:0032808	lacrimal gland development	1.19	1
GO:0032835	glomerulus development	0.09	1	GO:0032835	glomerulus development	1.19	1

GO:0032897	negative regulation of viral transcription	0.09	1	GO:0032897	negative regulation of viral transcription	1.19	1
GO:0032956	regulation of actin cytoskeleton organization	0.09	1	GO:0032956	regulation of actin cytoskeleton organization	1.19	1
GO:0033031	positive regulation of neutrophil apoptotic process	0.09	1	GO:0033031	positive regulation of neutrophil apoptotic process	1.19	1
GO:0033044	regulation of chromosome organization	0.09	1	GO:0033044	regulation of chromosome organization	1.19	1
GO:0033158	regulation of protein import into nucleus, translocation	0.09	1	GO:0033158	regulation of protein import into nucleus, translocation	1.19	1
GO:0033591	response to L-ascorbic acid	0.09	1	GO:0033591	response to L-ascorbic acid	1.19	1
GO:0034080	CENP-A containing nucleosome assembly	0.09	1	GO:0034080	CENP-A containing nucleosome assembly	1.19	1
GO:0034097	response to cytokine	0.09	1	GO:0034097	response to cytokine	1.19	1
GO:0034341	response to interferon-gamma	0.09	1	GO:0034341	response to interferon-gamma	1.19	1
GO:0034641	cellular nitrogen compound metabolic process	0.09	1	GO:0034641	cellular nitrogen compound metabolic process	1.19	1
GO:0034656	nucleobase-containing small molecule catabolic process	0.09	1	GO:0034656	nucleobase-containing small molecule catabolic process	1.19	1
GO:0034976	response to endoplasmic reticulum stress	0.09	1	GO:0034976	response to endoplasmic reticulum stress	1.19	1
GO:0035019	somatic stem cell population maintenance	0.09	1	GO:0035019	somatic stem cell population maintenance	1.19	1
GO:0035455	response to interferon-alpha	0.09	1	GO:0035455	response to interferon-alpha	1.19	1
GO:0035456	response to interferon-beta	0.09	1	GO:0035456	response to interferon-beta	1.19	1
GO:0035457	cellular response to interferon-alpha	0.09	1	GO:0035457	cellular response to interferon-alpha	1.19	1
GO:0035567	non-canonical Wnt signalling pathway	0.09	1	GO:0035567	non-canonical Wnt signalling pathway	1.19	1

	fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	0.09	1	GO:0035607	fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	1.19	1
GO:0035690	cellular response to drug	0.09	1	GO:0035690	cellular response to drug	1.19	1
GO:0035787	cell migration involved in kidney development	0.09	1	GO:0035787	cell migration involved in kidney development	1.19	1
GO:0035914	skeletal muscle cell differentiation	0.09	1	GO:0035914	skeletal muscle cell differentiation	1.19	1
GO:0035924	cellular response to vascular endothelial growth factor stimulus	0.09	1	GO:0035924	cellular response to vascular endothelial growth factor stimulus	1.19	1
GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	0.09	1	GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	1.19	1
GO:0036158	outer dynein arm assembly	0.09	1	GO:0036158	outer dynein arm assembly	1.19	1
GO:0036342	post-anal tail morphogenesis	0.09	1	GO:0036342	post-anal tail morphogenesis	1.19	1
GO:0036514	dopaminergic neuron axon guidance	0.09	1	GO:0036514	dopaminergic neuron axon guidance	1.19	1
GO:0036515	serotonergic neuron axon guidance	0.09	1	GO:0036515	serotonergic neuron axon guidance	1.19	1
GO:0038033	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway	0.09	1	GO:0038033	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway	1.19	1
GO:0038083	peptidyl-tyrosine autophosphorylation	0.09	1	GO:0038083	peptidyl-tyrosine autophosphorylation	1.19	1
GO:0038093	Fc receptor signaling pathway	0.09	1	GO:0038093	Fc receptor signaling pathway	1.19	1
GO:0042026	protein refolding	0.09	1	GO:0042026	protein refolding	1.19	1
GO:0042119	neutrophil activation	0.09	1	GO:0042119	neutrophil activation	1.19	1
GO:0042130	negative regulation of T cell proliferation	0.09	1	GO:0042130	negative regulation of T cell proliferation	1.19	1
GO:0042177	negative regulation of protein catabolic process	0.09	1	GO:0042177	negative regulation of protein catabolic process	1.19	1

GO:0042308	negative regulation of protein import into nucleus	0.09	1	GO:0042308	negative regulation of protein import into nucleus	1.19	1
GO:0042326	negative regulation of phosphorylation	0.09	1	GO:0042326	negative regulation of phosphorylation	1.19	1
GO:0042391	regulation of membrane potential	0.09	1	GO:0042391	regulation of membrane potential	1.19	1
GO:0042438	melanin biosynthetic process	0.09	1	GO:0042438	melanin biosynthetic process	1.19	1
GO:0042472	inner ear morphogenesis	0.09	1	GO:0042472	inner ear morphogenesis	1.19	1
GO:0042473	outer ear morphogenesis	0.09	1	GO:0042473	outer ear morphogenesis	1.19	1
GO:0042474	middle ear morphogenesis	0.09	1	GO:0042474	middle ear morphogenesis	1.19	1
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	0.09	1	GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	1.19	1
GO:0042851	L-alanine metabolic process	0.09	1	GO:0042851	L-alanine metabolic process	1.19	1
GO:0042853	L-alanine catabolic process	0.09	1	GO:0042853	L-alanine catabolic process	1.19	1
GO:0042981	regulation of apoptotic process	0.09	1	GO:0042981	regulation of apoptotic process	1.19	1
GO:0042993	positive regulation of transcription factor import into nucleus	0.09	1	GO:0042993	positive regulation of transcription factor import into nucleus	1.19	1
GO:0043009	chordate embryonic development	0.09	1	GO:0043009	chordate embryonic development	1.19	1
GO:0043068	positive regulation of programmed cell death	0.09	1	GO:0043068	positive regulation of programmed cell death	1.19	1
GO:0043086	negative regulation of catalytic activity	0.09	1	GO:0043086	negative regulation of catalytic activity	1.19	1
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	0.09	1	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	1.19	1
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	0.09	1	GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic process	1.19	1

GO:0043401	steroid hormone mediated signaling pathway	0.09	1	GO:0043401	steroid hormone mediated signaling pathway	1.19	1
GO:0043410	positive regulation of MAPK cascade	0.09	1	GO:0043410	positive regulation of MAPK cascade	1.19	1
GO:0043434	response to peptide hormone	0.09	1	GO:0043434	response to peptide hormone	1.19	1
GO:0043457	regulation of cellular respiration	0.09	1	GO:0043457	regulation of cellular respiration	1.19	1
GO:0043473	pigmentation	0.09	1	GO:0043473	pigmentation	1.19	1
GO:0043486	histone exchange	0.09	1	GO:0043486	histone exchange	1.19	1
GO:0043488	regulation of mRNA stability	0.09	1	GO:0043488	regulation of mRNA stability	1.19	1
GO:0043491	protein kinase B signaling	0.09	1	GO:0043491	protein kinase B signaling	1.19	1
GO:0043507	positive regulation of JUN kinase activity	0.09	1	GO:0043507	positive regulation of JUN kinase activity	1.19	1
GO:0043623	cellular protein complex assembly	0.09	1	GO:0043623	cellular protein complex assembly	1.19	1
GO:0043687	post-translational protein modification	0.09	1	GO:0043687	post-translational protein modification	1.19	1
GO:0044267	cellular protein metabolic process	0.09	1	GO:0044267	cellular protein metabolic process	1.19	1
GO:0045070	positive regulation of viral genome replication	0.09	1	GO:0045070	positive regulation of viral genome replication	1.19	1
GO:0045088	regulation of innate immune response	0.09	1	GO:0045088	regulation of innate immune response	1.19	1
GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	0.09	1	GO:0045197	establishment or maintenance of epithelial cell apical/basal polarity	1.19	1
GO:0045446	endothelial cell differentiation	0.09	1	GO:0045446	endothelial cell differentiation	1.19	1
GO:0045454	cell redox homeostasis	0.09	1	GO:0045454	cell redox homeostasis	1.19	1
GO:0045471	response to ethanol	0.09	1	GO:0045471	response to ethanol	1.19	1
GO:0045595	regulation of cell differentiation	0.09	1	GO:0045595	regulation of cell differentiation	1.19	1
GO:0045596	negative regulation of cell differentiation	0.09	1	GO:0045596	negative regulation of cell differentiation	1.19	1
GO:0045604	regulation of epidermal cell differentiation	0.09	1	GO:0045604	regulation of epidermal cell differentiation	1.19	1
GO:0045652	regulation of megakaryocyte differentiation	0.09	1	GO:0045652	regulation of megakaryocyte differentiation	1.19	1

GO:0045653	negative regulation of megakaryocyte differentiation	0.09	1	GO:0045653	negative regulation of megakaryocyte differentiation	1.19	1
GO:0045666	positive regulation of neuron differentiation	0.09	1	GO:0045666	positive regulation of neuron differentiation	1.19	1
GO:0045747	positive regulation of Notch signaling pathway	0.09	1	GO:0045747	positive regulation of Notch signaling pathway	1.19	1
GO:0045773	positive regulation of axon extension	0.09	1	GO:0045773	positive regulation of axon extension	1.19	1
GO:0045776	negative regulation of blood pressure	0.09	1	GO:0045776	negative regulation of blood pressure	1.19	1
GO:0045787	positive regulation of cell cycle	0.09	1	GO:0045787	positive regulation of cell cycle	1.19	1
GO:0045815	positive regulation of gene expression, epigenetic	0.09	1	GO:0045815	positive regulation of gene expression, epigenetic	1.19	1
GO:0045955	negative regulation of calcium ion-dependent exocytosis	0.09	1	GO:0045955	negative regulation of calcium ion-dependent exocytosis	1.19	1
GO:0045995	regulation of embryonic development	0.09	1	GO:0045995	regulation of embryonic development	1.19	1
GO:0046549	retinal cone cell development	0.09	1	GO:0046549	retinal cone cell development	1.19	1
GO:0046685	response to arsenic-containing substance	0.09	1	GO:0046685	response to arsenic-containing substance	1.19	1
GO:0046686	response to cadmium ion	0.09	1	GO:0046686	response to cadmium ion	1.19	1
GO:0046827	positive regulation of protein export from nucleus	0.09	1	GO:0046827	positive regulation of protein export from nucleus	1.19	1
GO:0047497	mitochondrion transport along microtubule	0.09	1	GO:0047497	mitochondrion transport along microtubule	1.19	1
GO:0048010	vascular endothelial growth factor receptor signaling pathway	0.09	1	GO:0048010	vascular endothelial growth factor receptor signaling pathway	1.19	1
GO:0048015	phosphatidylinositol-mediated signaling	0.09	1	GO:0048015	phosphatidylinositol-mediated signaling	1.19	1
GO:0048103	somatic stem cell division	0.09	1	GO:0048103	somatic stem cell division	1.19	1
GO:0048105	establishment of body hair planar orientation	0.09	1	GO:0048105	establishment of body hair planar orientation	1.19	1

GO:0048146	positive regulation of fibroblast proliferation	0.09	1	GO:0048146	positive regulation of fibroblast proliferation	1.19	1
GO:0048305	immunoglobulin secretion	0.09	1	GO:0048305	immunoglobulin secretion	1.19	1
GO:0048339	paraxial mesoderm development	0.09	1	GO:0048339	paraxial mesoderm development	1.19	1
GO:0048378	regulation of lateral mesodermal cell fate specification	0.09	1	GO:0048378	regulation of lateral mesodermal cell fate specification	1.19	1
GO:0048469	cell maturation	0.09	1	GO:0048469	cell maturation	1.19	1
GO:0048546	digestive tract morphogenesis	0.09	1	GO:0048546	digestive tract morphogenesis	1.19	1
GO:0048568	embryonic organ development	0.09	1	GO:0048568	embryonic organ development	1.19	1
GO:0048661	positive regulation of smooth muscle cell proliferation	0.09	1	GO:0048661	positive regulation of smooth muscle cell proliferation	1.19	1
GO:0048675	axon extension	0.09	1	GO:0048675	axon extension	1.19	1
GO:0048699	generation of neurons	0.09	1	GO:0048699	generation of neurons	1.19	1
GO:0048705	skeletal system morphogenesis	0.09	1	GO:0048705	skeletal system morphogenesis	1.19	1
GO:0048706	embryonic skeletal system development	0.09	1	GO:0048706	embryonic skeletal system development	1.19	1
GO:0048762	mesenchymal cell differentiation	0.09	1	GO:0048762	mesenchymal cell differentiation	1.19	1
GO:0048839	inner ear development	0.09	1	GO:0048839	inner ear development	1.19	1
GO:0050434	positive regulation of viral transcription	0.09	1	GO:0050434	positive regulation of viral transcription	1.19	1
GO:0050688	regulation of defense response to virus	0.09	1	GO:0050688	regulation of defense response to virus	1.19	1
GO:0050689	negative regulation of defense response to virus by host	0.09	1	GO:0050689	negative regulation of defense response to virus by host	1.19	1
GO:0050727	regulation of inflammatory response	0.09	1	GO:0050727	regulation of inflammatory response	1.19	1
GO:0050790	regulation of catalytic activity	0.09	1	GO:0050790	regulation of catalytic activity	1.19	1
GO:0050796	regulation of insulin secretion	0.09	1	GO:0050796	regulation of insulin secretion	1.19	1
GO:0050819	negative regulation of coagulation	0.09	1	GO:0050819	negative regulation of coagulation	1.19	1
GO:0050829	defense response to Gram-negative bacterium	0.09	1	GO:0050829	defense response to Gram-negative bacterium	1.19	1

GO:0050853	B cell receptor signaling pathway	0.09	1	GO:0050853	B cell receptor signaling pathway	1.19	1
GO:0050862	positive regulation of T cell receptor signaling pathway	0.09	1	GO:0050862	positive regulation of T cell receptor signaling pathway	1.19	1
GO:0050868	negative regulation of T cell activation	0.09	1	GO:0050868	negative regulation of T cell activation	1.19	1
GO:0050927	positive regulation of positive chemotaxis	0.09	1	GO:0050927	positive regulation of positive chemotaxis	1.19	1
GO:0051026	chiasma assembly	0.09	1	GO:0051026	chiasma assembly	1.19	1
GO:0051097	negative regulation of helicase activity	0.09	1	GO:0051097	negative regulation of helicase activity	1.19	1
GO:0051131	chaperone-mediated protein complex assembly	0.09	1	GO:0051131	chaperone-mediated protein complex assembly	1.19	1
GO:0051174	regulation of phosphorus metabolic process	0.09	1	GO:0051174	regulation of phosphorus metabolic process	1.19	1
GO:0051209	release of sequestered calcium ion into cytosol	0.09	1	GO:0051209	release of sequestered calcium ion into cytosol	1.19	1
GO:0051249	regulation of lymphocyte activation	0.09	1	GO:0051249	regulation of lymphocyte activation	1.19	1
GO:0051259	protein oligomerization	0.09	1	GO:0051259	protein oligomerization	1.19	1
GO:0051290	protein heterotetramerization	0.09	1	GO:0051290	protein heterotetramerization	1.19	1
GO:0051412	response to corticosterone	0.09	1	GO:0051412	response to corticosterone	1.19	1
GO:0051480	regulation of cytosolic calcium ion concentration	0.09	1	GO:0051480	regulation of cytosolic calcium ion concentration	1.19	1
GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	0.09	1	GO:0051482	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G-protein coupled signaling pathway	1.19	1
GO:0051496	positive regulation of stress fiber assembly	0.09	1	GO:0051496	positive regulation of stress fiber assembly	1.19	1

GO:0051497	negative regulation of stress fiber assembly	0.09	1	GO:0051497	negative regulation of stress fiber assembly	1.19	1
GO:0051591	response to cAMP	0.09	1	GO:0051591	response to cAMP	1.19	1
GO:0051712	positive regulation of killing of cells of other organism	0.09	1	GO:0051712	positive regulation of killing of cells of other organism	1.19	1
GO:0051726	regulation of cell cycle	0.09	1	GO:0051726	regulation of cell cycle	1.19	1
GO:0051797	regulation of hair follicle development	0.09	1	GO:0051797	regulation of hair follicle development	1.19	1
GO:0051798	positive regulation of hair follicle development	0.09	1	GO:0051798	positive regulation of hair follicle development	1.19	1
GO:0055059	asymmetric neuroblast division	0.09	1	GO:0055059	asymmetric neuroblast division	1.19	1
GO:0055070	copper ion homeostasis	0.09	1	GO:0055070	copper ion homeostasis	1.19	1
GO:0055093	response to hyperoxia	0.09	1	GO:0055093	response to hyperoxia	1.19	1
GO:0060028	convergent extension involved in axis elongation	0.09	1	GO:0060028	convergent extension involved in axis elongation	1.19	1
GO:0060029	convergent extension involved in organogenesis	0.09	1	GO:0060029	convergent extension involved in organogenesis	1.19	1
GO:0060045	positive regulation of cardiac muscle cell proliferation	0.09	1	GO:0060045	positive regulation of cardiac muscle cell proliferation	1.19	1
GO:0060078	regulation of postsynaptic membrane potential	0.09	1	GO:0060078	regulation of postsynaptic membrane potential	1.19	1
GO:0060117	auditory receptor cell development	0.09	1	GO:0060117	auditory receptor cell development	1.19	1
GO:0060119	inner ear receptor cell development	0.09	1	GO:0060119	inner ear receptor cell development	1.19	1
GO:0060173	limb development	0.09	1	GO:0060173	limb development	1.19	1
GO:0060333	interferon-gamma-mediated signaling pathway	0.09	1	GO:0060333	interferon-gamma-mediated signaling pathway	1.19	1
GO:0060348	bone development	0.09	1	GO:0060348	bone development	1.19	1
GO:0060402	calcium ion transport into cytosol	0.09	1	GO:0060402	calcium ion transport into cytosol	1.19	1
GO:0060445	branching involved in salivary gland morphogenesis	0.09	1	GO:0060445	branching involved in salivary gland morphogenesis	1.19	1
GO:0060484	lung-associated mesenchyme development	0.09	1	GO:0060484	lung-associated mesenchyme development	1.19	1

	orthogonal dichotomous subdivision of terminal units involved in lung branching morphogenesis	0.09	1	GO:0060488	orthogonal dichotomous subdivision of terminal units involved in lung branching morphogenesis	1.19	1
GO:0060489	planar dichotomous subdivision of terminal units involved in lung branching morphogenesis	0.09	1	GO:0060489	planar dichotomous subdivision of terminal units involved in lung branching morphogenesis	1.19	1
GO:0060490	lateral sprouting involved in lung morphogenesis	0.09	1	GO:0060490	lateral sprouting involved in lung morphogenesis	1.19	1
GO:0060574	intestinal epithelial cell maturation	0.09	1	GO:0060574	intestinal epithelial cell maturation	1.19	1
GO:0060576	intestinal epithelial cell development	0.09	1	GO:0060576	intestinal epithelial cell development	1.19	1
GO:0060665	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	0.09	1	GO:0060665	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	1.19	1
GO:0060674	placenta blood vessel development	0.09	1	GO:0060674	placenta blood vessel development	1.19	1
GO:0060707	trophoblast giant cell differentiation	0.09	1	GO:0060707	trophoblast giant cell differentiation	1.19	1
GO:0060721	regulation of spongiotrophoblast cell proliferation	0.09	1	GO:0060721	regulation of spongiotrophoblast cell proliferation	1.19	1
GO:0060849	regulation of transcription involved in lymphatic endothelial cell fate commitment	0.09	1	GO:0060849	regulation of transcription involved in lymphatic endothelial cell fate commitment	1.19	1
GO:0060947	cardiac vascular smooth muscle cell differentiation	0.09	1	GO:0060947	cardiac vascular smooth muscle cell differentiation	1.19	1
GO:0060964	regulation of gene silencing by miRNA	0.09	1	GO:0060964	regulation of gene silencing by miRNA	1.19	1
GO:0060993	kidney morphogenesis	0.09	1	GO:0060993	kidney morphogenesis	1.19	1
GO:0061042	vascular wound healing	0.09	1	GO:0061042	vascular wound healing	1.19	1

GO:0061087	positive regulation of histone H3-K27 methylation	0.09	1	GO:0061087	positive regulation of histone H3-K27 methylation	1.19	1
GO:0061162	establishment of monopolar cell polarity	0.09	1	GO:0061162	establishment of monopolar cell polarity	1.19	1
GO:0061346	planar cell polarity pathway involved in heart morphogenesis	0.09	1	GO:0061346	planar cell polarity pathway involved in heart morphogenesis	1.19	1
GO:0065002	intracellular protein transmembrane transport	0.09	1	GO:0065002	intracellular protein transmembrane transport	1.19	1
GO:0070194	synaptonemal complex disassembly	0.09	1	GO:0070194	synaptonemal complex disassembly	1.19	1
GO:0070207	protein homotrimerization	0.09	1	GO:0070207	protein homotrimerization	1.19	1
GO:0070208	protein heterotrimerization	0.09	1	GO:0070208	protein heterotrimerization	1.19	1
GO:0070424	regulation of nucleotide-binding oligomerization domain containing signaling pathway	0.09	1	GO:0070424	regulation of nucleotide-binding oligomerization domain containing signaling pathway	1.19	1
GO:0070527	platelet aggregation	0.09	1	GO:0070527	platelet aggregation	1.19	1
GO:0070634	transepithelial ammonium transport	0.09	1	GO:0070634	transepithelial ammonium transport	1.19	1
GO:0070640	vitamin D3 metabolic process	0.09	1	GO:0070640	vitamin D3 metabolic process	1.19	1
GO:0070829	heterochromatin maintenance	0.09	1	GO:0070829	heterochromatin maintenance	1.19	1
GO:0070873	regulation of glycogen metabolic process	0.09	1	GO:0070873	regulation of glycogen metabolic process	1.19	1
GO:0071260	cellular response to mechanical stimulus	0.09	1	GO:0071260	cellular response to mechanical stimulus	1.19	1
GO:0071320	cellular response to cAMP	0.09	1	GO:0071320	cellular response to cAMP	1.19	1
GO:0071354	cellular response to interleukin-6	0.09	1	GO:0071354	cellular response to interleukin-6	1.19	1
GO:0071356	cellular response to tumor necrosis factor	0.09	1	GO:0071356	cellular response to tumor necrosis factor	1.19	1
GO:0071363	cellular response to growth factor stimulus	0.09	1	GO:0071363	cellular response to growth factor stimulus	1.19	1

GO:0071377	cellular response to glucagon stimulus	0.09	1	GO:0071377	cellular response to glucagon stimulus	1.19	1
GO:0071480	cellular response to gamma radiation	0.09	1	GO:0071480	cellular response to gamma radiation	1.19	1
GO:0071850	mitotic cell cycle arrest	0.09	1	GO:0071850	mitotic cell cycle arrest	1.19	1
GO:0072331	signal transduction by p53 class mediator	0.09	1	GO:0072331	signal transduction by p53 class mediator	1.19	1
GO:0072604	interleukin-6 secretion	0.09	1	GO:0072604	interleukin-6 secretion	1.19	1
GO:0072606	interleukin-8 secretion	0.09	1	GO:0072606	interleukin-8 secretion	1.19	1
GO:0090080	positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway	0.09	1	GO:0090080	positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway	1.19	1
GO:0090084	negative regulation of inclusion body assembly	0.09	1	GO:0090084	negative regulation of inclusion body assembly	1.19	1
GO:0090102	cochlea development	0.09	1	GO:0090102	cochlea development	1.19	1
GO:0090140	regulation of mitochondrial fission	0.09	1	GO:0090140	regulation of mitochondrial fission	1.19	1
GO:0090175	regulation of establishment of planar polarity	0.09	1	GO:0090175	regulation of establishment of planar polarity	1.19	1
GO:0090177	establishment of planar polarity involved in neural tube closure	0.09	1	GO:0090177	establishment of planar polarity involved in neural tube closure	1.19	1
GO:0090263	positive regulation of canonical Wnt signaling pathway	0.09	1	GO:0090263	positive regulation of canonical Wnt signaling pathway	1.19	1
GO:0090272	negative regulation of fibroblast growth factor production	0.09	1	GO:0090272	negative regulation of fibroblast growth factor production	1.19	1
GO:0090307	mitotic spindle assembly	0.09	1	GO:0090307	mitotic spindle assembly	1.19	1
GO:0090314	positive regulation of protein targeting to membrane	0.09	1	GO:0090314	positive regulation of protein targeting to membrane	1.19	1
GO:0090398	cellular senescence	0.09	1	GO:0090398	cellular senescence	1.19	1
GO:0090399	replicative senescence	0.09	1	GO:0090399	replicative senescence	1.19	1

GO:0090400	stress-induced premature senescence	0.09	1	GO:0090400	stress-induced premature senescence	1.19	1
GO:0090481	pyrimidine nucleotide-sugar transmembrane transport	0.09	1	GO:0090481	pyrimidine nucleotide-sugar transmembrane transport	1.19	1
GO:0090501	RNA phosphodiester bond hydrolysis	0.09	1	GO:0090501	RNA phosphodiester bond hydrolysis	1.19	1
GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	0.09	1	GO:0090502	RNA phosphodiester bond hydrolysis, endonucleolytic	1.19	1
GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	0.09	1	GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	1.19	1
GO:0097053	L-kynurenine catabolic process	0.09	1	GO:0097053	L-kynurenine catabolic process	1.19	1
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	0.09	1	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	1.19	1
GO:0097193	intrinsic apoptotic signaling pathway	0.09	1	GO:0097193	intrinsic apoptotic signaling pathway	1.19	1
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	0.09	1	GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	1.19	1
GO:0097755	positive regulation of blood vessel diameter	0.09	1	GO:0097755	positive regulation of blood vessel diameter	1.19	1
GO:0098703	calcium ion import across plasma membrane	0.09	1	GO:0098703	calcium ion import across plasma membrane	1.19	1
GO:0099641	anterograde axonal protein transport	0.09	1	GO:0099641	anterograde axonal protein transport	1.19	1
GO:1900015	regulation of cytokine production involved in inflammatory response	0.09	1	GO:1900015	regulation of cytokine production involved in inflammatory response	1.19	1
GO:1900034	regulation of cellular response to heat	0.09	1	GO:1900034	regulation of cellular response to heat	1.19	1

GO:1901896	positive regulation of calcium-transporting ATPase activity	0.09	1	GO:1901896	positive regulation of calcium-transporting ATPase activity	1.19	1
GO:1902036	regulation of hematopoietic stem cell differentiation	0.09	1	GO:1902036	regulation of hematopoietic stem cell differentiation	1.19	1
GO:1902530	positive regulation of protein linear polyubiquitination	0.09	1	GO:1902530	positive regulation of protein linear polyubiquitination	1.19	1
GO:1903209	positive regulation of oxidative stress-induced cell death	0.09	1	GO:1903209	positive regulation of oxidative stress-induced cell death	1.19	1
GO:1903465	positive regulation of mitotic cell cycle DNA replication	0.09	1	GO:1903465	positive regulation of mitotic cell cycle DNA replication	1.19	1
GO:1903543	positive regulation of exosomal secretion	0.09	1	GO:1903543	positive regulation of exosomal secretion	1.19	1
GO:1903547	regulation of growth hormone activity	0.09	1	GO:1903547	regulation of growth hormone activity	1.19	1
GO:1903553	positive regulation of extracellular exosome assembly	0.09	1	GO:1903553	positive regulation of extracellular exosome assembly	1.19	1
GO:1904030	negative regulation of cyclin-dependent protein kinase activity	0.09	1	GO:1904030	negative regulation of cyclin-dependent protein kinase activity	1.19	1
GO:1904031	positive regulation of cyclin-dependent protein kinase activity	0.09	1	GO:1904031	positive regulation of cyclin-dependent protein kinase activity	1.19	1
GO:1904837	beta-catenin-TCF complex assembly	0.09	1	GO:1904837	beta-catenin-TCF complex assembly	1.19	1
GO:1904938	planar cell polarity pathway involved in axon guidance	0.09	1	GO:1904938	planar cell polarity pathway involved in axon guidance	1.19	1
GO:1905515	non-motile cilium assembly	0.09	1	GO:1905515	non-motile cilium assembly	1.19	1
GO:1905564	positive regulation of vascular endothelial cell proliferation	0.09	1	GO:1905564	positive regulation of vascular endothelial cell proliferation	1.19	1
GO:1990001	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	0.09	1	GO:1990001	inhibition of cysteine-type endopeptidase activity involved in apoptotic process	1.19	1

GO:1990034	calcium ion export across plasma membrane	0.09	1	GO:1990034	calcium ion export across plasma membrane	1.19	1
GO:1990830	cellular response to leukemia inhibitory factor	0.09	1	GO:1990830	cellular response to leukemia inhibitory factor	1.19	1
GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	0.09	1	GO:2000134	negative regulation of G1/S transition of mitotic cell cycle	1.19	1
GO:2000278	regulation of DNA biosynthetic process	0.09	1	GO:2000278	regulation of DNA biosynthetic process	1.19	1
GO:2000298	regulation of Rho-dependent protein serine/threonine kinase activity	0.09	1	GO:2000298	regulation of Rho-dependent protein serine/threonine kinase activity	1.19	1
GO:2000404	regulation of T cell migration	0.09	1	GO:2000404	regulation of T cell migration	1.19	1
GO:2000546	positive regulation of endothelial cell chemotaxis to fibroblast growth factor	0.09	1	GO:2000546	positive regulation of endothelial cell chemotaxis to fibroblast growth factor	1.19	1
GO:2000830	positive regulation of parathyroid hormone secretion	0.09	1	GO:2000830	positive regulation of parathyroid hormone secretion	1.19	1
GO:2001028	positive regulation of endothelial cell chemotaxis	0.09	1	GO:2001028	positive regulation of endothelial cell chemotaxis	1.19	1
GO:2001234	negative regulation of apoptotic signaling pathway	0.09	1	GO:2001234	negative regulation of apoptotic signaling pathway	1.19	1
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	0.09	1	GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	1.19	1
GO:2001275	positive regulation of glucose import in response to insulin stimulus	0.09	1	GO:2001275	positive regulation of glucose import in response to insulin stimulus	1.19	1

A blank 6x10 grid of 60 empty cells, arranged in 6 rows and 10 columns. The grid is defined by black lines on a white background.

SupptbI35_RNAseq_QuickGO_shareddiffgenes				GO IDs (by protein)			
Code	Name	Percentage	Count	Code	Name	Percentage	Count
GO:0008543	fibroblast growth factor receptor signaling pathway	4.85	16	GO:0008543	fibroblast growth factor receptor signaling pathway	6.25	1
GO:0008284	positive regulation of cell proliferation	3.03	10	GO:0008284	positive regulation of cell proliferation	6.25	1
GO:0018108	peptidyl-tyrosine phosphorylation	1.52	5	GO:0018108	peptidyl-tyrosine phosphorylation	12.50	2
GO:0006468	protein phosphorylation	1.21	4	GO:0006468	protein phosphorylation	12.50	2
GO:0006898	receptor-mediated endocytosis	1.21	4	GO:0006898	receptor-mediated endocytosis	25.00	4
GO:0009408	response to heat	1.21	4	GO:0009408	response to heat	6.25	1
GO:0009409	response to cold	1.21	4	GO:0009409	response to cold	6.25	1
GO:0007165	signal transduction	0.91	3	GO:0007165	signal transduction	18.75	3
GO:0007283	spermatogenesis	0.91	3	GO:0007283	spermatogenesis	6.25	1
GO:0016310	phosphorylation	0.91	3	GO:0016310	phosphorylation	18.75	3
GO:0016477	cell migration	0.91	3	GO:0016477	cell migration	18.75	3
GO:0048013	ephrin receptor signaling pathway	0.91	3	GO:0048013	ephrin receptor signaling pathway	6.25	1
GO:0051607	defense response to virus	0.91	3	GO:0051607	defense response to virus	6.25	1
GO:0000165	MAPK cascade	0.61	2	GO:0000165	MAPK cascade	6.25	1
GO:0001525	angiogenesis	0.61	2	GO:0001525	angiogenesis	12.50	2
GO:0001657	ureteric bud development	0.61	2	GO:0001657	ureteric bud development	12.50	2
GO:0006811	ion transport	0.61	2	GO:0006811	ion transport	6.25	1
GO:0006814	sodium ion transport	0.61	2	GO:0006814	sodium ion transport	6.25	1
GO:0006816	calcium ion transport	0.61	2	GO:0006816	calcium ion transport	6.25	1
	mitochondrial calcium ion transmembrane transport	0.61	2		mitochondrial calcium ion transmembrane transport	6.25	1
GO:0006851	transport	0.61	2	GO:0006851	transport	6.25	1
GO:0006874	cellular calcium ion homeostasis	0.61	2	GO:0006874	cellular calcium ion homeostasis	6.25	1
GO:0006915	apoptotic process	0.61	2	GO:0006915	apoptotic process	12.50	2
GO:0006955	immune response	0.61	2	GO:0006955	immune response	12.50	2
GO:0007140	male meiotic nuclear division	0.61	2	GO:0007140	male meiotic nuclear division	6.25	1
GO:0007286	spermatid development	0.61	2	GO:0007286	spermatid development	6.25	1
GO:0007420	brain development	0.61	2	GO:0007420	brain development	12.50	2
GO:0007612	learning	0.61	2	GO:0007612	learning	6.25	1
GO:0007613	memory	0.61	2	GO:0007613	memory	6.25	1
GO:0009615	response to virus	0.61	2	GO:0009615	response to virus	6.25	1
GO:0010468	regulation of gene expression	0.61	2	GO:0010468	regulation of gene expression	12.50	2
GO:0014819	regulation of skeletal muscle contraction	0.61	2	GO:0014819	regulation of skeletal muscle contraction	6.25	1
GO:0030154	cell differentiation	0.61	2	GO:0030154	cell differentiation	12.50	2
GO:0030324	lung development	0.61	2	GO:0030324	lung development	12.50	2
GO:0035725	sodium ion transmembrane transport	0.61	2	GO:0035725	sodium ion transmembrane transport	6.25	1
GO:0042060	wound healing	0.61	2	GO:0042060	wound healing	12.50	2
GO:0042127	regulation of cell proliferation	0.61	2	GO:0042127	regulation of cell proliferation	12.50	2
GO:0042255	myelination	0.61	2	GO:0042255	myelination	6.25	1
GO:0043406	positive regulation of MAP kinase activity	0.61	2	GO:0043406	positive regulation of MAP kinase activity	6.25	1
GO:0045071	negative regulation of viral genome replication	0.61	2	GO:0045071	negative regulation of viral genome replication	6.25	1
GO:0048709	oligodendrocyte differentiation	0.61	2	GO:0048709	oligodendrocyte differentiation	6.25	1
GO:0051560	mitochondrial calcium ion homeostasis	0.61	2	GO:0051560	mitochondrial calcium ion homeostasis	6.25	1
GO:0060291	long-term synaptic potentiation	0.61	2	GO:0060291	long-term synaptic potentiation	6.25	1
GO:0060326	cell chemotaxis	0.61	2	GO:0060326	cell chemotaxis	6.25	1
GO:0070588	calcium ion transmembrane transport	0.61	2	GO:0070588	calcium ion transmembrane transport	6.25	1
GO:0071456	cellular response to hypoxia	0.61	2	GO:0071456	cellular response to hypoxia	6.25	1
GO:0090238	positive regulation of arachidonic acid secretion	0.61	2	GO:0090238	positive regulation of arachidonic acid secretion	6.25	1
GO:0000122	negative regulation of transcription by RNA polymerase II	0.30	1	GO:0000122	negative regulation of transcription by RNA polymerase II	6.25	1
GO:0000226	microtubule cytoskeleton organization	0.30	1	GO:0000226	microtubule cytoskeleton organization	6.25	1
GO:0001501	skeletal system development	0.30	1	GO:0001501	skeletal system development	6.25	1
GO:0001503	ossification	0.30	1	GO:0001503	ossification	6.25	1
GO:0001523	retinoid metabolic process	0.30	1	GO:0001523	retinoid metabolic process	6.25	1
GO:0001578	microtubule bundle formation	0.30	1	GO:0001578	microtubule bundle formation	6.25	1
GO:0001649	osteoblast differentiation	0.30	1	GO:0001649	osteoblast differentiation	6.25	1
GO:0001701	in utero embryonic development	0.30	1	GO:0001701	in utero embryonic development	6.25	1
GO:0001759	organ induction	0.30	1	GO:0001759	organ induction	6.25	1
GO:0001764	neuron migration	0.30	1	GO:0001764	neuron migration	6.25	1
GO:0001816	cytokine production	0.30	1	GO:0001816	cytokine production	6.25	1
GO:0001843	neural tube closure	0.30	1	GO:0001843	neural tube closure	6.25	1
GO:0001890	placenta development	0.30	1	GO:0001890	placenta development	6.25	1
GO:0001934	positive regulation of protein phosphorylation	0.30	1	GO:0001934	positive regulation of protein phosphorylation	6.25	1
GO:0001937	negative regulation of endothelial cell proliferation	0.30	1	GO:0001937	negative regulation of endothelial cell proliferation	6.25	1
	positive regulation of mesenchymal cell proliferation	0.30	1		positive regulation of mesenchymal cell proliferation	6.25	1
GO:0002053	proliferation	0.30	1	GO:0002053	proliferation	6.25	1
GO:0002062	chondrocyte differentiation	0.30	1	GO:0002062	chondrocyte differentiation	6.25	1
GO:0002244	hematopoietic progenitor cell differentiation	0.30	1	GO:0002244	hematopoietic progenitor cell differentiation	6.25	1
GO:0002376	immune system process	0.30	1	GO:0002376	immune system process	6.25	1
GO:0002446	neutrophil mediated immunity	0.30	1	GO:0002446	neutrophil mediated immunity	6.25	1
GO:0002576	platelet degranulation	0.30	1	GO:0002576	platelet degranulation	6.25	1
GO:0006024	glycosaminoglycan biosynthetic process	0.30	1	GO:0006024	glycosaminoglycan biosynthetic process	6.25	1
GO:0006027	glycosaminoglycan catabolic process	0.30	1	GO:0006027	glycosaminoglycan catabolic process	6.25	1
GO:0006351	transcription, DNA-templated	0.30	1	GO:0006351	transcription, DNA-templated	6.25	1
GO:0006355	regulation of transcription, DNA-templated	0.30	1	GO:0006355	regulation of transcription, DNA-templated	6.25	1

GO:0006457	protein folding	0.30	1	GO:0006457	protein folding	6.25	1
GO:0006897	endocytosis	0.30	1	GO:0006897	endocytosis	6.25	1
GO:0006986	response to unfolded protein	0.30	1	GO:0006986	response to unfolded protein	6.25	1
GO:0007141	male meiosis I	0.30	1	GO:0007141	male meiosis I	6.25	1
GO:0007154	cell communication	0.30	1	GO:0007154	cell communication	6.25	1
GO:0007155	cell adhesion	0.30	1	GO:0007155	cell adhesion	6.25	1
	transmembrane receptor protein tyrosine kinase signaling pathway	0.30	1	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	6.25	1
GO:0007275	multicellular organism development	0.30	1	GO:0007275	multicellular organism development	6.25	1
GO:0007399	nervous system development	0.30	1	GO:0007399	nervous system development	6.25	1
GO:0007409	axonogenesis	0.30	1	GO:0007409	axonogenesis	6.25	1
GO:0007435	salivary gland morphogenesis	0.30	1	GO:0007435	salivary gland morphogenesis	6.25	1
GO:0007507	heart development	0.30	1	GO:0007507	heart development	6.25	1
GO:0007605	sensory perception of sound	0.30	1	GO:0007605	sensory perception of sound	6.25	1
	extrinsic apoptotic signaling pathway via death domain receptors	0.30	1	GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	6.25	1
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	0.30	1	GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	6.25	1
GO:0009435	NAD biosynthetic process	0.30	1	GO:0009435	NAD biosynthetic process	6.25	1
GO:0009629	response to gravity	0.30	1	GO:0009629	response to gravity	6.25	1
GO:0009887	animal organ morphogenesis	0.30	1	GO:0009887	animal organ morphogenesis	6.25	1
GO:0009987	cellular process	0.30	1	GO:0009987	cellular process	6.25	1
GO:0010288	response to lead ion	0.30	1	GO:0010288	response to lead ion	6.25	1
GO:0010518	positive regulation of phospholipase activity	0.30	1	GO:0010518	positive regulation of phospholipase activity	6.25	1
GO:0010591	regulation of lamellipodium assembly	0.30	1	GO:0010591	regulation of lamellipodium assembly	6.25	1
				GO:0010595	positive regulation of endothelial cell migration	6.25	1
GO:0010629	negative regulation of gene expression	0.30	1	GO:0010629	negative regulation of gene expression	6.25	1
	negative regulation of striated muscle cell apoptotic process	0.30	1	GO:0010664	negative regulation of striated muscle cell apoptotic process	6.25	1
GO:0010762	regulation of fibroblast migration	0.30	1	GO:0010762	regulation of fibroblast migration	6.25	1
GO:0010863	positive regulation of phospholipase C activity	0.30	1	GO:0010863	positive regulation of phospholipase C activity	6.25	1
GO:0010966	regulation of phosphate transport	0.30	1	GO:0010966	regulation of phosphate transport	6.25	1
GO:0010976	positive regulation of neuron projection development	0.30	1	GO:0010976	positive regulation of neuron projection development	6.25	1
	positive regulation of phosphatidylinositol 3-kinase signaling	0.30	1	GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	6.25	1
GO:0016032	viral process	0.30	1	GO:0016032	viral process	6.25	1
GO:0016358	dendrite development	0.30	1	GO:0016358	dendrite development	6.25	1
GO:0016525	negative regulation of angiogenesis	0.30	1	GO:0016525	negative regulation of angiogenesis	6.25	1
GO:0019363	pyridine nucleotide biosynthetic process	0.30	1	GO:0019363	pyridine nucleotide biosynthetic process	6.25	1
GO:0019674	NAD metabolic process	0.30	1	GO:0019674	NAD metabolic process	6.25	1
GO:0021510	spinal cord development	0.30	1	GO:0021510	spinal cord development	6.25	1
GO:0021537	telencephalon development	0.30	1	GO:0021537	telencephalon development	6.25	1
GO:0021769	orbitofrontal cortex development	0.30	1	GO:0021769	orbitofrontal cortex development	6.25	1
GO:0021847	ventricular zone neuroblast division	0.30	1	GO:0021847	ventricular zone neuroblast division	6.25	1
GO:0022604	regulation of cell morphogenesis	0.30	1	GO:0022604	regulation of cell morphogenesis	6.25	1
GO:0030001	metal ion transport	0.30	1	GO:0030001	metal ion transport	6.25	1
GO:0030198	extracellular matrix organization	0.30	1	GO:0030198	extracellular matrix organization	6.25	1
GO:0030203	glycosaminoglycan metabolic process	0.30	1	GO:0030203	glycosaminoglycan metabolic process	6.25	1
GO:0030216	keratinocyte differentiation	0.30	1	GO:0030216	keratinocyte differentiation	6.25	1
GO:0030316	osteoclast differentiation	0.30	1	GO:0030316	osteoclast differentiation	6.25	1
GO:0030326	embryonic limb morphogenesis	0.30	1	GO:0030326	embryonic limb morphogenesis	6.25	1
GO:0030334	regulation of cell migration	0.30	1	GO:0030334	regulation of cell migration	6.25	1
GO:0030901	midbrain development	0.30	1	GO:0030901	midbrain development	6.25	1
	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle	0.30	1	GO:0031662	positive regulation of cyclin-dependent protein serine/threonine kinase activity involved in G2/M transition of mitotic cell cycle	6.25	1
GO:0032387	negative regulation of intracellular transport	0.30	1	GO:0032387	negative regulation of intracellular transport	6.25	1
GO:0032496	response to lipopolysaccharide	0.30	1	GO:0032496	response to lipopolysaccharide	6.25	1
GO:0032781	positive regulation of ATPase activity	0.30	1	GO:0032781	positive regulation of ATPase activity	6.25	1
				GO:0033031	positive regulation of neutrophil apoptotic process	6.25	1
GO:0033591	response to L-ascorbic acid	0.30	1	GO:0033591	response to L-ascorbic acid	6.25	1
GO:0033598	mammary gland epithelial cell proliferation	0.30	1	GO:0033598	mammary gland epithelial cell proliferation	6.25	1
				GO:0033628	regulation of cell adhesion mediated by integrin	6.25	1
GO:0034097	response to cytokine	0.30	1	GO:0034097	response to cytokine	6.25	1
GO:0034605	cellular response to heat	0.30	1	GO:0034605	cellular response to heat	6.25	1
GO:0035457	cellular response to interferon-alpha	0.30	1	GO:0035457	cellular response to interferon-alpha	6.25	1
	fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	0.30	1	GO:0035607	fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	6.25	1
GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	0.30	1	GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	6.25	1
GO:0038093	Fc receptor signaling pathway	0.30	1	GO:0038093	Fc receptor signaling pathway	6.25	1
GO:0042026	protein refolding	0.30	1	GO:0042026	protein refolding	6.25	1
GO:0042119	neutrophil activation	0.30	1	GO:0042119	neutrophil activation	6.25	1
GO:0042130	negative regulation of T cell proliferation	0.30	1	GO:0042130	negative regulation of T cell proliferation	6.25	1

GO:0042472	inner ear morphogenesis	0.30	1	GO:0042472	inner ear morphogenesis	6.25	1
GO:0042473	outer ear morphogenesis	0.30	1	GO:0042473	outer ear morphogenesis	6.25	1
GO:0042474	middle ear morphogenesis	0.30	1	GO:0042474	middle ear morphogenesis	6.25	1
GO:0042993	positive regulation of transcription factor import into nucleus	0.30	1	GO:0042993	positive regulation of transcription factor import into nucleus	6.25	1
GO:0043009	chordate embryonic development	0.30	1	GO:0043009	chordate embryonic development	6.25	1
GO:0043066	negative regulation of apoptotic process	0.30	1	GO:0043066	negative regulation of apoptotic process	6.25	1
GO:0043312	neutrophil degranulation	0.30	1	GO:0043312	neutrophil degranulation	6.25	1
GO:0043410	positive regulation of MAPK cascade	0.30	1	GO:0043410	positive regulation of MAPK cascade	6.25	1
GO:0043434	response to peptide hormone	0.30	1	GO:0043434	response to peptide hormone	6.25	1
GO:0043473	pigmentation	0.30	1	GO:0043473	pigmentation	6.25	1
GO:0043491	protein kinase B signaling	0.30	1	GO:0043491	protein kinase B signaling	6.25	1
GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	0.30	1	GO:0043517	positive regulation of DNA damage response, signal transduction by p53 class mediator	6.25	1
GO:0043535	regulation of blood vessel endothelial cell migration	0.30	1	GO:0043535	regulation of blood vessel endothelial cell migration	6.25	1
GO:0043536	positive regulation of blood vessel endothelial cell migration	0.30	1	GO:0043536	positive regulation of blood vessel endothelial cell migration	6.25	1
GO:0043583	ear development	0.30	1	GO:0043583	ear development	6.25	1
GO:0045087	innate immune response	0.30	1	GO:0045087	innate immune response	6.25	1
GO:0045471	response to ethanol	0.30	1	GO:0045471	response to ethanol	6.25	1
GO:0045595	regulation of cell differentiation	0.30	1	GO:0045595	regulation of cell differentiation	6.25	1
GO:0045666	positive regulation of neuron differentiation	0.30	1	GO:0045666	positive regulation of neuron differentiation	6.25	1
GO:0045765	regulation of angiogenesis	0.30	1	GO:0045765	regulation of angiogenesis	6.25	1
GO:0045773	positive regulation of axon extension	0.30	1	GO:0045773	positive regulation of axon extension	6.25	1
GO:0045787	positive regulation of cell cycle	0.30	1	GO:0045787	positive regulation of cell cycle	6.25	1
GO:0045860	positive regulation of protein kinase activity	0.30	1	GO:0045860	positive regulation of protein kinase activity	6.25	1
GO:0045995	regulation of embryonic development	0.30	1	GO:0045995	regulation of embryonic development	6.25	1
GO:0046058	cAMP metabolic process	0.30	1	GO:0046058	cAMP metabolic process	6.25	1
GO:0046686	response to cadmium ion	0.30	1	GO:0046686	response to cadmium ion	6.25	1
GO:0046718	viral entry into host cell	0.30	1	GO:0046718	viral entry into host cell	6.25	1
GO:0046777	protein autophosphorylation	0.30	1	GO:0046777	protein autophosphorylation	6.25	1
GO:0046827	positive regulation of protein export from nucleus	0.30	1	GO:0046827	positive regulation of protein export from nucleus	6.25	1
GO:0046849	bone remodeling	0.30	1	GO:0046849	bone remodeling	6.25	1
GO:0046854	phosphatidylinositol phosphorylation	0.30	1	GO:0046854	phosphatidylinositol phosphorylation	6.25	1
GO:0047497	mitochondrion transport along microtubule	0.30	1	GO:0047497	mitochondrion transport along microtubule	6.25	1
GO:0048015	phosphatidylinositol-mediated signaling	0.30	1	GO:0048015	phosphatidylinositol-mediated signaling	6.25	1
GO:0048339	paraxial mesoderm development	0.30	1	GO:0048339	paraxial mesoderm development	6.25	1
GO:0048378	regulation of lateral mesodermal cell fate specification	0.30	1	GO:0048378	regulation of lateral mesodermal cell fate specification	6.25	1
GO:0048469	cell maturation	0.30	1	GO:0048469	cell maturation	6.25	1
GO:0048514	blood vessel morphogenesis	0.30	1	GO:0048514	blood vessel morphogenesis	6.25	1
GO:0048675	axon extension	0.30	1	GO:0048675	axon extension	6.25	1
GO:0048699	generation of neurons	0.30	1	GO:0048699	generation of neurons	6.25	1
GO:0048705	skeletal system morphogenesis	0.30	1	GO:0048705	skeletal system morphogenesis	6.25	1
GO:0048762	mesenchymal cell differentiation	0.30	1	GO:0048762	mesenchymal cell differentiation	6.25	1
GO:0048839	inner ear development	0.30	1	GO:0048839	inner ear development	6.25	1
GO:0048870	cell motility	0.30	1	GO:0048870	cell motility	6.25	1
GO:0050790	regulation of catalytic activity	0.30	1	GO:0050790	regulation of catalytic activity	6.25	1
GO:0050821	protein stabilization	0.30	1	GO:0050821	protein stabilization	6.25	1
GO:0050900	leukocyte migration	0.30	1	GO:0050900	leukocyte migration	6.25	1
GO:0051174	regulation of phosphorus metabolic process	0.30	1	GO:0051174	regulation of phosphorus metabolic process	6.25	1
GO:0051384	response to glucocorticoid	0.30	1	GO:0051384	response to glucocorticoid	6.25	1
GO:0051496	positive regulation of stress fiber assembly	0.30	1	GO:0051496	positive regulation of stress fiber assembly	6.25	1
GO:0051591	response to cAMP	0.30	1	GO:0051591	response to cAMP	6.25	1
GO:0051592	response to calcium ion	0.30	1	GO:0051592	response to calcium ion	6.25	1
GO:0051894	positive regulation of focal adhesion assembly	0.30	1	GO:0051894	positive regulation of focal adhesion assembly	6.25	1
GO:0051897	positive regulation of protein kinase B signaling	0.30	1	GO:0051897	positive regulation of protein kinase B signaling	6.25	1
GO:0051898	negative regulation of protein kinase B signaling	0.30	1	GO:0051898	negative regulation of protein kinase B signaling	6.25	1
GO:0055085	transmembrane transport	0.30	1	GO:0055085	transmembrane transport	6.25	1
GO:0060045	positive regulation of cardiac muscle cell proliferation	0.30	1	GO:0060045	positive regulation of cardiac muscle cell proliferation	6.25	1
GO:0060078	regulation of postsynaptic membrane potential	0.30	1	GO:0060078	regulation of postsynaptic membrane potential	6.25	1
GO:0060117	auditory receptor cell development	0.30	1	GO:0060117	auditory receptor cell development	6.25	1
GO:0060122	inner ear receptor cell stereocilium organization	0.30	1	GO:0060122	inner ear receptor cell stereocilium organization	6.25	1
GO:0060333	interferon-gamma-mediated signaling pathway	0.30	1	GO:0060333	interferon-gamma-mediated signaling pathway	6.25	1
GO:0060337	type I interferon signaling pathway	0.30	1	GO:0060337	type I interferon signaling pathway	6.25	1
GO:0060348	bone development	0.30	1	GO:0060348	bone development	6.25	1
GO:0060402	calcium ion transport into cytosol	0.30	1	GO:0060402	calcium ion transport into cytosol	6.25	1
GO:0060444	branching involved in mammary gland duct morphogenesis	0.30	1	GO:0060444	branching involved in mammary gland duct morphogenesis	6.25	1
GO:0060445	branching involved in salivary gland morphogenesis	0.30	1	GO:0060445	branching involved in salivary gland morphogenesis	6.25	1

GO:0060484	lung-associated mesenchyme development	0.30	1	GO:0060484	lung-associated mesenchyme development	6.25	1
GO:0060665	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	0.30	1	GO:0060665	regulation of branching involved in salivary gland morphogenesis by mesenchymal-epithelial signaling	6.25	1
GO:0060721	regulation of spongiotrophoblast cell proliferation	0.30	1	GO:0060721	regulation of spongiotrophoblast cell proliferation	6.25	1
GO:0061162	establishment of monopolar cell polarity	0.30	1	GO:0061162	establishment of monopolar cell polarity	6.25	1
GO:0070194	synaptonemal complex disassembly	0.30	1	GO:0070194	synaptonemal complex disassembly	6.25	1
GO:0070309	lens fiber cell morphogenesis	0.30	1	GO:0070309	lens fiber cell morphogenesis	6.25	1
GO:0070372	regulation of ERK1 and ERK2 cascade	0.30	1	GO:0070372	regulation of ERK1 and ERK2 cascade	6.25	1
GO:0070640	vitamin D3 metabolic process	0.30	1	GO:0070640	vitamin D3 metabolic process	6.25	1
GO:0070848	response to growth factor	0.30	1	GO:0070848	response to growth factor	6.25	1
GO:0070873	regulation of glycogen metabolic process	0.30	1	GO:0070873	regulation of glycogen metabolic process	6.25	1
GO:0071222	cellular response to lipopolysaccharide	0.30	1	GO:0071222	cellular response to lipopolysaccharide	6.25	1
GO:0071260	cellular response to mechanical stimulus	0.30	1	GO:0071260	cellular response to mechanical stimulus	6.25	1
GO:0071320	cellular response to cAMP	0.30	1	GO:0071320	cellular response to cAMP	6.25	1
GO:0071346	cellular response to interferon-gamma	0.30	1	GO:0071346	cellular response to interferon-gamma	6.25	1
GO:0071354	cellular response to interleukin-6	0.30	1	GO:0071354	cellular response to interleukin-6	6.25	1
GO:0071356	cellular response to tumor necrosis factor	0.30	1	GO:0071356	cellular response to tumor necrosis factor	6.25	1
GO:0071363	cellular response to growth factor stimulus	0.30	1	GO:0071363	cellular response to growth factor stimulus	6.25	1
GO:0072593	reactive oxygen species metabolic process	0.30	1	GO:0072593	reactive oxygen species metabolic process	6.25	1
GO:0090080	positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway	0.30	1	GO:0090080	positive regulation of MAPKKK cascade by fibroblast growth factor receptor signaling pathway	6.25	1
GO:0090084	negative regulation of inclusion body assembly	0.30	1	GO:0090084	negative regulation of inclusion body assembly	6.25	1
GO:0090272	negative regulation of fibroblast growth factor production	0.30	1	GO:0090272	negative regulation of fibroblast growth factor production	6.25	1
GO:0090399	replicative senescence	0.30	1	GO:0090399	replicative senescence	6.25	1
GO:0090403	oxidative stress-induced premature senescence	0.30	1	GO:0090403	oxidative stress-induced premature senescence	6.25	1
GO:0090630	activation of GTPase activity	0.30	1	GO:0090630	activation of GTPase activity	6.25	1
GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	0.30	1	GO:0097011	cellular response to granulocyte macrophage colony-stimulating factor stimulus	6.25	1
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	0.30	1	GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	6.25	1
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	0.30	1	GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	6.25	1
GO:0098703	calcium ion import across plasma membrane	0.30	1	GO:0098703	calcium ion import across plasma membrane	6.25	1
GO:1900034	regulation of cellular response to heat	0.30	1	GO:1900034	regulation of cellular response to heat	6.25	1
GO:1900138	negative regulation of phospholipase A2 activity	0.30	1	GO:1900138	negative regulation of phospholipase A2 activity	6.25	1
GO:1900139	negative regulation of arachidonic acid secretion	0.30	1	GO:1900139	negative regulation of arachidonic acid secretion	6.25	1
GO:1901896	positive regulation of calcium-transporting ATPase activity	0.30	1	GO:1901896	positive regulation of calcium-transporting ATPase activity	6.25	1
GO:1903078	positive regulation of protein localization to plasma membrane	0.30	1	GO:1903078	positive regulation of protein localization to plasma membrane	6.25	1
GO:1903209	positive regulation of oxidative stress-induced cell death	0.30	1	GO:1903209	positive regulation of oxidative stress-induced cell death	6.25	1
GO:1903465	positive regulation of mitotic cell cycle DNA replication	0.30	1	GO:1903465	positive regulation of mitotic cell cycle DNA replication	6.25	1
GO:1903543	positive regulation of exosomal secretion	0.30	1	GO:1903543	positive regulation of exosomal secretion	6.25	1
GO:1903547	regulation of growth hormone activity	0.30	1	GO:1903547	regulation of growth hormone activity	6.25	1
GO:1903553	positive regulation of extracellular exosome assembly	0.30	1	GO:1903553	positive regulation of extracellular exosome assembly	6.25	1
GO:1903779	regulation of cardiac conduction	0.30	1	GO:1903779	regulation of cardiac conduction	6.25	1
GO:1905564	positive regulation of vascular endothelial cell proliferation	0.30	1	GO:1905564	positive regulation of vascular endothelial cell proliferation	6.25	1
GO:1990034	calcium ion export across plasma membrane	0.30	1	GO:1990034	calcium ion export across plasma membrane	6.25	1
GO:2000546	positive regulation of endothelial cell chemotaxis to fibroblast growth factor	0.30	1	GO:2000546	positive regulation of endothelial cell chemotaxis to fibroblast growth factor	6.25	1
GO:2000830	positive regulation of parathyroid hormone secretion	0.30	1	GO:2000830	positive regulation of parathyroid hormone secretion	6.25	1
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	0.30	1	GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	6.25	1

Supptb136_HALOmeasurements

P-Nr.

P16_900_T1_wt1

Mittelwert Standardabw Verhältnis Leber zu... (aus Mittelwerten)

file name	912.svs	912.svs	912.svs	912.svs	912.svs	
Classified Area (mm²2)	0.40666	1.10855	0.09778	1.08091	1.53551	0.44802
CD3 positive Lymphozyten Area (mm²2)	0.2489	0.65367	0.09496	0.59416	0.90409	0.33099
CD3 negative Lymphozyten Area (mm²2)	0.06286	0.18772	0.01252	0.08387	0.23291	0.06556
Bindegewebe Area (mm²2)	0.00454	0.02649	0.0029	0.02805	0.07996	0.008
optisch leer Area (mm²2)	0	0.00054	0	0.00006	0.0027	0.00006
Leber Area (mm²2)	0.09036	0.24113	0.0329	0.27477	0.31585	0.04341
% CD3 positive Lymphozyten Area	61.21	58.88	50.59	64.22	58.88	73.88
% CD3 negative Lymphozyten Area	15.46	16.93	12.8	7.76	15.17	14.63
% Bindegewebe Area	1.12	2.39	2.97	2.59	5.21	1.79
% optisch leer Area	0	0.05	0	0.01	0.18	0.01
% Leber Area	22.22	21.75	33.65	25.42	20.57	9.69
Summe Lyphos	76.67	75.81	63.39	71.98	74.05	88.51
Verhältnis Leber:Lymphos	0.2898135	0.286901464	0.530840827	0.353153654	0.27778528	0.109479155
						0.307995644
						0.12436253

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	61.21	58.91	50.59	66.23	58.99	73.89	61.63666667	7.16348767
% CD3 negative Lymphozyten Area	15.46	16.94	12.8	7.76	15.2	14.63	13.79833332	2.06495216
% Bindegewebe Area	1.12	2.39	2.97	2.59	5.22	1.79	2.68	1.28150953
% Leber Area	22.22	21.76	33.65	25.42	20.61	9.69	22.225	7.07918722

P-Nr.

P17_407_2374_wt

file name	915.svs	915.svs	915.svs	915.svs	915.svs	
Classified Area (mm²2)	0.9986	0.29333	0.43173	0.24128	0.31362	0.52668
CD3 positive Lymphozyten Area (mm²2)	0.30417	0.10716	0.18289	0.09005	0.0887	0.03421
CD3 negative Lymphozyten Area (mm²2)	0.00917	0.03008	0.00766	0.00134	0.00486	0.00766
Bindegewebe Area (mm²2)	0.14143	0.02552	0.01699	0.02361	0.02045	0.01666
optisch leer Area (mm²2)	0.0012	0.00063	0.00005	0.00014	0.00069	0.00006
Leber Area (mm²2)	0.54264	0.11569	0.22413	0.12614	0.19892	0.26809
% CD3 positive Lymphozyten Area	30.46	36.53	42.36	37.32	28.28	44.47
% CD3 negative Lymphozyten Area	0.92	1.05	1.77	0.56	1.55	1.45
% Bindegewebe Area	14.16	8.7	3.94	9.79	6.52	3.16
% optisch leer Area	0.12	0.21	0.01	0.06	0.22	0.01
% Leber Area	54.34	53.51	51.92	52.28	63.43	50.9
Summe Lyphos	31.38	37.58	44.13	37.88	29.83	45.92
Verhältnis Leber:Lymphos	1.7316762	1.423895689	1.176523907	1.380147835	2.126382836	1.108449477
						1.491179329
						0.34729131

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	30.5	36.61	42.36	37.34	28.34	44.48	36.605	5.79161966
% CD3 negative Lymphozyten Area	0.93	1.05	1.77	0.56	1.55	1.45	1.216666667	0.41205447
% Bindegewebe Area	14.18	8.72	3.94	9.8	6.53	3.16	7.721666667	3.73175748
% Leber Area	54.4	53.62	51.93	52.31	63.57	50.91	54.45666667	4.22940369

P-Nr.

P13_154_752_wt

file name	918.svs	918.svs	918.svs	918.svs	918.svs	
Classified Area (mm²2)	0.20058	0.24992	0.35223	0.049	0.20058	0.02117
CD3 positive Lymphozyten Area (mm²2)	0.12408	0.17132	0.22219	0.02815	0.12408	0.01296
CD3 negative Lymphozyten Area (mm²2)	0.01184	0.00717	0.02219	0.00267	0.01184	0.00121
Bindegewebe Area (mm²2)	0.02879	0.02696	0.05371	0.00694	0.02879	0.00328
optisch leer Area (mm²2)	0.00286	0.0015	0.00295	0.00098	0.00286	0.00011
Leber Area (mm²2)	0.03301	0.04928	0.05118	0.01026	0.03301	0.00362
% CD3 positive Lymphozyten Area	61.86	68.55	63.08	57.44	61.86	61.19
% CD3 negative Lymphozyten Area	5.9	2.87	6.3	5.45	5.9	5.7
% Bindegewebe Area	14.35	10.79	15.25	14.17	14.35	15.47
% optisch leer Area	1.43	0.6	0.84	2.01	1.43	0.53
% Leber Area	16.46	17.2	14.53	20.93	16.46	17.1
Summe Lyphos	67.76	71.42	69.38	62.89	67.76	66.89
Verhältnis Leber:Lymphos	0.2429162	0.240828899	0.209426348	0.332803307	0.242916175	0.255643594
						0.254089083
						0.03790032

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	62.76	68.96	63.61	58.62	62.76	61.52	63.03830599	3.09445394
% CD3 negative Lymphozyten Area	5.99	2.89	6.35	5.56	5.09	5.73	5.41807487	1.15807555
% Bindegewebe Area	14.56	10.86	15.38	14.46	14.56	15.55	14.23	1.56672433
% Leber Area	16.70	17.30	14.65	21.36	16.70	17.19	17.32	2.00902915

P-Nr.

P16_902_1_vTR

file name	913.svs	913.svs	913.svs	913.svs	913.svs	
Classified Area (mm²2)	2.275	2.02765	2.22174	1.95751	2.15288	2.24403
CD3 positive Lymphozyten Area (mm²2)	0.7403	1.32002	0.97483	1.10541	1.28115	0.98273
CD3 negative Lymphozyten Area (mm²2)	0.79681	0.3973	0.92318	0.58694	0.27723	0.61941
Bindegewebe Area (mm²2)	0.45727	0.12364	0.19624	0.12033	0.25411	0.45925
optisch leer Area (mm²2)	0.00093	0.00063	0.00027	0.0013	0.0011	0.0016
Leber Area (mm²2)	0.27978	0.27587	0.17271	0.14353	0.3393	0.32505
% CD3 positive Lymphozyten Area	32.54	60.67	43.88	56.47	59.51	37.38
% CD3 negative Lymphozyten Area	35.02	19.59	41.55	29.98	12.88	27.76
% Bindegewebe Area	20.1	6.1	8.83	6.15	11.8	20.47
% optisch leer Area	0.04	0.03	0.01	0.07	0.05	0.07
% Leber Area	12.3	13.61	5.73	7.33	15.76	14.49
Summe Lyphos	67.56	80.26	85.43	86.45	72.39	64.98
Verhältnis Leber:Lymphos	0.1820604	0.169573885	0.067072457	0.084788895	0.217709628	0.22299169
						0.157366158
						0.06072793

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	32.55	60.69	43.88	56.51	59.54	37.41	48.43	11.0546777
% CD3 negative Lymphozyten Area	35.03	19.60	41.55	30.00	12.89	27.62	27.78	9.4525533
% Bindegewebe Area	20.11	6.10	8.83	6.15	11.81	20.48	12.25	6.0055277

Leerer Raum abgezogen

P16_900_T1_wt1	P17_407_2374_wt	P13_154_752_wt	P16_902_1_vTR	P15_376_1173_vTR	P16_263_control_liver
% CD3 positive	61.64	36.61	62.04	48.43	68.04
STABW	7.16	5.79	3.09	11.05	9.12
% CD3 negative	13.8	1.22	5.42	27.78	12.12
STABW	2.97	0.41	1.16	9.45	6.82
% Bindegewebe	2.68	7.72	14.23	12.25	11.52
STABW	1.28	3.73	1.57	6.01	2.15
% Leber Area	22.23	54.46	17.32	11.54	8.31
STABW	7.08	4.23	2.01	3.72	1.11
					6.74
					1.13

% Leber Area	12.30	13.61	5.73	7.34	15.77	14.50	11.54	3.71830449
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P-Nr. P16_902_2_2353_vTR

file name	914.svs	914.svs	914.svs	914.svs	914.svs	914.svs	914.svs	
Classified Area (mm²)	1.68643	2.3777	1.6858	2.41316	1.84928	3.748		
CD3 positive Lymphozyten Area (mm²)	1.24017	1.85892	0.98941	1.82511	1.25136	1.99884		
CD3 negative Lymphozyten Area (mm²)	0.12403	0.20225	0.28911	0.16187	0.14266	0.94118		
Bindegewebe Area (mm²)	0.16911	0.16223	0.24409	0.22476	0.27248	0.50756		
optisch leer Area (mm²)	0.00228	0.00558	0.00466	0.01133	0.00944	0.00424		
Leber Area (mm²)	0.15084	0.14849	0.15854	0.19008	0.17335	0.29617		
% CD3 positive Lymphozyten Area	73.54	78.18	58.69	75.63	67.67	53.33	67.84	9.07727198 0.12219929
% CD3 negative Lymphozyten Area	7.35	8.51	17.15	6.71	7.71	25.11	12.09	6.81342792 0.10371575
% Bindegewebe Area	10.03	6.82	14.48	9.31	14.73	13.54		
% optisch leer Area	0.14	0.24	0.28	0.47	0.51	0.11		
% Leber Area	8.94	6.25	9.4	7.88	9.37	7.9	8.29	1.10323766
Summe Lymphos	80.89	86.69	75.84	82.34	75.38	78.44		
Verhältnis Leber:Lymphos	0.1105205	0.072095974	0.123945148	0.095700753	0.124303529	0.100713921	0.104546631	0.01801994

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	73.64	78.37	58.85	75.99	68.02	53.39	68.04	9.13098521
% CD3 negative Lymphozyten Area	7.36	8.53	17.20	6.74	7.75	25.14	12.12	6.81681309
% Bindegewebe Area	10.04	6.84	14.52	9.35	14.81	13.55	11.52	2.96404843
% Leber Area	8.95	6.27	9.43	7.92	9.42	7.91	8.31	1.1093536

P-Nr. P15_376_1173_vTR

file name	917.svs	917.svs	917.svs	917.svs	917.svs	917.svs	917.svs	
Classified Area (mm²)	0.05094	0.03371	0.21693	0.27469	0.25634	0.37352		
CD3 positive Lymphozyten Area (mm²)	0.03881	0.02526	0.15762	0.1861	0.17059	0.29762		
CD3 negative Lymphozyten Area (mm²)	0.00188	0.00392	0.00353	0.00233	0.00389	0.00899		
Bindegewebe Area (mm²)	0.00202	0.00046	0.00393	0.00507	0.00792	0.00277		
optisch leer Area (mm²)	0.00072	0	0	0.00014	0.00001	0.00007		
Leber Area (mm²)	0.00751	0.00407	0.05185	0.08105	0.07374	0.06407		
% CD3 positive Lymphozyten Area	76.19	74.92	72.66	67.75	66.6	70.68	72.96666667	4.60283125 0.28816811
% CD3 negative Lymphozyten Area	3.69	11.64	1.63	0.85	1.52	2.41	3.623333333	3.69306407 0.27453454
% Bindegewebe Area	3.97	1.36	1.81	1.85	3.09	0.74		
% optisch leer Area	1.41	0	0	0.05	0	0.02		
% Leber Area	14.74	12.07	23.9	29.51	28.79	17.15	21.02666667	6.77329232
Summe Lymphos	79.88	86.56	74.29	68.6	68.12	82.09		
Verhältnis Leber:Lymphos	0.1845268	0.13944085	0.321712209	0.430174927	0.422636524	0.208917042	0.284568057	0.11433663

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	77.38	74.92	72.66	67.78	66.6	70.70	72.16	4.74395214
% CD3 negative Lymphozyten Area	3.74	11.64	1.63	0.85	1.52	2.41	3.69319524	
% Bindegewebe Area	4.03	1.36	1.81	1.85	3.09	0.74	2.15	1.09716608
% Leber Area	14.95	12.07	23.9	29.52	28.79	17.15	21.06	6.74381456

P-Nr. P16_263_Leber nicht inf

file name	916.svs	916.svs	916.svs	916.svs	916.svs	916.svs	916.svs	
Classified Area (mm²)	1.39863	1.14296						
CD3 positive Lymphozyten Area (mm²)	0.18309	0.19171						
CD3 negative Lymphozyten Area (mm²)	0.02972	0.01347						
Bindegewebe Area (mm²)	0.20355	0.18489						
optisch leer Area (mm²)	0.01897	0.0221						
Leber Area (mm²)	0.8633	0.7308						
% CD3 positive Lymphozyten Area	14.1	16.77			15.435	1.335	4.22481374	
% CD3 negative Lymphozyten Area	2.29	1.18			1.735	0.555	3.79790332	
% Bindegewebe Area	15.67	16.18						
% optisch leer Area	1.46	1.93						
% Leber Area	66.48	63.94			65.21	1.27		
Summe Lymphos	16.39	17.95						
Verhältnis Leber:Lymphos	4.0561318	3.562116992			3.80912439	0.2470074		

Leerer Raum abgezogen

% CD3 positive Lymphozyten Area	14.31	17.30			15.70447034	1.39556035		
% CD3 negative Lymphozyten Area	2.32	1.20				1.76	1.56035359	
% Bindegewebe Area	15.90	16.50				16.20	0.29812389	
% Leber Area	67.46	65.20				66.33	1.13333056	

P16_900_T1.wt1 P17_407_2374.wt P13_154_752.wt P16_902_1.vTR P16_902_2_2353.vTR P15_376_1173.vTR

Mittelwert %Leber	22.32	54.4	17.41	11.54	8.29	21.03	
Standardabweichung %Leber	7.08	4.92	1.92	3.72	1.1	6.77	
Mittelwert %CD3+	61.28	36.57	62.33	51.58	67.84	72.97	
Standardabweichung %CD3+	6.99	5.81	3.29	11.05	9.08	4.6	

Aus mittelwerten Verhältnis Leber:CD3+

0.36	1.49	0.27	0.22	0.12	0.29	
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Aus mittelwerten Verhältnis Leber:Lymphos

0.3	1.44	0.25	0.15	0.1	0.28	
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Verhältnis Leber:Lymphos

0.31	1.49	0.25	0.16	0.1	0.25	
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Standardabweichung Verhältnis

0.12	0.34	0.04	0.06	0.02	0.11	
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Supptbl37_ProteinTable_Dim1lbl_vTRvsTcells

Row	User Flag	OK	Accession	Protein	MW [kDa]	pI	#Alt. Proteins	Scores	#Peptides	SC [%]	RMS90 [ppm]	Rank	Median(SoK)	#(SoK)	CV [%](SoK)
1	true	ENSGALP00000025600	2,4-dienoyl CoA reductase 1 mitochondrial - CGNC Symbol 11873		35.7	9.5	1	225.1 (M:225.1)	6	9.8	8.02	714	1.8	3	66.55
2	true	ENSGALP00000005468	2' 3'-cyclic nucleotide 3' phosphodiesterase - CGNC Symbol 49552		47.2	9.2	1	113.7 (M:113.7)	2	3.3	1.11	1138	0.85!	1	
3	true	ENSGALP00000028664	2'-5'-oligoadenylate synthetase-like - CGNC Symbol 49545		54.2	8.4	2	192.5 (M:192.5)	3	6.5	5.88	819	2.19	1	
4	true	ENSGALP00000037772	3'(2') 5'-bisphosphate nucleotidase 1 - CGNC Symbol 7291		32.9	5.6	1	180.7 (M:180.7)	2	2.6	6.63	865	0.36!	1	
5	true	ENSGALP00000017139	3'-phosphoadenosine 5'-phosphosulfate synthase 1 - CGNC Symbol 8007		70.8	6.3	1	157.1 (M:157.1)	4	3.8	8.97	939	0.82!	1	
6	true	ENSGALP00000023936	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble) - CGNC Symbol 49779		57.6	5.5	1	155.2 (M:55.2)	2	3.4	12.17	1396			
7	true	ENSGALP00000020134	3-hydroxybutyrate dehydrogenase type 2 - CGNC Symbol 9371		26.8	6.8	1	182.8 (M:182.8)	4	15.1	12.4	856	0.88!	1	
8	true	ENSGALP00000036263	3-hydroxyisobutyryl-CoA hydrolase - CGNC Symbol 1646		42.8	8.6	1	116.3 (M:116.3)	4	7.8	7.5	1115	0.43!	2	2.69
9	true	ENSGALP00000023917	3-oxoacid CoA transferase 1 - CGNC Symbol 53012		56.1	8	1	470.7 (M:470.7)	10	19	5.74	315	0.83!	6	68.49
10	true	ENSGALP00000035595	40S ribosomal protein S11 - Refseq NP_001026004		18.2	10.4	1	563.0 (M:563.0)	13	52.9	4.86	263	0.74!	3	10.85
11	true	ENSGALP00000013622	5'-3' exoribonuclease 2 - CGNC Symbol 6344		108.5	7.5	1	134.0 (M:134.0)	3	4.1	13.91	1047	0.84!	1	
12	true	ENSGALP00000013294	5'-nucleotidase cytosolic II - CGNC Symbol 6204		65.9	5.3	1	245.2 (M:245.2)	5	7.4	13.92	657	0.84!	3	20.32
13	true	ENSGALP00000005776	5'-nucleotidase cytosolic IIIB - CGNC Symbol 2665		33.1	5.3	1	102.0 (M:102.0)	1	5.9	2.85	1194	0.55!	1	
14	true	ENSGALP00000024086	5'-nucleotidase domain containing 1 - CGNC Symbol 11115		52	5.2	1	49.9 (M:49.9)	1	3.7	5.63	1427			
15	true	ENSGALP00000005643	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase - CGNC Symbol		64.4	8.4	1	1285.3 (M:1285.3)	23	28.5	6.73	68	0.98!	11	60.91
16	true	ENSGALP00000042140	6-phosphogluconolactonase - CGNC Symbol 10027		13.7	6.1	1	135.8 (M:135.8)	4	46.5	12.92	1034	0.90!	1	
17	true	ENSGALP0000036963	60S ribosomal protein L15 - Refseq NP_001292094		24.1	11.6	1	273.5 (M:273.5)	6	17.2	3.77	597	0.44!	3	92.14
18	true	ENSGALP00000015160	A kinase (PRKA) anchor protein 9 - CGNC Symbol 49433		455	5	1	463.5 (M:463.5)	2	0.4	18.55	324	2.98!	1	
19	true	ENSGALP00000024767	abhydrolase domain containing 10 - CGNC Symbol 11454		33.3	9	1	66.5 (M:66.5)	2	3.7	6.54	1352	1.05	1	
20	true	ENSGALP00000027665	acetyl-CoA acetyltransferase 1 - CGNC Symbol 12890		44.1	9.1	1	284.4 (M:284.4)	4	10.2	5.29	572	1.19!	2	15.63
21	true	ENSGALP00000019037	acetyl-CoA acetyltransferase 2 - CGNC Symbol 8861		40.9	7.6	1	396.6 (M:396.6)	7	20.3	5.38	393	0.53!	1	
22	true	ENSGALP00000009408	acyl-CoA acyltransferase 1 - CGNC Symbol 4375		44.6	9.3	1	135.9 (M:135.9)	2	3	1.61	1032	0.90!	1	
23	true	ENSGALP00000004375	acyl-CoA acyltransferase 2 - CGNC Symbol 2003		41.6	8	1	225.6 (M:225.6)	5	9.3	12.94	713	0.92!	2	13.68
24	true	ENSGALP00000022084	achalasia adrenocortical insufficiency alacrimia - CGNC Symbol 62874		32.5	7.6	1	58.0 (M:58.0)	1	4.7	8.12	1384	0.96	1	
25	true	ENSGALP00000026345	acid phosphatase 1 soluble - CGNC Symbol 12245		18.2	6.8	1	288.1 (M:288.1)	6	21.5	2.76	557	0.81	3	9.25
26	true	ENSGALP00000013053	acidic (leucine-rich) nuclear phosphoprotein 32 family member A - CGNC Symbol 50017		32.2	3.9	2	535.3 (M:535.3)	8	17.1	8.56	281	0.47!	4	40.44
27	true	ENSGALP00000021907	acidic (leucine-rich) nuclear phosphoprotein 32 family member E - CGNC Symbol 52680		28.9	3.7	1	333.9 (M:333.9)	6	15.6	8.22	470	0.38!	2	15.52
28	true	ENSGALP000000040836	acidic residue methyltransferase 1 - CGNC Symbol 9819		49.1	5.7	1	80.9 (M:80.9)	2	5.9	16.36	1288			
29	true	ENSGALP00000003381	aconitase 1 soluble - CGNC Symbol 48955		98	7	1	534.3 (M:534.3)	11	8.8	6.51	282	1.47!	5	65.15
30	true	ENSGALP00000019468	aconitase 2 - CGNC Symbol 9059		85.6	8	1	1328.6 (M:1328.6)	25	25.5	5.92	65	0.79!	10	73.11
31	true	ENSGALP00000018042	actin alpha 1 skeletal muscle - CGNC Symbol 8420		42	5.2	2	2143.4 (M:2143.4)	35	45.1	6.5	16	1.10!	18	89.76
32	true	ENSGALP00000010239	actin alpha 2 smooth muscle aorta - CGNC Symbol 52051		42	5.2	1	1959.0 (M:1959.0)	33	45.1	6.2	25	1.21!	17	77.36
33	true	ENSGALP00000015657	actin beta - CGNC Symbol 49855		41.7	5.3	1	4606.8 (M:4606.8)	64	70.7	6.43	3	1.27!	29	69.26
34	true	ENSGALP00000023523	actin beta-like 2 - CGNC Symbol 52851		42	5.2	1	1901.5 (M:1901.5)	32	42.7	6.21	29	1.13!	16	72.69
35	true	ENSGALP00000039995	actin related protein 2/3 complex subunit 1A 41kDa - CGNC Symbol 3478		41.7	8.6	1	41.1 (M:41.1)	1	4.6	12.86	1444			
36	true	ENSGALP00000074766	actin related protein 2/3 complex subunit 1B 41kDa - CGNC Symbol 15421		41	8.6	1	680.9 (M:680.9)	11	26.8	5.23	195	1.06!	5	280.89
37	true	ENSGALP00000018652	actin related protein 2/3 complex subunit 2 34kDa - CGNC Symbol 8704		42.5	9.1	2	407.8 (M:407.8)	8	12.6	8.05	378	1.19!	4	42.68
38	true	ENSGALP0000006046	actin related protein 2/3 complex subunit 3 - CGNC Symbol 2797		21.3	8.8	1	265.0 (M:265.0)	6	19.4	4.44	613	0.74!	3	71.38
39	true	ENSGALP00000010800	actin related protein 2/3 complex subunit 4 20kDa - CGNC Symbol 50145		19.7	8.6	1	336.6 (M:336.6)	7	29.2	3.39	465	0.58!	3	20.79
40	true	ENSGALP00000038587	actin related protein 2/3 complex subunit 5 16kDa - CGNC Symbol 14362		11.1	9.6	1	109.5 (M:109.5)	2	11.7	0.39	1158	0.93!	1	
41	true	ENSGALP00000038778	actin-like 6A - CGNC Symbol 6893		47.5	5.5	1	338.6 (M:338.6)	7	18.4	5.46	459	0.57!	2	48.31
42	true	ENSGALP00000015409	actinin alpha 1 - CGNC Symbol 48956		101.8	5.2	5	2126.8 (M:2126.8)	39	34.8	7.68	17	0.90!	21	82.69
43	true	ENSGALP00000023085	actinin alpha 4 - CGNC Symbol 49612		71.6	5.7	1	1023.7 (M:1023.7)	17	26.9	12.77	97	1.25!	8	78.15
44	true	ENSGALP00000015027	acyl-CoA binding domain containing 3 - CGNC Symbol 7024		59.5	5.1	1	222.5 (M:222.5)	2	7.9	10.1	725	1.44!	1	
45	true	ENSGALP00000011441	acyl-CoA dehydrogenase C-2 to C-3 short chain - CGNC Symbol 5341		44.6	8.7	1	235.2 (M:235.2)	6	15.4	2.98	682	0.95!	2	38.51
46	true	ENSGALP00000008056	acyl-CoA dehydrogenase family member 9 - CGNC Symbol 3741		67.8	7.2	1	654.7 (M:654.7)	12	21.1	9.54	207	0.97!	3	63.63
47	true	ENSGALP00000004548	acyl-CoA dehydrogenase long chain - CGNC Symbol 2086		47.8	8.3	1	151.4 (M:151.4)	4	11.1	10.59	964	2.51!	2	11.1
48	true	ENSGALP0000000924	acyl-CoA thioesterase 7 - CGNC Symbol 50978		43.7	9.1	1	238.7 (M:238.7)	6	12.6	15.41	670	0.8	2	3.19
49	true	ENSGALP00000026327	acyl-CoA thioesterase 9 - CGNC Symbol 12234		48.5	8.4	1	103.5 (M:103.5)	3	3.8	12.97	1186	1.24!	1	
50	true	ENSGALP00000036932	acylphosphatase 1 erythrocyte (common) type - CGNC Symbol 7842		11.1	9.9	1	40.9 (M:40.9)	1	17.2	12.64	1445	0.79	1	
51	true	ENSGALP00000013724	adaptor related protein complex 2 mu 1 subunit - CGNC Symbol 6392		49.4	9.6	1	302.2 (M:302.2)	5	6.7	4.31	526	0.84!	2	49.73
52	true	ENSGALP00000063030	adaptor-related protein complex 1 mu 1 subunit - CGNC Symbol 51191		48.5	6.8	1	265.0 (M:265.0)	4	8.3	11.57	612	0.59!	3	27.79
53	true	ENSGALP00000010984	adaptor-related protein complex 2 alpha 2 subunit - CGNC Symbol 51890		108.9	6.1	1	255.0 (M:255.0)	6	6.2	12.15	637	1.07!	3	141.36
54	true	ENSGALP00000003342	adaptor-related protein complex 2 beta 1 subunit - CGNC Symbol 1528		105.7	5.2	2	438.5 (M:438.5)	7	6.8	2.35	347	1.32!	4	82.25
55	true	ENSGALP000000041532	adenine phosphoribosyltransferase - CGNC Symbol 65844		23.5	9	1	355.9 (M:355.9)	7	15.8	10.92	439	0.78!	3	19.89
56	true	ENSGALP00000008095	adenosine kinase - CGNC Symbol 3760		38.1	5.8	1	134.9 (M:134.9)	3	12	11.18	1039			
57	true	ENSGALP0000003152	adenosylhomocysteinase - CGNC Symbol 1443		74.4	9.4	1	410.2 (M:410.2)	10	10.6	6.19	374	0.36!	5	68.41

58	true	ENSGALP00000042094	adenylate kinase 1 - CGNC Symbol 49598	21.7	8.7	1 170.1 (M:170.1)	4	14.9	5.17	898	0.95!	1	
59	true	ENSGALP00000005680	adenylyl kinase 2 - CGNC Symbol 2627	27.3	8.6	1 383.1 (M:383.1)	6	14.7	4.9	406	1.63	3	65.73
60	true	ENSGALP0000019613	adenylosuccinate lyase - CGNC Symbol 9122	54.6	6.7	1 184.5 (M:184.5)	4	5.6	12.54	847	0.49!	2	16.13
61	true	ENSGALP0000017386	adenylosuccinate synthase - CGNC Symbol 53408	43.9	6	1 335.0 (M:335.0)	7	19.9	5.7	466	1.34!	2	88.49
62	true	ENSGALP0000008336	adhesion regulating molecule 1 - CGNC Symbol 3870	42.2	5	1 150.5 (M:150.5)	3	7.4	13.41	965	0.93!	2	39.12
63	true	ENSGALP0000028073	ADP ribosylation factor like GTPase 6 interacting protein 5 - CGNC Symbol 13078	21.6	9.5	1 73.6 (M:73.6)	2	10.6	5.01	1314	0.48!	1	
64	true	ENSGALP0000002754	ADP-dependent glucokinase - CGNC Symbol 1256	53.1	5.5	1 56.7 (M:56.7)	1	2.9	3.72	1391			
65	true	ENSGALP0000009007	ADP-ribosylation factor 4 - CGNC Symbol 55483	18.1	4.8	2 414.0 (M:414.0)	6	18.9	6.41	369	1.61!	3	108.47
66	true	ENSGALP0000013410	ADP-ribosylation factor GTPase activating protein 2 - CGNC Symbol 51916	57.2	7.1	1 104.6 (M:104.6)	3	5.2	11.87	1181	0.44!	1	
67	true	ENSGALP0000003617	ADP-ribosylhydrolase like 2 - CGNC Symbol 1642	39.9	5.3	1 220.1 (M:220.1)	3	7.6	3.5	733	0.48!	1	
68	true	ENSGALP0000022434	AFG3-like AAA ATPase 2 - CGNC Symbol 10366	89.2	8.9	1 174.2 (M:174.2)	6	7.3	7.3	884	0.71!	2	10.46
69	true	ENSGALP0000017014	AHA1 activator of heat shock 90kDa protein ATPase homolog 1 (yeast) - CGNC Symbol 7960	38	5.6	1 30.4 (M:30.4)	1	2.4	23.04	1472	0.43	1	
70	true	ENSGALP0000030043	alanyl-tRNA synthetase - CGNC Symbol 50043	101.3	5.6	1 155.4 (M:155.4)	3	2.2	10.74	948	0.91!	2	28.88
71	true	ENSGALP0000019031	albumin - CGNC Symbol 14106	64	5.3	1 1982.2 (M:1982.2)	31	63.9	6.1	23	0.85!	8	22.68
72	true	ENSGALP0000019967	alcohol dehydrogenase 5 (class III) chi polypeptide - CGNC Symbol 9300	39.6	8.1	1 120.4 (M:120.4)	3	15.8	5.37	1100	1.16!	1	
73	true	ENSGALP0000007586	aldehyde dehydrogenase 3 family member A2 - CGNC Symbol 50558	54.1	8.2	1 96.9 (M:96.9)	3	4.5	10.6	1218	1.04!	1	
74	true	ENSGALP0000020641	aldehyde dehydrogenase 5 family member A1 - CGNC Symbol 9610	57.9	9.2	1 175.7 (M:175.7)	1	1.6	0.71	880			
75	true	ENSGALP0000013377	aldehyde dehydrogenase 7 family member A1 - CGNC Symbol 6235	58	7	1 69.7 (M:69.7)	1	2.8	2.27	1329	3.45	1	
76	true	ENSGALP0000005520	aldehyde dehydrogenase 9 family member A1 - CGNC Symbol 2550	57.1	9.3	1 404.3 (M:404.3)	6	14.3	6.18	381	2.83!	1	
77	true	ENSGALP0000016630	aldo-keto reductase family 1 member A1 (aldo-keto reductase) - CGNC Symbol 7795	37.1	7.7	1 323.1 (M:323.1)	9	16.8	6.54	491	1.03!	5	59.96
78	true	ENSGALP0000040985	aldo-keto reductase family 1 member B1-like (aldose reductase) - CGNC Symbol 50692	35.8	7.1	4 616.7 (M:616.7)	14	30.4	8	225	1.02!	5	24.09
79	true	ENSGALP0000021315	aldo-keto reductase family 1 member B10 (aldo reductase) - CGNC Symbol 49273	36.4	7.6	1 141.3 (M:141.3)	3	10.1	4.62	1005	1.43!	1	
80	true	ENSGALP0000021301	aldo-keto reductase family 1 member B10 (aldo reductase) - CGNC Symbol 50690	36.4	6.7	1 533.8 (M:533.8)	10	25.6	11.46	283	0.89!	4	21.23
81	true	ENSGALP0000021303	aldo-keto reductase family 1 member B10-like - CGNC Symbol 50691	35.6	8	2 446.0 (M:446.0)	8	24.2	7.81	340	0.94!	2	8.31
82	true	ENSGALP0000006372	aldo-keto reductase family 7 member A2 (afлатоксин aldehyde reductase) - CGNC Symbol 51005	40.9	8.7	1 180.1 (M:180.1)	3	7.1	0.25	866	2.06	2	40.56
83	true	ENSGALP0000043256	aldolase C fructose-biphosphate - CGNC Symbol 49343	39.3	6.2	1 1653.2 (M:1653.2)	29	48.1	7.03	37	1.46!	11	88.48
84	true	ENSGALP0000012723	alpha thalassemia/mental retardation syndrome X-linked - CGNC Symbol 51707	276.1	7.1	1 250.3 (M:250.3)	5	1.9	14.08	648	0.62!	3	161.25
85	true	ENSGALP0000036406	alpha-2-macroglobulin - CGNC Symbol 50716	164.8	6	1 112.7 (M:112.7)	2	1.9	14.61	1146			
86	true	ENSGALP0000000383	alpha-2-macroglobulin-like 4 - CGNC Symbol 65057	163.2	6	1 400.4 (M:400.4)	10	7.5	9.24	389	1.26!	2	40.21
87	true	ENSGALP0000038912	alpha-D-globin - CGNC Symbol 50309	15.7	7	1 760.3 (M:760.3)	10	50.4	6.54	163	1.98!	5	77.41
88	true	ENSGALP0000004546	alveolar soft part sarcoma chromosome region candidate 1 - CGNC Symbol 2085	53	5.2	1 110.9 (M:110.9)	2	3.8	7.24	1152	0.46	1	
89	true	ENSGALP0000011696	Aly/REF export factor - CGNC Symbol 5467	27.9	11.4	1 429.2 (M:429.2)	5	15	11.62	354	0.39	2	19.53
90	true	ENSGALP0000017152	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 - CGNC Symbol 8013	35.9	8.9	1 234.5 (M:234.5)	4	8.8	9.76	685	0.98!	2	14.44
91	true	ENSGALP0000005367	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2 - CGNC Symbol 54930	30.3	6.3	1 68.4 (M:68.4)	1	3.3	5.21	1337			
92	true	ENSGALP0000042870	aminoacylase 1 - CGNC Symbol 64270	45.9	6	1 190.8 (M:190.8)	4	12.8	6.14	825			
93	true	ENSGALP0000022243	aminopeptidase puromycin sensitive - CGNC Symbol 10259	97.2	5.3	2 506.1 (M:506.1)	12	8.8	6.94	300	1.35!	5	24.66
94	true	ENSGALP0000012240	amyloid beta (A4) precursor protein-binding family B member 1 interacting protein - CGNC Symbol 571	72.8	5.7	1 243.7 (M:243.7)	8	9.1	6.57	662	0.71!	5	66.38
95	true	ENSGALP0000032184	annexin A1 - CGNC Symbol 11272	38.5	7.1	1 186.4 (M:186.4)	3	7	6.05	843			
96	true	ENSGALP0000004186	annexin A11 - CGNC Symbol 52013	57.2	8.6	1 253.0 (M:253.0)	8	9.8	5.94	642	0.74!	4	21.42
97	true	ENSGALP000005971	annexin A2 - CGNC Symbol 49740	38.6	6.9	1 311.9 (M:311.9)	7	19.8	6.24	514	2.31!	2	39.99
98	true	ENSGALP0000013359	annexin A4 - CGNC Symbol 57513	36	5.2	1 131.2 (M:131.2)	4	5.6	4.41	1063	1.64	2	54.03
99	true	ENSGALP0000019365	annexin A5 - CGNC Symbol 9009	36.2	5.6	1 313.0 (M:313.0)	7	23.7	7.78	511			
100	true	ENSGALP0000006939	annexin A6 - CGNC Symbol 49340	86.9	5.9	2 2178.5 (M:2178.5)	42	38.5	6.01	15	0.86!	18	54.27
101	true	ENSGALP0000000236	antigen peptide transporter 2 - Refseq NP_001092827	75.9	6.9	1 246.1 (M:246.1)	7	11.4	11.97	656	1.55	1	
102	true	ENSGALP0000006626	antioxidant 1 copper chaperone - CGNC Symbol 3066	8	6.3	1 70.4 (M:70.4)	2	28.2	9.93	1326			
103	true	ENSGALP0000011510	apolipoprotein A-I - CGNC Symbol 49860	30.7	5.6	1 504.7 (M:504.7)	10	34.1	6.42	302	0.66!	2	205.64
104	true	ENSGALP0000006298	apolipoprotein H (beta-2-glycoprotein I) - CGNC Symbol 2904	41.1	8.6	1 79.3 (M:79.3)	3	10.7	14.66	1293			
105	true	ENSGALP0000012938	apoptosis inhibitor 5 - CGNC Symbol 16313	57.2	7.7	1 295.5 (M:295.5)	4	8.8	12.39	546	0.45!	2	23.1
106	true	ENSGALP0000015978	ariabius intron-binding spliceosomal factor - CGNC Symbol 7473	174.1	6.2	1 481.6 (M:481.6)	12	6.5	6.94	312	0.58!	6	37.14
107	true	ENSGALP0000012007	archain 1 - CGNC Symbol 5606	57	5.8	1 225.6 (M:225.6)	5	7.3	6	712	0.76!	4	52.14
108	true	ENSGALP0000038774	argininosuccinate synthase 1 - CGNC Symbol 50457	46.9	6.1	1 662.9 (M:662.9)	14	25.2	4.6	202	7.92!	2	184.85
109	true	ENSGALP0000002862	arginyl-tRNA synthetase - CGNC Symbol 1305	75.4	6.5	1 472.7 (M:472.7)	11	9.1	8.28	313	0.95!	5	14.67
110	true	ENSGALP0000026044	argonaute RISC catalytic component 2 - CGNC Symbol 64972	97.8	9.3	3 331.2 (M:331.2)	12	14.4	7.49	474	0.54!	4	18.69
111	true	ENSGALP0000002785	ariadne RBR E3 ubiquitin protein ligase 1 - CGNC Symbol 1344	41.4	7.4	1 98.1 (M:98.1)	3	6	8.37	1214	0.78	2	11.01
112	true	ENSGALP0000014260	ARP2 actin-related protein 2 homolog (yeast) - CGNC Symbol 49669	43	6.3	1 696.1 (M:696.1)	11	28.3	5.14	189	0.70!	5	98.35
113	true	ENSGALP0000019832	ARP3 actin-related protein 3 homolog (yeast) - CGNC Symbol 49080	47.4	5.6	2 1177.6 (M:1177.6)	24	38.8	7.37	75	0.85!	11	31.83
114	true	ENSGALP00000043018	arsA arsenite transporter ATP-binding homolog 1 (bacterial) - CGNC Symbol 63380	26.1	4.6	1 90.7 (M:90.7)	3	6.3	2.84	1248	0.58	2	1.03
115	true	ENSGALP0000015844	arylsulfatase A - CGNC Symbol 7409	54.9	6.2	1 85.3 (M:85.3)	2	4	8.14	1265	1.00!	1	
116	true	ENSGALP0000015846	asparagine synthetase (glutamine-hydrolyzing) - CGNC Symbol 7411	64	6.3	1 317.9 (M:317.9)	7	11.9	4.55	503	2.01!	1	

117	true	ENSGALP00000004871	asparaginyl-tRNA synthetase - CGNC Symbol 2238	64.1	5.7	1 408.5 (M:408.5)	11	13.4	5.74	377	0.69!	4	66.19
118	true	ENSGALP00000018441	aspartyl aminopeptidase - CGNC Symbol 8600	51.9	6.4	1 626.2 (M:626.2)	10	18.2	8.6	217	0.9	6	24.63
119	true	ENSGALP00000020154	aspartyl-tRNA synthetase - CGNC Symbol 9384	57.2	6.1	1 791.7 (M:791.7)	18	21.9	6.05	150	0.52!	8	34.8
120	true	ENSGALP00000015719	AT-rich interaction domain 2 - CGNC Symbol 7350	197.4	7.2	1 156.7 (M:156.7)	4	2.6	13.04	940			
121	true	ENSGALP00000016175	ATP binding cassette subfamily E member 1 - CGNC Symbol 7569	67.3	8.6	1 188.2 (M:188.2)	5	8.7	13.06	832	0.85!	1	
122	true	ENSGALP00000021752	ATP binding cassette subfamily F member 2 - CGNC Symbol 10054	71.2	6.9	1 331.8 (M:331.8)	5	6.1	13.54	471	0.92!	3	21.07
123	true	ENSGALP00000039157	ATP citrate lyase - CGNC Symbol 2533	120.1	7.5	1 287.9 (M:287.9)	7	6.2	10.01	558	0.76!	2	17.65
124	true	ENSGALP00000042610	ATP synthase H+ transporting mitochondrial F1 complex delta subunit - CGNC Symbol 56808	7.1	4.1	1 102.4 (M:102.4)	2	20.3	6.04	1192	1.22	1	
125	true	ENSGALP00000010899	ATP synthase H+ transporting mitochondrial F1 complex gamma polypeptide 1 - CGNC Symbol 5096	32.7	9.4	1 54.2 (M:54.2)	1	3.7	18.98	1402	1.29	1	
126	true	ENSGALP00000002205	ATP synthase H+ transporting mitochondrial Fo complex subunit B1 - CGNC Symbol 1004	28.6	9.2	1 261.2 (M:261.2)	4	15.3	7.58	623	0.75!	3	36.87
127	true	ENSGALP00000012854	ATP synthase H+ transporting mitochondrial Fo complex subunit D - CGNC Symbol 5993	18.4	8.7	1 121.8 (M:121.8)	4	26.5	9.79	1094	1.19!	3	95.77
128	true	ENSGALP00000025356	ATP synthase H+ transporting mitochondrial Fo complex subunit F6 - CGNC Symbol 11749	12.5	9.4	1 90.8 (M:90.8)	2	12.8	18.3	1247	1.16	1	
129	true	ENSGALP0000002373	ATPase Ca++ transporting ubiquitous - CGNC Symbol 1084	115.3	5.7	1 456.0 (M:456.0)	9	8	7.07	334	0.41!	4	34.35
130	true	ENSGALP00000011629	ATPase H+ transporting lysosomal 13kDa V1 subunit G1 - CGNC Symbol 5433	13.5	9.3	1 93.9 (M:93.9)	2	9.3	5.32	1236	2.61!	1	
131	true	ENSGALP00000015002	ATPase H+ transporting lysosomal 16kDa V0 subunit c - CGNC Symbol 7004	13	9.9	1 107.2 (M:107.2)	2	13.8	6.97	1170	2.08!	1	
132	true	ENSGALP00000023850	ATPase H+ transporting lysosomal 70kDa V1 subunit A - CGNC Symbol 10976	68.3	5.6	2 272.7 (M:272.7)	7	9.5	9.47	598	1.48!	2	202.13
133	true	ENSGALP00000024150	ATPase Na+/K+ transporting alpha 1 polypeptide - CGNC Symbol 49857	112	5.4	1 424.0 (M:424.0)	11	10	3.98	363	0.73!	5	36.41
134	true	ENSGALP0000004355	ATPase Na+/K+ transporting beta 3 polypeptide - CGNC Symbol 1995	31.8	8.1	1 33.6 (M:33.6)	1	5	11.11	1466			
135	true	ENSGALP00000024484	autophagy related 3 - CGNC Symbol 11313	35.6	4.6	1 124.8 (M:124.8)	2	7	11.98	1079	0.62	1	
136	true	ENSGALP00000042659	B-cell lymphoma/leukemia 11B-like - CGNC Symbol 63941	73.9	6.7	2 258.8 (M:258.8)	3	4.8	18.2	626	0.12!	1	
137	true	ENSGALP00000017553	basic leucine zipper and W2 domains 2 - CGNC Symbol 8215	48.3	6.4	1 306.9 (M:306.9)	7	11.5	2.79	522	0.78!	4	18.23
138	true	ENSGALP00000039454	beta-2-microglobulin - CGNC Symbol 1542	13	5.8	1 362.2 (M:362.2)	5	37	9.45	427	2.33!	4	124.93
139	true	ENSGALP00000021253	BH3 interacting domain death agonist - CGNC Symbol 9863	21.7	4.9	1 249.8 (M:249.8)	4	16.6	10.26	650	0.50!	2	3.14
140	true	ENSGALP0000006762	bloomyrin hydrolase - CGNC Symbol 3131	52.7	5.6	1 593.5 (M:593.5)	11	18.7	9.16	242	1.30!	6	59.7
141	true	ENSGALP00000036341	brain abundant membrane attached signal protein 1 - CGNC Symbol 9805	25.4	4.6	1 105.1 (M:105.1)	1	8.6	2.02	1176			
142	true	ENSGALP00000016287	brain and reproductive organ-expressed (TNFRSF1A modulator) - CGNC Symbol 7632	43.4	5.6	1 122.2 (M:122.2)	3	7	5.5	1092	0.31!	1	
143	true	ENSGALP00000004589	BRI3 binding protein - CGNC Symbol 2105	20.3	6.1	1 42.6 (M:42.6)	1	4	6.73	1439	0.99	1	
144	true	ENSGALP00000002111	bromodomain containing 2 - CGNC Symbol 50420	80.3	8.7	1 113.2 (M:113.2)	1	1.8	8.4	1141	1.83!	1	
145	true	ENSGALP0000005322	BRX1 biogenesis of ribosomes - CGNC Symbol 2456	40.3	9.9	1 83.9 (M:83.9)	1	6.9	5.8	1273			
146	true	ENSGALP00000041722	BTB domain containing 10 - CGNC Symbol 4000	53.6	7.6	1 53.9 (M:53.9)	2	4.6	4.23	1404			
147	true	ENSGALP0000007481	BUD31 homolog - CGNC Symbol 3487	17	9.1	1 204.1 (M:204.1)	6	27.1	7.76	784	0.60!	4	22.79
148	true	ENSGALP0000005482	bystin like - CGNC Symbol 2527	49.4	7.3	1 184.6 (M:184.6)	6	11.3	10.04	845	0.75!	2	45.01
149	true	ENSGALP00000020080	c-src tyrosine kinase - CGNC Symbol 902	59.3	8.1	1 386.9 (M:386.9)	4	5.3	7.98	401	0.64!	2	23.17
150	true	ENSGALP00000025299	C-terminal binding protein 1 - CGNC Symbol 11723	46.8	6.2	2 316.8 (M:316.8)	8	12.8	6.81	504	0.49	5	50.07
151	true	ENSGALP0000012349	C-terminal binding protein-like - CGNC Symbol 50231	48	6.3	1 298.6 (M:298.6)	7	10.9	11.51	535	0.72	3	37.09
152	true	ENSGALP0000041816	calcium binding protein 39 - HGNC:20292	39.9	6.4	1 187.1 (M:187.1)	4	7.6	14.82	838	0.71!	2	22.02
153	true	ENSGALP0000006050	calcium homeostasis endoplasmic reticulum protein - CGNC Symbol 2800	44.5	4.9	1 189.2 (M:189.2)	2	3.3	18.71	828	0.51	1	
154	true	ENSGALP0000007236	calcyclin binding protein - CGNC Symbol 3365	25.6	8.6	1 220.5 (M:220.5)	3	10	6.57	731	1.26!	1	
155	true	ENSGALP0000021314	caldesmon 1 - CGNC Symbol 9884	86.4	5.5	1 314.8 (M:314.8)	2	3.7	6.33	507			
156	true	ENSGALP0000016260	calmodulin 2 (phosphorylase kinase delta) - CGNC Symbol 49513	16.7	4.1	3 781.9 (M:781.9)	13	45.9	4.75	154	0.75!	7	53.81
157	true	ENSGALP0000009549	calnexin - CGNC Symbol 4443	68.3	4.4	1 65.1 (M:65.1)	2	5.8	15.51	1356	1.50!	1	
158	true	ENSGALP0000016538	calpain 11 - CGNC Symbol 54348	80.3	4.9	1 360.1 (M:360.1)	8	10.1	7.03	433	1.73!	1	
159	true	ENSGALP0000041815	calponin-2 - Refseq NP_001135728	31	8.1	1 383.7 (M:383.7)	9	28.3	5.88	405	0.39!	5	37.37
160	true	ENSGALP0000006222	calreticulin 3 - CGNC Symbol 2868	48	5.2	1 121.7 (M:121.7)	3	4.8	12.87	1096	0.59	2	62.45
161	true	ENSGALP0000038292	cAMP-regulated phosphoprotein 19kDa - CGNC Symbol 54805	12.3	9.1	1 64.2 (M:64.2)	1	13.4	4.16	1361			
162	true	ENSGALP0000006218	CAP adenylate cyclase-associated protein 1 (yeast) - CGNC Symbol 2866	57.6	8.2	1 1054.8 (M:1054.8)	15	19.4	6.71	93	0.70!	8	33.74
163	true	ENSGALP0000006414	capping actin protein of muscle Z-line beta subunit - CGNC Symbol 2959	30.6	5.7	2 858.0 (M:858.0)	15	32.4	8.61	129	1.01!	8	33.11
164	true	ENSGALP0000002349	capping protein (actin filament) muscle Z-line alpha 1 - CGNC Symbol 1070	32.9	5.4	1 782.2 (M:782.2)	13	43	6.74	153	1.02!	6	25.48
165	true	ENSGALP0000015277	capping protein (actin filament) muscle Z-line alpha 2 - CGNC Symbol 7136	32.8	5.5	1 643.8 (M:643.8)	9	29.4	5.76	209	0.95!	3	9.52
166	true	ENSGALP0000026615	carbamoyl-phosphate synthetase 2 aspartate transcarbamylase and dihydroorotate - HGNC:1424	200.7	5.9	1 337.2 (M:337.2)	8	4.9	8.72	462	0.59!	4	27.22
167	true	ENSGALP0000025525	carbonic anhydrase II - CGNC Symbol 11834	29	6.6	1 118.1 (M:118.1)	3	10	4.26	1109	1.82!	1	
168	true	ENSGALP0000025516	carbonic anhydrase III-like - CGNC Symbol 51206	30.5	8.3	1 42.4 (M:42.4)	1	3.8	7.36	1441			
169	true	ENSGALP0000040233	casein kinase 1 alpha 1 - CGNC Symbol 49554	38.7	9.6	2 78.9 (M:78.9)	1	3.3	4.37	1297	0.77!	1	
170	true	ENSGALP0000009985	casein kinase 2 alpha 1 polypeptide - CGNC Symbol 54315	45.2	7.3	1 487.1 (M:487.1)	12	22.8	5.84	308	1.29!	4	18.26
171	true	ENSGALP0000001302	casein kinase 2 alpha prime polypeptide - CGNC Symbol 585	41.2	8.2	1 152.8 (M:152.8)	5	16	5.56	959	1.01!	2	54.09
172	true	ENSGALP00000017288	caspase 3 apoptosis-related cysteine peptidase - CGNC Symbol 8080	31.7	6.5	2 237.0 (M:237.0)	6	17.7	6.44	676	0.67!	2	23.6
173	true	ENSGALP00000019870	caspase 6 - CGNC Symbol 9250	34.5	6.8	1 132.9 (M:132.9)	2	5.3	7.18	1053	0.83	1	
174	true	ENSGALP00000020304	caspase recruitment domain family member 10 - CGNC Symbol 9445	79.2	5.2	1 23.5 (M:23.5)	1	1.3	22.46	1477			
175	true	ENSGALP0000023319	catalase - CGNC Symbol 51998	55.4	7.3	1 108.9 (M:108.9)	3	4.9	6.78	1160	0.8	1	

176	true	ENSGALP00000019402	catenin (cadherin-associated protein) beta 1 88kDa - CGNC Symbol 49578	85.4	5.5	1 109.9 (M:109.9)	3	4.4	6.76	1157	1.85!	1
177	true	ENSGALP00000011006	catenin beta like 1 - CGNC Symbol 5146	65.1	4.9	1 234.7 (M:234.7)	5	5.9	6.92	684	0.65!	1
178	true	ENSGALP00000011124	cathepsin A - CGNC Symbol 5190	53.1	6.1	1 208.0 (M:208.0)	4	10.2	9.39	767	2.05!	1
179	true	ENSGALP00000035933	cathepsin B - CGNC Symbol 12486	37.6	5.5	1 509.2 (M:509.2)	8	17.6	6.13	298	1.84!	3
180	true	ENSGALP00000027816	cathepsin C - CGNC Symbol 12954	52	7.9	1 221.1 (M:221.1)	4	10.8	7.99	730	2.72!	1
181	true	ENSGALP0000001120	cathepsin S - CGNC Symbol 494	36.3	6.6	1 62.5 (M:62.5)	1	2.4	24.69	1372		
182	true	ENSGALP00000012053	cathepsin Z - CGNC Symbol 5626	33.8	7.5	1 165.1 (M:165.1)	5	19.7	12.11	909	2.18!	1
183	true	ENSGALP00000010935	Cbl proto-oncogene E3 ubiquitin protein ligase - CGNC Symbol 49015	95.5	5.6	2 301.8 (M:301.8)	4	6.6	12.43	528	0.37!	2
184	true	ENSGALP0000002808	CCTC-binding factor (zinc finger protein) - CGNC Symbol 49729	84	6.3	1 538.8 (M:538.8)	10	14	6.63	279	0.74!	4
185	true	ENSGALP00000035496	CCHC-type zinc finger nucleic acid binding protein - CGNC Symbol 3717	19	7.8	1 624.5 (M:624.5)	10	41.3	8.88	218	0.54	6
186	true	ENSGALP0000003612	CCR4-NOT transcription complex subunit 1 - CGNC Symbol 64685	266.6	6.7	2 430.7 (M:430.7)	10	4.7	4.93	352	0.61!	3
187	true	ENSGALP00000027036	CCR4-NOT transcription complex subunit 11 - CGNC Symbol 12583	46.3	5.5	1 139.2 (M:139.2)	4	14.5	9.58	1016	0.39!	1
188	true	ENSGALP00000022159	CCR4-NOT transcription complex subunit 7 - CGNC Symbol 10229	32.7	4.8	1 59.5 (M:59.5)	2	7.4	19.09	1376	0.73!	1
189	true	ENSGALP0000011984	CD3d molecule delta (CD3-TCR complex) - CGNC Symbol 49849	19.5	8.2	1 196.6 (M:196.6)	6	42	4.69	809	0.65!	1
190	true	ENSGALP0000011982	CD3e molecule - CGNC Symbol 5597	19	6.3	1 128.4 (M:128.4)	4	14.9	6.52	1069	0.48!	1
191	true	ENSGALP0000012731	CD44 molecule (Indian blood group) - CGNC Symbol 5938	43.2	5.5	1 323.6 (M:323.6)	7	9.8	10.38	489	0.82	4
192	true	ENSGALP0000024734	CD47 molecule - CGNC Symbol 11437	33.2	8.6	3 78.9 (M:78.9)	1	4.7	4.02	1298	0.63	1
193	true	ENSGALP0000032097	CD5 molecule - CGNC Symbol 3864	51	8.8	1 141.8 (M:141.8)	4	9.1	9.09	1002	0.61!	1
194	true	ENSGALP0000008329	CD72 molecule - CGNC Symbol 49553	38.4	5.2	1 72.6 (M:72.6)	1	2.3	24.01	1320	3.55!	1
195	true	ENSGALP0000039736	CD74 molecule - CGNC Symbol 3398	24.8	9.2	2 113.3 (M:113.3)	2	12.6	16.36	1140		
196	true	ENSGALP0000043162	CDGSH iron sulfur domain 2 - HGNC:24212	15.2	9.7	1 56.9 (M:56.9)	1	9	14.95	1388		
197	true	ENSGALP0000036822	CDV3 homolog - HGNC:26928	19.1	4.7	1 101.6 (M:101.6)	2	32.5	2.71	1199		
198	true	ENSGALP0000034254	cell division cycle 42 - CGNC Symbol 3561	21.3	6.2	1 372.4 (M:372.4)	7	22.5	4.15	416	0.63!	4
199	true	ENSGALP0000035905	cell division cycle 5 like - CGNC Symbol 12520	92.3	7.6	1 208.5 (M:208.5)	4	6.6	8.81	765		
200	true	ENSGALP0000036760	centrosomal protein 135kDa - CGNC Symbol 10315	134.6	5.7	1 355.3 (M:355.3)	6	4.2	16.15	440	1.37!	1
201	true	ENSGALP0000016196	chaperonin containing TCP1 subunit 2 (beta) - CGNC Symbol 7582	57.4	5.9	1 1293.0 (M:1293.0)	18	30.3	7.26	66	0.63!	8
202	true	ENSGALP0000014308	chaperonin containing TCP1 subunit 4 - CGNC Symbol 6688	57.7	7.9	1 817.2 (M:817.2)	12	21.3	5.21	140	1.03!	7
203	true	ENSGALP0000021255	chaperonin containing TCP1 subunit 5 - CGNC Symbol 9864	59.7	5.5	1 944.3 (M:944.3)	20	27.4	7.98	109	0.91!	9
204	true	ENSGALP0000003850	chaperonin containing TCP1 subunit 6A (zeta 1) - CGNC Symbol 50541	57.7	6.4	1 443.1 (M:443.1)	8	10.9	6.05	343	0.81!	3
205	true	ENSGALP0000036304	chaperonin containing TCP1 subunit 7 - CGNC Symbol 12022	60	5.8	1 805.5 (M:805.5)	18	32.5	5.57	144	0.92!	10
206	true	ENSGALP0000025461	chaperonin containing TCP1 subunit 8 - CGNC Symbol 11805	59.5	5.4	1 855.4 (M:855.4)	18	19.1	4.21	130	1.08!	8
207	true	ENSGALP00000003263	charged multivesicular body protein 4B - CGNC Symbol 50929	25.1	4.7	1 104.3 (M:104.3)	2	4.4	6.94	1182	1.15!	1
208	true	ENSGALP0000009122	checkpoint kinase 2 - CGNC Symbol 4245	58.9	6.4	1 84.2 (M:84.2)	1	4.6	10.54	1270		
209	true	ENSGALP0000007523	chloride intracellular channel 2 - CGNC Symbol 51647	28.1	5.4	1 923.0 (M:923.0)	13	36.5	10.18	113	0.98!	6
210	true	ENSGALP0000011170	choroeremria (Rab escort protein 1) - CGNC Symbol 51680	73.1	4.7	1 218.2 (M:218.2)	6	6.1	8.37	741	0.62	3
211	true	ENSGALP0000042891	chromatin target of PRMT1 - HGNC:24511	26.3	12.2	1 207.6 (M:207.6)	4	11.7	6.1	769	0.44	2
212	true	ENSGALP0000029248	chromobox homolog 1 - CGNC Symbol 49096	21.5	4.9	1 122.5 (M:122.5)	2	6.5	6.3	1089	0.47!	1
213	true	ENSGALP0000040761	chromobox homolog 5 - CGNC Symbol 58306	6.5	4.8	2 143.7 (M:143.7)	3	49.1	1.48	993	0.47!	1
214	true	ENSGALP0000023294	chromodomain helicase DNA binding protein 4 - CGNC Symbol 10176	219	5.6	2 553.8 (M:553.8)	11	6.4	10.76	269	0.38!	4
215	true	ENSGALP0000014100	chromosome 1 open reading frame 52 - HGNC:24871	23.1	5.2	1 70.0 (M:70.0)	1	4.3	2.98	1327	1.09	1
216	true	ENSGALP0000027779	chromosome 1 open reading frame human C11orf54 - Refseq NP_001264206	34.7	6.2	1 296.1 (M:296.1)	4	12.3	10.54	544	0.56!	2
217	true	ENSGALP0000002442	chromosome 17 open reading frame 62 - HGNC:28672	21.2	4.8	1 136.4 (M:136.4)	2	16.9	10.03	1028	0.63!	1
218	true	ENSGALP0000039158	chromosome 22 open reading frame 39 - CGNC Symbol 62321	12	9	1 33.3 (M:33.3)	1	16.7	10.76	1468		
219	true	ENSGALP0000043136	citrate synthase - CGNC Symbol 64209	42.5	6.5	1 100.7 (M:100.7)	4	5	5.56	1207	0.86	2
220	true	ENSGALP0000008236	clathrin heavy chain (Hc) - CGNC Symbol 49238	189.9	5.5	2 2289.1 (M:2289.1)	47	21.1	6.62	13	0.84!	24
221	true	ENSGALP0000005281	clathrin light chain B - CGNC Symbol 50199	28.1	4.9	1 90.1 (M:90.1)	3	9.4	2.72	1252	1.03!	1
222	true	ENSGALP0000016173	cleavage and polyadenylation specific factor 6 - CGNC Symbol 13843	59.1	6.9	1 158.5 (M:158.5)	5	8.9	16.58	933	0.55!	3
223	true	ENSGALP0000012563	cleavage stimulation factor 3' pre-RNA subunit 1 - CGNC Symbol 5864	48.3	6.1	1 59.2 (M:59.2)	1	4.4	3.89	1378		
224	true	ENSGALP0000010910	cleavage stimulation factor 3' pre-RNA subunit 2 64kDa - CGNC Symbol 51677	49.9	5.9	1 136.5 (M:136.5)	3	8.2	11.8	1026		
225	true	ENSGALP0000009393	clustered mitochondria (cluA/CLU1) homolog - CGNC Symbol 4370	150.4	5.7	1 178.3 (M:178.3)	2	1.3	9.67	875		
226	true	ENSGALP0000022235	CNDP dipeptidase 2 (metallopeptidase M20 family) - CGNC Symbol 13892	53	5.7	1 252.6 (M:252.6)	8	13.5	8.28	643	1.05!	4
227	true	ENSGALP0000028283	coactosin-like F-actin binding protein 1 - CGNC Symbol 54450	16.1	5.3	1 338.4 (M:338.4)	9	48.6	6.28	460	0.98!	3
228	true	ENSGALP0000039965	coatomer protein complex subunit alpha - CGNC Symbol 6964	138.4	7.5	1 886.4 (M:886.4)	22	18.3	12.12	125	0.63!	8
229	true	ENSGALP0000009665	coatomer protein complex subunit beta 1 - CGNC Symbol 4506	107.1	5.7	1 630.9 (M:630.9)	11	10.4	5.92	213	0.56!	3
230	true	ENSGALP0000008578	coatomer protein complex subunit beta 2 (beta prime) - CGNC Symbol 3988	103.1	5.1	1 581.3 (M:581.3)	14	12.8	8.78	254	1.00!	9
231	true	ENSGALP0000004982	coatomer protein complex subunit epsilon - CGNC Symbol 2286	34.3	5	1 133.8 (M:133.8)	3	11.4	13.25	1048	1.34	1
232	true	ENSGALP0000009420	coatomer protein complex subunit gamma 1 - CGNC Symbol 4382	97.5	5.3	2 269.8 (M:269.8)	7	7.7	3.08	607	0.64!	4
233	true	ENSGALP0000008798	coiled-coil domain containing 12 - CGNC Symbol 4088	20	5.1	1 103.6 (M:103.6)	4	26.3	14.73	1185	0.83!	1
234	true	ENSGALP0000007165	coiled-coil domain containing 17 - CGNC Symbol 3327	35.7	11.5	1 168.6 (M:168.6)	4	13.1	17.28	905	0.93!	2

235	true	ENSGALP00000023242	coiled-coil domain containing 58 - CGNC Symbol 10725	16.7	7.7	1 35.6 (M:35.6)	1	13.9	6.31	1460		
236	true	ENSGALP00000042528	cold inducible RNA binding protein - CGNC Symbol 9285	18.6	9.5	1 89.0 (M:89.0)	2	14	8.02	1254		
237	true	ENSGALP00000039235	cold shock domain containing E1 - CGNC Symbol 51115	88.6	5.9	1 489.7 (M:489.7)	12	9.5	3.98	307 1.30!	5	54.12
238	true	ENSGALP00000015687	collagen type I alpha 2 - CGNC Symbol 49716	128.8	9.2	1 68.5 (M:68.5)	2	1.4	16.89	1336		
239	true	ENSGALP00000003945	collagen type V alpha 2 - CGNC Symbol 1798	53.9	5.6	1 33.7 (M:33.7)	1	2.5	14.64	1465		
240	true	ENSGALP00000038878	collagen type VI alpha 1 - CGNC Symbol 4468	107.9	5.6	1 95.8 (M:95.8)	3	3	7.65	1225	0.85	1
241	true	ENSGALP00000009873	collagen type VI alpha 2 - CGNC Symbol 4597	109.1	5.7	2 201.0 (M:201.0)	5	5.2	13.46	797	0.8	1
242	true	ENSGALP00000006240	collagen type VI alpha 3 - CGNC Symbol 2875	339.4	6.3	1 617.6 (M:617.6)	14	5.9	6.99	222 0.49!	2	33.15
243	true	ENSGALP0000014389	COMM domain containing 5 - CGNC Symbol 6733	24.9	6.8	1 133.6 (M:133.6)	2	9.7	5.17	1050	1.01	1
244	true	ENSGALP0000012814	COMM domain containing 9 - CGNC Symbol 51912	21.8	5.9	1 55.5 (M:55.5)	1	6.5	19.29	1393		
245	true	ENSGALP0000002522	complement component 1 q subcomponent binding protein - CGNC Symbol 1156	23.5	4.4	1 88.5 (M:88.5)	2	14	3.98	1257 1.58!	1	
246	true	ENSGALP0000001779	complement component 4 binding protein alpha - CGNC Symbol 49292	48.7	5.9	1 38.9 (M:38.9)	1	3.3	2.11	1453		
247	true	ENSGALP0000042661	complement factor D (adipsin) - CGNC Symbol 65437	29	7.6	1 105.0 (M:105.0)	3	16.2	6	1178		
248	true	ENSGALP0000007709	COP9 signalosome subunit 3 - CGNC Symbol 3588	47.9	6.3	1 92.0 (M:92.0)	2	7.6	9.88	1243		
249	true	ENSGALP0000018122	COP9 signalosome subunit 4 - CGNC Symbol 8452	46.8	5.7	1 242.0 (M:242.0)	2	7.3	12.21	663		
250	true	ENSGALP0000012557	COP9 signalosome subunit 7B - CGNC Symbol 5861	30.1	5.8	1 45.1 (M:45.1)	1	3.4	4.51	1433		
251	true	ENSGALP0000006264	COP9 signalosome subunit 8 - CGNC Symbol 52112	23	5.3	2 40.0 (M:40.0)	1	10.1	12.2	1448		
252	true	ENSGALP0000002482	copine I - CGNC Symbol 50925	59.7	5.5	5 270.6 (M:270.6)	5	6	11.9	604 0.84!	2	4.65
253	true	ENSGALP0000005013	core-binding factor beta subunit - CGNC Symbol 2299	14.8	5.3	1 160.5 (M:160.5)	3	18.1	8.55	927	0.73	2
254	true	ENSGALP0000038753	coronin 7 - CGNC Symbol 50317	100	5.5	1 324.7 (M:324.7)	6	6.7	3.72	487 0.57!	2	5.33
255	true	ENSGALP0000007822	coronin actin binding protein 1C - CGNC Symbol 50369	53.2	6.2	4 1497.1 (M:1497.1)	24	33.1	7.08	51 0.63!	11	66.41
256	true	ENSGALP0000012463	cortactin - CGNC Symbol 5818	63.2	5.3	1 71.3 (M:71.3)	2	4.6	5.79	1325		
257	true	ENSGALP0000018742	creatine kinase brain - CGNC Symbol 49719	40.2	5.9	1 232.1 (M:232.1)	4	10.6	13.02	692		
258	true	ENSGALP0000007487	CSE1 chromosome segregation 1-like (yeast) - CGNC Symbol 3489	110.4	5.4	1 675.0 (M:675.0)	15	13.6	6.75	198 0.64!	7	33.76
259	true	ENSGALP0000013337	CTD small phosphatase like 2 - CGNC Symbol 6215	53.1	6.1	1 115.7 (M:115.7)	2	2.6	19.44	1118	0.4	1
260	true	ENSGALP000000955	CTP synthase 1 - CGNC Symbol 429	69.7	7	1 163.3 (M:163.3)	4	4.5	5.17	916 1.51!	1	
261	true	ENSGALP0000009002	CTR9 homolog Paf1/RNA polymerase II complex component - CGNC Symbol 4182	132.7	6.4	1 235.3 (M:235.3)	5	3.3	7.16	679	0.49	2
262	true	ENSGALP0000010844	CUGBP Elav-like family member 2 - CGNC Symbol 49047	51.9	8.7	3 266.3 (M:266.3)	5	8	6.61	610 0.36!	2	22.32
263	true	ENSGALP0000013926	cullin 4B - CGNC Symbol 6494	101.3	8	1 155.1 (M:155.1)	4	3.6	11.58	949 0.50!	1	
264	true	ENSGALP0000005129	CWF19-like 1 cell cycle control (S. pombe) - CGNC Symbol 2360	59.9	7.5	1 161.9 (M:161.9)	4	7.3	6.02	920 0.91!	2	1.29
265	true	ENSGALP0000027682	CWF19-like 2 cell cycle control (S. pombe) - HGNC:26508	106	8.5	1 166.2 (M:166.2)	3	3.5	3.01	907 0.33!	1	
266	true	ENSGALP0000018144	cyclin K - CGNC Symbol 8459	65.5	8.6	1 52.1 (M:52.1)	1	2.9	3.46	1412		
267	true	ENSGALP0000042598	cyclin-dependent kinase 1 - CGNC Symbol 2236	34.6	8.8	2 114.7 (M:114.7)	2	4.3	5.62	1130	1.03	1
268	true	ENSGALP0000015412	cyclin-dependent kinase 6 - CGNC Symbol 51286	36.8	5.6	1 105.0 (M:105.0)	2	2.8	0.95	1177	1.09	1
269	true	ENSGALP0000008078	cyclin-dependent kinase 9 - CGNC Symbol 3750	39.4	9.3	1 127.0 (M:127.0)	1	3.5	8.25	1073		
270	true	ENSGALP0000018469	cystathione gamma-lyase - CGNC Symbol 8612	43.9	6.9	1 137.6 (M:137.6)	4	6.8	13.52	1023	0.81	2
271	true	ENSGALP00000023239	cystatin B (stefin B) - CGNC Symbol 10723	11.2	6.2	1 180.9 (M:180.9)	3	30.6	13.09	864 1.41!	1	
272	true	ENSGALP0000041804	cysteine and histidine-rich domain-containing protein 1 - Refseq NP_001026003	37.3	6.9	1 38.1 (M:38.1)	1	5.1	1.59	1454		
273	true	ENSGALP0000043636	cysteine-rich protein 1 - CGNC Symbol 52178	8.6	9.1	1 178.6 (M:178.6)	5	55.8	10.26	873 1.75!	2	354.69
274	true	ENSGALP0000017049	cytidine/uridine monophosphate kinase 1 - CGNC Symbol 7971	22.2	6.8	2 352.3 (M:352.3)	7	20.9	3.11	445	0.93	4
275	true	ENSGALP0000022250	cytochrome b5 type A (microsomal) - CGNC Symbol 10264	15.5	5	1 289.5 (M:289.5)	4	24.6	5.7	556	0.68	2
276	true	ENSGALP0000034615	Cytochrome c oxidase subunit 2 - UP P18944	25.6	4.6	1 393.9 (M:393.9)	7	25.1	4.33	396 0.44!	2	68.7
277	true	ENSGALP0000022815	cytochrome c oxidase subunit 5A - CGNC Symbol 10534	17	6.8	1 157.7 (M:157.7)	4	21.9	11.89	936 0.62!	1	
278	true	ENSGALP0000030189	cytochrome c oxidase subunit 6C - CGNC Symbol 13868	8.8	10.1	1 169.5 (M:169.5)	6	48.1	10.34	902 0.78!	2	2.63
279	true	ENSGALP000009217	cytochrome c oxidase subunit IV isoform 1 - CGNC Symbol 4285	19.6	8.9	1 283.7 (M:283.7)	5	11.1	11.59	574	0.71	2
280	true	ENSGALP0000011647	cytochrome c oxidase subunit Vla polypeptide 1 - CGNC Symbol 50396	11.8	9.4	1 238.9 (M:238.9)	6	38.9	4.78	669 0.54!	2	17.19
281	true	ENSGALP0000017934	cytochrome c somatic - CGNC Symbol 8375	11.7	9.5	1 172.4 (M:172.4)	3	17.1	7.01	887 1.04!	2	18.36
282	true	ENSGALP0000003187	cytochrome p450 oxidoreductase - CGNC Symbol 1457	76.9	5.4	1 237.5 (M:237.5)	4	5.6	11.03	674 0.55!	1	
283	true	ENSGALP0000001808	cytokine induced apoptosis inhibitor 1 - CGNC Symbol 812	32.9	5.2	1 205.6 (M:205.6)	5	18.9	6.94	776 0.85!	2	5.57
284	true	ENSGALP0000005184	cytokine receptor-like factor 3 - CGNC Symbol 2384	44.6	4.9	1 49.9 (M:49.9)	1	4.5	6.81	1426		
285	true	ENSGALP000006043	cytoplasmic FMR1 interacting protein 2 - CGNC Symbol 2795	145.6	6.6	2 277.2 (M:277.2)	8	7.5	5.07	585 0.92!	5	48.38
286	true	ENSGALP0000008338	damage-specific DNA binding protein 1 127kDa - CGNC Symbol 3871	127	5.1	1 525.7 (M:525.7)	9	7.7	6.79	288 0.53!	4	42.26
287	true	ENSGALP0000024479	DAZ associated protein 1 - CGNC Symbol 11311	43.6	8.9	1 292.7 (M:292.7)	7	13.2	3.23	550 0.63!	4	18.79
288	true	ENSGALP0000014300	DCN1 defective in cullin neddylation 1 domain containing 1 - CGNC Symbol 6684	30	5.2	1 101.6 (M:101.6)	2	6.6	12.31	1200	0.7	1
289	true	ENSGALP0000006969	DDB1 and CUL4 associated factor 7 - CGNC Symbol 313	38.9	5.3	1 90.4 (M:90.4)	2	5.6	2.56	1251	0.75	1
290	true	ENSGALP0000026509	DEAD (Asp-Glu-Ala-Asp) box helicase 1 - CGNC Symbol 12324	81.8	6.9	1 592.3 (M:592.3)	13	13.6	7.49	247 0.58!	6	40.49
291	true	ENSGALP0000019975	DEAD (Asp-Glu-Ala-Asp) box helicase 17 - CGNC Symbol 9302	75.1	9	1 1678.6 (M:1678.6)	31	33.6	7.28	35 0.51!	15	36.81
292	true	ENSGALP0000005576	DEAD (Asp-Glu-Ala-Asp) box helicase 5 - CGNC Symbol 49411	66.7	8.9	1 1286.8 (M:1286.8)	26	26.6	4.88	67 0.63!	14	39.83
293	true	ENSGALP0000038272	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27 - CGNC Symbol 5262	85.6	9.4	1 153.3 (M:153.3)	4	4.2	9.02	957 1.15!	3	2.46

294	true	ENSGALP00000026123	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3 X-linked - CGNC Symbol 50794	72.6	6.7	3 1272.0 (M:1272.0)	24	25.6	5.48	72	0.79!	12	48.11
295	true	ENSGALP00000006581	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50 - CGNC Symbol 3039	77.1	9.4	1 104.0 (M:104.0)	2	4.6	10.12	1183		6	30.97
296	true	ENSGALP00000023214	DEAH (Asp-Glu-Ala-His) box helicase 15 - CGNC Symbol 10712	87.6	7	2 539.2 (M:539.2)	15	15.6	4.6	278	0.86!	1	
297	true	ENSGALP00000016822	DEAH-box helicase 36 - CGNC Symbol 7873	112.6	8.3	1 186.4 (M:186.4)	4	5.5	11.26	842	0.92!	2	21.84
298	true	ENSGALP00000001617	decapping enzyme scavenger - CGNC Symbol 735	38.1	7.9	1 146.5 (M:146.5)	4	11.4	13.17	981	0.56!	2	
299	true	ENSGALP00000008524	decapping mRNA 1A - CGNC Symbol 3963	67.8	7.3	1 108.4 (M:108.4)	1	2	0.13	1167			
300	true	ENSGALP00000003234	dedicator of cytokinesis 2 - CGNC Symbol 1476	212.8	7	1 226.8 (M:226.8)	3	1.5	7.18	708	0.50!	2	23.52
301	true	ENSGALP00000016490	dedicator of cytokinesis 8 - CGNC Symbol 7720	238.9	6.3	1 460.7 (M:460.7)	10	4.6	11.71	330	0.73!	4	52.16
302	true	ENSGALP0000000261	defender against cell death 1 - CGNC Symbol 111	12.9	8.7	1 101.9 (M:101.9)	3	17.9	8.45	1196	0.86	2	35.29
303	true	ENSGALP00000019423	dehydrogenase/reductase (SDR family) member 7 - CGNC Symbol 9039	37.7	9.2	1 113.2 (M:113.2)	4	10.1	13.34	1142	0.70!	2	25.65
304	true	ENSGALP00000020666	DEK proto-oncogene - CGNC Symbol 9623	42.1	8.6	1 441.5 (M:441.5)	9	18.7	7.23	344	0.70!	5	38.17
305	true	ENSGALP00000009344	deleted in lung and esophageal cancer 1 - CGNC Symbol 4351	184.9	5.4	1 128.4 (M:128.4)	3	1.4	14.04	1070			
306	true	ENSGALP00000007930	deoxyuridine triphosphatase - CGNC Symbol 3681	17.8	5.9	1 147.9 (M:147.9)	2	9	12.37	977	1.76!	1	
307	true	ENSGALP00000018424	desmin - CGNC Symbol 49543	48.8	5.3	1 389.0 (M:389.0)	7	11.8	8.05	399	3.07!	2	111.2
308	true	ENSGALP00000014097	estrin (actin depolymerizing factor) - CGNC Symbol 6580	18.4	8.2	1 1276.8 (M:1276.8)	25	62.2	6.34	70	0.93!	14	34.21
309	true	ENSGALP00000011055	diaphanous homolog 1 (Drosophila) - CGNC Symbol 49017	90.7	6.1	1 204.4 (M:204.4)	6	4.7	6.75	782	0.79!	2	48.19
310	true	ENSGALP00000004108	differentially expressed in FDCP 6 homolog (mouse) - CGNC Symbol 1882	73.2	5.7	1 237.1 (M:237.1)	8	14.6	9.28	675	0.54!	3	128.08
311	true	ENSGALP00000016054	digestive organ expansion factor homolog (zebrafish) - CGNC Symbol 7511	88.9	5.7	1 92.6 (M:92.6)	3	2.5	13.52	1241	1.1	1	
312	true	ENSGALP00000012869	dihydrolipoamide dehydrogenase - CGNC Symbol 5998	53.9	8.2	1 310.6 (M:310.6)	4	10	8.56	517	0.81!	2	4.13
313	true	ENSGALP00000012815	dihydrolipoamide S-acetyltransferase - CGNC Symbol 5977	66.5	8	1 183.0 (M:183.0)	4	4	11.89	853	0.83	2	1.81
314	true	ENSGALP00000030864	dihydropyrimidinase-like 2 - CGNC Symbol 129	73.4	6	2 588.6 (M:588.6)	8	12.3	7.76	248	1.02	5	108.83
315	true	ENSGALP00000014813	dipeptidyl-peptidase 7 - CGNC Symbol 6929	54.5	5.8	1 360.7 (M:360.7)	6	10.9	3.19	432	2.56!	1	
316	true	ENSGALP00000013649	diphosphoinositol pentakisphosphate kinase 1 - CGNC Symbol 6353	135.3	5.8	2 154.4 (M:154.4)	3	3.2	8.37	955	1.56!	2	397.74
317	true	ENSGALP00000027317	D13S homolog exosome endoribonuclease and 3'-5' exoribonuclease - CGNC Symbol 12709	112.7	6.9	1 297.3 (M:297.3)	7	3.9	10	540	0.45!	3	25.36
318	true	ENSGALP00000001565	discs large (Drosophila) homolog-associated protein 4 - CGNC Symbol 708	107.7	6.6	1 207.9 (M:207.9)	5	6.1	14.16	768	2.00!	1	
319	true	ENSGALP00000021795	DNA ligase 1 - HGNC:6598	85.5	6.7	1 261.9 (M:261.9)	4	5.3	11.15	622	0.63	2	30.8
320	true	ENSGALP00000036774	Dnaj (Hsp40) homolog subfamily A member 1 - CGNC Symbol 53066	44.7	6.9	1 170.4 (M:170.4)	3	6.8	2.92	896	1.35	2	55.22
321	true	ENSGALP00000005132	Dnaj (Hsp40) homolog subfamily A member 4 - CGNC Symbol 2362	48	6.8	1 430.7 (M:430.7)	8	15.9	7.05	351	1.14!	3	47.25
322	true	ENSGALP00000039901	DnaJ heat shock protein family (Hsp40) member B12 - CGNC Symbol 52030	42.3	8.2	1 35.6 (M:35.6)	1	2.1	24.08	1459			
323	true	ENSGALP00000014379	DnaJ heat shock protein family (Hsp40) member C10 - CGNC Symbol 6729	91.4	6.6	1 131.7 (M:131.7)	4	3.5	8.01	1061	1.09!	2	54.11
324	true	ENSGALP0000000889	DnaJ heat shock protein family (Hsp40) member C11 - CGNC Symbol 391	63.4	8.6	1 107.4 (M:107.4)	2	3.2	6.95	1169	0.67!	1	
325	true	ENSGALP00000019064	DnaJ heat shock protein family (Hsp40) member C13 - CGNC Symbol 8873	254.8	6.3	1 341.8 (M:341.8)	6	2.9	6.34	455	0.55!	3	83.88
326	true	ENSGALP00000013413	DnaJ heat shock protein family (Hsp40) member C2 - CGNC Symbol 6249	71.4	8.7	1 52.2 (M:52.2)	2	3.9	2.32	1411			
327	true	ENSGALP00000005453	DnaJ heat shock protein family (Hsp40) member C7 - CGNC Symbol 2515	55.4	6.6	1 244.1 (M:244.1)	6	9.7	2.05	660	0.56!	2	1.04
328	true	ENSGALP00000004248	DnaJ heat shock protein family (Hsp40) member C9 - CGNC Symbol 1946	29.8	6	1 268.4 (M:268.4)	5	18.5	11.38	608	1.18!	2	66.14
329	true	ENSGALP00000038313	dolichyl-diphosphooligosaccharide-protein glycosyltransferase non-catalytic subunit - CGNC Symbol 71	48.7	5.4	1 344.0 (M:344.0)	9	11.6	6.45	453	0.98!	4	32.55
330	true	ENSGALP00000001483	dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit STT3A-like - CGNC Symbol 658:	80.5	8.1	1 274.4 (M:274.4)	5	7.7	13.32	593	0.15!	2	375.45
331	true	ENSGALP00000035143	drebrin like - CGNC Symbol 15268	45.4	5.2	1 358.1 (M:358.1)	9	21.6	13.26	435	0.90!	3	21.28
332	true	ENSGALP00000007207	dynactin subunit 4 - CGNC Symbol 3352	53.2	6.9	1 15.5 (M:15.5)	1	3.6	0.39	1479			
333	true	ENSGALP00000021055	dynamin 1-like - CGNC Symbol 9791	77.6	6.2	1 265.5 (M:265.5)	6	8.5	8.93	611	0.79!	1	
334	true	ENSGALP00000011499	dynein axonemal heavy chain 17 - CGNC Symbol 26405	506.9	5.4	1 258.6 (M:258.6)	4	0.9	11.62	627	1.09!	1	
335	true	ENSGALP00000036720	dynein cytoplasmic 1 heavy chain 1 - CGNC Symbol 8611	525.5	6.1	1 1055.5 (M:1055.5)	20	4.5	7.04	91	0.74!	11	34.79
336	true	ENSGALP00000027700	dynein cytoplasmic 2 heavy chain 1 - CGNC Symbol 12906	491.7	6	1 380.0 (M:380.0)	8	2	14.88	410	1.07!	1	
337	true	ENSGALP00000011574	dynein light chain 1 cytoplasmic - CGNC Symbol 53172	11.2	7.1	3 88.1 (M:88.1)	3	29.6	3.52	1259	0.71!	1	
338	true	ENSGALP00000008091	dyskerin pseudouridine synthase 1 - CGNC Symbol 3757	58.1	9.3	1 197.9 (M:197.9)	6	8.7	9.28	805	0.57!	3	2.1
339	true	ENSGALP00000018382	early endosome antigen 1 - CGNC Symbol 8572	161.6	5.6	1 389.0 (M:389.0)	4	3	14.08	398	1.26!	1	
340	true	ENSGALP00000016105	echinoderm microtubule associated protein like 4 - CGNC Symbol 7532	109.3	5.9	1 279.7 (M:279.7)	4	5.8	5.75	580	0.74	1	
341	true	ENSGALP00000033741	EH-hand domain family member D1 - CGNC Symbol 52247	26.9	5.1	1 366.8 (M:366.8)	8	17.6	6.18	425	0.74!	3	31.27
342	true	ENSGALP00000014768	EH-domain containing 3 - CGNC Symbol 51465	60.9	6.1	2 412.1 (M:412.1)	10	12.9	8.3	370	0.85!	5	47.86
343	true	ENSGALP0000001027	ELAV like RNA binding protein 1 - CGNC Symbol 49416	36.1	9.1	2 426.5 (M:426.5)	8	27.6	5.16	357	0.75!	5	49.58
344	true	ENSGALP00000004621	electron-transfer-flavoprotein alpha polypeptide - CGNC Symbol 2114	36.6	8.7	1 67.3 (M:67.3)	1	2.9	3.28	1347	0.77	1	
345	true	ENSGALP0000001456	elongation factor Tu GTP binding domain containing 2 - CGNC Symbol 656	109.4	4.9	1 795.2 (M:795.2)	19	15.1	4.09	146	0.79!	10	46.28
346	true	ENSGALP00000022724	embryonic ectoderm development - CGNC Symbol 10494	50.3	6.5	1 161.8 (M:161.8)	4	9.4	6.71	922	0.76!	1	
347	true	ENSGALP00000018258	Enah/Vasp-like - CGNC Symbol 8513	44.7	9.1	1 733.1 (M:733.1)	14	29.2	5.16	174	0.42!	6	35.61
348	true	ENSGALP00000023617	endoplasmic reticulum aminopeptidase 1 - CGNC Symbol 52992	102.4	5.8	1 59.4 (M:59.4)	2	2.6	13.82	1377	1	1	
349	true	ENSGALP00000038209	endoplasmic reticulum protein 29 - CGNC Symbol 50366	29.1	8.2	1 263.9 (M:263.9)	4	9.6	8.13	615	1.64	2	0.97
350	true	ENSGALP00000021892	endoplasmic reticulum protein 44 - CGNC Symbol 10115	46.9	5.2	1 302.0 (M:302.0)	5	14.3	11.46	527	1.44!	1	
351	true	ENSGALP00000004508	endoplasmic reticulum-golgi intermediate compartment 1 - CGNC Symbol 2067	32.5	6.2	1 204.0 (M:204.0)	6	15.2	4.78	786	0.94!	3	23.47
352	true	ENSGALP00000042251	endosulfine alpha - CGNC Symbol 23246	12.7	9.5	1 135.6 (M:135.6)	4	38.5	9.33	1035	0.30!	1	

353	true	ENSGALP0000014641	endothelial differentiation related factor 1 - CGNC Symbol 6846	16.4	9.9	1 263.3 (M:263.3)	5	33.1	18.55	618	0.58!	3	41.08
354	true	ENSGALP0000019726	engulfment and cell motility 1 - CGNC Symbol 51330	83.7	5.9	1 155.6 (M:155.6)	3	5.2	11.26	946	0.31!	1	
355	true	ENSGALP0000028016	enhancer of rudimentary homolog (Drosophila) - CGNC Symbol 13056	12.3	5.6	1 301.6 (M:301.6)	7	32.7	3.64	530	0.69	4	65.84
356	true	ENSGALP0000004835	enhancer of zeste homolog 1 (Drosophila) - CGNC Symbol 2222	85.4	8.2	2 81.8 (M:81.8)	1	1.1	23.08	1283			
357	true	ENSGALP0000003737	enolase 1 (alpha) - CGNC Symbol 49607	47.3	6.4	2 2033.4 (M:2033.4)	35	53	6.42	22	1.09!	16	34.62
358	true	ENSGALP0000040189	enoyl CoA hydratase short chain 1 mitochondrial - CGNC Symbol 56301	31.6	9	1 338.3 (M:338.3)	5	15.9	10.27	461	0.51!	1	
359	true	ENSGALP0000012529	enoyl-CoA delta isomerase 1 - CGNC Symbol 50312	32.9	9.1	1 286.8 (M:286.8)	5	13.9	7.72	562	0.66!	2	14.75
360	true	ENSGALP0000020867	enoyl-CoA delta isomerase 2 - CGNC Symbol 9709	44	8.7	1 181.7 (M:181.7)	2	3.8	4.27	860	0.52!	1	
361	true	ENSGALP0000016743	epoxide hydrolase 1-like - CGNC Symbol 51488	55.6	9	1 117.6 (M:117.6)	3	3.7	6.94	1113	0.57	1	
362	true	ENSGALP0000037486	epsin 3 - CGNC Symbol 63844	53.9	4.9	1 73.2 (M:73.2)	3	5.7	13.55	1319	0.36	1	
363	true	ENSGALP000006355	Era-like 12S mitochondrial rRNA chaperone 1 - CGNC Symbol 2934	51.2	9.6	1 69.3 (M:69.3)	2	5.4	0.37	1331	0.85!	1	
364	true	ENSGALP0000016416	ERI1 exoribonuclease family member 3 - CGNC Symbol 7679	29.8	8.8	1 34.2 (M:34.2)	1	6.8	22.83	1462	0.66	1	
365	true	ENSGALP0000017597	ERO1-like beta (S. cerevisiae) - CGNC Symbol 8234	51.5	7.3	1 98.8 (M:98.8)	2	5.8	7.3	1211			
366	true	ENSGALP0000041687	erythrocyte membrane protein band 4.1 (elliptocytosis 1 RH-linked) - CGNC Symbol 49834	96.8	5.7	4 295.3 (M:295.3)	6	6.5	4.05	547	0.44!	3	38.76
367	true	ENSGALP0000027299	ES1 protein homolog mitochondrial-like - CGNC Symbol 50857	26.4	6.5	3 162.0 (M:162.0)	4	6.8	2.44	919	0.49!	2	11.86
368	true	ENSGALP0000027399	esterase D - CGNC Symbol 12753	36.9	7.7	1 218.8 (M:218.8)	4	10.3	5.51	738	0.71	2	7.38
369	true	ENSGALP0000025606	eukaryotic translation elongation factor 1 alpha 1 - CGNC Symbol 48980	50.1	9.1	1 1139.7 (M:1139.7)	21	36.8	5.57	81	1.08!	9	34.4
370	true	ENSGALP0000009371	eukaryotic translation elongation factor 1 alpha 2 - CGNC Symbol 50948	50.5	9.1	1 746.1 (M:746.1)	16	21.4	6.33	166	1.35!	6	77.23
371	true	ENSGALP0000025937	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) - CGNC Symbol	76.1	4.9	1 256.7 (M:256.7)	5	7.4	4.36	634	0.88!	2	48.03
372	true	ENSGALP0000002828	eukaryotic translation elongation factor 2 - CGNC Symbol 1287	95.2	6.4	2 2550.6 (M:2550.6)	55	41.5	6.69	10	1.06!	29	43.69
373	true	ENSGALP0000019452	eukaryotic translation initiation factor 1B - CGNC Symbol 9051	12.8	6.8	2 67.3 (M:67.3)	2	22.1	5.49	1346	0.80!	1	
374	true	ENSGALP0000015560	eukaryotic translation initiation factor 2 subunit alpha - CGNC Symbol 7281	36.2	5.1	1 210.0 (M:210.0)	7	15.9	6.84	761	0.32!	3	273.14
375	true	ENSGALP0000003175	eukaryotic translation initiation factor 2 subunit beta - CGNC Symbol 49248	37.9	5.9	1 169.2 (M:169.2)	5	10.6	8.64	904	0.72!	2	3.35
376	true	ENSGALP0000016918	eukaryotic translation initiation factor 2A - CGNC Symbol 7921	62.7	9	1 115.0 (M:115.0)	3	5.3	7.98	1126	0.55!	1	
377	true	ENSGALP0000015176	eukaryotic translation initiation factor 3 subunit A - CGNC Symbol 7090	163.2	6.7	1 715.8 (M:715.8)	15	10.1	6.21	179	0.70!	7	41.41
378	true	ENSGALP0000006778	eukaryotic translation initiation factor 3 subunit B - CGNC Symbol 55528	85.6	5	1 850.8 (M:850.8)	19	19.3	7.99	132	0.79!	9	27.17
379	true	ENSGALP0000020439	eukaryotic translation initiation factor 3 subunit D - CGNC Symbol 56714	34.7	9.5	1 308.1 (M:308.1)	4	11.5	14.4	520	0.54!	1	
380	true	ENSGALP0000025883	eukaryotic translation initiation factor 3 subunit E - CGNC Symbol 12026	52.1	5.7	1 294.9 (M:294.9)	6	12.1	5.51	548	1.05!	2	55.6
381	true	ENSGALP0000008530	eukaryotic translation initiation factor 3 subunit F - CGNC Symbol 3965	35.2	5.3	1 347.8 (M:347.8)	4	9.9	12.67	452	0.65!	2	0.84
382	true	ENSGALP0000025924	eukaryotic translation initiation factor 3 subunit H - CGNC Symbol 12051	39.5	6	1 79.5 (M:79.5)	1	5.7	4.76	1290			
383	true	ENSGALP0000005271	eukaryotic translation initiation factor 3 subunit I - CGNC Symbol 2428	36.5	5.4	1 39.8 (M:39.8)	1	4.9	2.74	1449			
384	true	ENSGALP0000043461	eukaryotic translation initiation factor 3 subunit K - HGNC:24656	34.2	5.9	1 69.7 (M:69.7)	2	9.8	13.94	1328	0.49!	1	
385	true	ENSGALP0000020064	eukaryotic translation initiation factor 3 subunit L - CGNC Symbol 9341	66.6	5.9	1 411.8 (M:411.8)	9	15.8	14.2	371	1.02!	5	46.67
386	true	ENSGALP0000019755	eukaryotic translation initiation factor 3 subunit M - CGNC Symbol 9182	42.6	5.3	1 132.3 (M:132.3)	2	8.3	5.9	1057			
387	true	ENSGALP0000013862	eukaryotic translation initiation factor 4 gamma 1 - CGNC Symbol 6463	178.9	5.4	1 489.9 (M:489.9)	8	4.2	6.54	306	1.00!	2	8.78
388	true	ENSGALP0000008953	eukaryotic translation initiation factor 4 gamma 2 - CGNC Symbol 4160	97.5	6.6	2 352.5 (M:352.5)	8	8.3	9.23	444	0.83!	4	11.48
389	true	ENSGALP0000016375	eukaryotic translation initiation factor 4 gamma 3 - CGNC Symbol 7664	176.1	5.1	1 133.7 (M:133.7)	3	2.1	13.8	1049	0.78!	1	
390	true	ENSGALP00000038935	eukaryotic translation initiation factor 4A2 - CGNC Symbol 49225	46.3	5.3	2 1370.1 (M:1370.1)	24	37.8	7.67	60	0.89!	12	72.99
391	true	ENSGALP00000038179	eukaryotic translation initiation factor 4A3 - CGNC Symbol 6471	46.8	6.3	1 924.2 (M:924.2)	18	21.4	7.56	112	0.75!	8	42.88
392	true	ENSGALP0000001997	eukaryotic translation initiation factor 4H - CGNC Symbol 897	16.2	5.5	1 148.3 (M:148.3)	5	26	13.93	975	1.28	1	
393	true	ENSGALP0000018669	eukaryotic translation initiation factor 5 - CGNC Symbol 8711	49	5.2	1 144.0 (M:144.0)	5	6	8.95	992	1.26!	2	6.75
394	true	ENSGALP00000038570	eukaryotic translation initiation factor 5A2 - CGNC Symbol 49863	16.7	5.4	1 287.4 (M:287.4)	4	24.2	4.24	559	1.72!	1	
395	true	ENSGALP0000002796	eukaryotic translation initiation factor 6 - CGNC Symbol 1275	26.5	4.6	1 387.5 (M:387.5)	7	26.5	4.35	400	1.3	4	28.21
396	true	ENSGALP0000003538	eukaryotic translation termination factor 1 - CGNC Symbol 1614	49	5.5	1 58.7 (M:58.7)	1	2.7	7.56	1381			
397	true	ENSGALP0000037232	EWS RNA binding protein 1 - CGNC Symbol 50409	71.7	9.3	1 301.6 (M:301.6)	4	7.7	3.69	529	0.89!	2	81.71
398	true	ENSGALP0000010925	exocyst complex component 6 - CGNC Symbol 52056	87.4	5.7	1 138.1 (M:138.1)	4	4.7	17.09	1022	0.52!	2	15.39
399	true	ENSGALP0000006970	exportin 1 - CGNC Symbol 3224	122.8	5.7	1 583.4 (M:583.4)	16	12.9	6.66	251	0.78!	7	73.91
400	true	ENSGALP0000016816	exportin 5 - CGNC Symbol 7870	137.6	5.6	1 370.4 (M:370.4)	7	4.8	15.4	420	0.89!	3	80.92
401	true	ENSGALP0000002839	exportin 7 - CGNC Symbol 1294	123.8	5.9	1 171.4 (M:171.4)	4	3.2	7.83	889	0.49!	2	38.99
402	true	ENSGALP0000015971	exportin for tRNA - CGNC Symbol 7470	109.8	5.1	1 45.6 (M:45.6)	1	1.5	5.71	1432			
403	true	ENSGALP0000016164	extra spindle pole bodies like 1 separase - CGNC Symbol 7565	204.2	8.5	1 125.8 (M:125.8)	3	2.2	4.8	1077	1.52!	1	
404	true	ENSGALP00000039691	extracellular fatty acid-binding protein precursor - Refseq NP_990753	20.2	5.6	1 62.6 (M:62.6)	1	5.1	12.7	1371			
405	true	ENSGALP0000022293	ezrin - CGNC Symbol 10288	69.3	5.9	1 942.3 (M:942.3)	18	14	7.44	110	1.40!	7	70.97
406	true	ENSGALP0000007389	F-box protein 6 - CGNC Symbol 51014	32.4	8.3	1 121.6 (M:121.6)	4	11.3	10.96	1098	0.57	2	6.22
407	true	ENSGALP0000009656	family with sequence similarity 103 member A1 - CGNC Symbol 49987	14.1	9.4	2 206.7 (M:206.7)	4	31.9	3.51	771	0.17!	1	
408	true	ENSGALP0000008299	family with sequence similarity 120A - CGNC Symbol 3854	122.5	9	1 284.9 (M:284.9)	8	8.5	5.67	567	0.56!	3	34.4
409	true	ENSGALP0000007671	family with sequence similarity 129 member A - CGNC Symbol 3572	90.7	5	1 165.1 (M:165.1)	4	4	10.76	910	0.59!	2	30.76
410	true	ENSGALP00000026511	family with sequence similarity 49 member A - CGNC Symbol 12326	37.3	5.7	1 235.2 (M:235.2)	6	22	7.31	681	1.43!	1	
411	true	ENSGALP0000030147	family with sequence similarity 49 member B - CGNC Symbol 12196	36.8	6	2 656.5 (M:656.5)	10	28.4	5.75	204	0.53!	3	29.64

412	true	ENSGALP00000008144	family with sequence similarity 83 member G - HGNC:32554	91.8	6.5	1 53.4 (M:53.4)	1	2.1	4.73	1408	0.77	1
413	true	ENSGALP00000015840	family with sequence similarity 98 member B - CGNC Symbol 7407	44.7	9	1 100.8 (M:100.8)	1	2.8	6.09	1205	0.74!	1
414	true	ENSGALP0000014509	far upstream element (FUSE) binding protein 1 - CGNC Symbol 6789	55.2	7.7	1 889.0 (M:889.0)	25	30.4	7.39	121	0.67!	12
415	true	ENSGALP0000038764	far upstream element (FUSE) binding protein 3 - CGNC Symbol 2892	57.9	7.7	1 283.6 (M:283.6)	7	11.1	6.42	575	1.58!	2
416	true	ENSGALP0000043372	farnesyl diphosphate synthase - CGNC Symbol 23240	27.1	5.7	1 115.3 (M:115.3)	3	14.6	10.2	1122	0.88!	1
417	true	ENSGALP0000005262	Fas associated factor family member 2 - CGNC Symbol 2423	52.6	5.5	1 125.3 (M:125.3)	3	5.4	8.81	1078	0.67	2
418	true	ENSGALP0000012326	Fas associated via death domain - CGNC Symbol 51906	22.9	6	1 220.4 (M:220.4)	4	10.2	12.06	732	0.38!	2
419	true	ENSGALP0000033359	fasin actin-bundling protein 1 - CGNC Symbol 14444	54.1	6.8	1 284.6 (M:284.6)	7	12.9	6.77	570	6.35!	1
420	true	ENSGALP0000038124	fatty acid synthase - CGNC Symbol 1983	274.6	5.9	2 496.9 (M:496.9)	10	3.7	4.03	303	1.12!	4
421	true	ENSGALP0000011673	ferritin heavy polypeptide 1 - CGNC Symbol 49581	21.1	5.8	1 736.3 (M:736.3)	12	32.2	6.4	172	1.67!	5
422	true	ENSGALP0000041208	ferritin light polypeptide - Refseq NP_989714	30.9	8.9	1 206.5 (M:206.5)	2	3.6	2.57	773	0.41!	1
423	true	ENSGALP0000015061	fibrinogen alpha chain - CGNC Symbol 49746	82.3	5.7	1 339.2 (M:339.2)	6	10.9	10.61	458	1.06!	1
424	true	ENSGALP0000015057	fibrinogen beta chain - CGNC Symbol 7036	54.5	6.8	2 144.4 (M:144.4)	4	12	13.4	991		
425	true	ENSGALP0000015063	fibrinogen gamma chain - CGNC Symbol 7041	49.9	5.5	1 178.7 (M:178.7)	4	14.8	7.59	872		
426	true	ENSGALP0000005653	fibronectin 1 - CGNC Symbol 2613	259	5.8	2 284.7 (M:284.7)	9	5.9	14.44	568		
427	true	ENSGALP0000035478	filamin B beta - CGNC Symbol 49141	277	5.6	1 2108.4 (M:2108.4)	44	15.6	6.83	18	1.66!	18
428	true	ENSGALP0000042635	FK506 binding protein 1A 12kDa - CGNC Symbol 20061	8.9	6.8	1 71.5 (M:71.5)	1	17.5	2.24	1323	28.72	1
429	true	ENSGALP0000020346	FK506 binding protein 3 - CGNC Symbol 9468	25	9.2	1 435.7 (M:435.7)	7	28.2	2.94	348	0.80!	2
430	true	ENSGALP0000023115	FK506 binding protein 4 59kDa - CGNC Symbol 10671	50.4	5.5	1 557.1 (M:557.1)	11	22.6	11.46	268	1.08!	5
431	true	ENSGALP0000014935	fragile X mental retardation 1 - CGNC Symbol 51729	70	8.9	1 223.9 (M:223.9)	5	4.9	6.22	721	2.69	2
432	true	ENSGALP0000020563	fructose-1-6-bisphosphatase 1 - CGNC Symbol 9572	44.6	8.7	1 59.6 (M:59.6)	1	2.6	23.49	1375		
433	true	ENSGALP0000021472	fumurate hydratase - CGNC Symbol 9939	54.3	9.2	1 331.3 (M:331.3)	7	16.2	11.27	472	0.83!	3
434	true	ENSGALP0000039767	fumarylacetoacetate hydrolase domain containing 1 - CGNC Symbol 16972	24.7	6.6	1 67.7 (M:67.7)	2	13.5	17.97	1342	0.23!	1
435	true	ENSGALP0000033650	FYN binding protein - CGNC Symbol 2773	92	7.2	2 472.7 (M:472.7)	7	14.1	9.85	314	0.80!	3
436	true	ENSGALP0000020523	G kinase anchoring protein 1 - CGNC Symbol 9552	42.2	7.7	1 53.4 (M:53.4)	2	4.4	12.57	1407		
437	true	ENSGALP0000004453	G protein pathway suppressor 1 - CGNC Symbol 2036	55.2	6.2	1 225.1 (M:225.1)	4	8	9.33	715	0.59!	2
438	true	ENSGALP0000000054	G protein subunit alpha i3 - HGNC:4387	39.1	5.6	1 526.7 (M:526.7)	9	20.7	7.49	287	0.56!	6
439	true	ENSGALP0000040337	G1 to S phase transition 1 - CGNC Symbol 54531	67.6	5.1	1 85.1 (M:85.1)	1	1.8	8.79	1267		
440	true	ENSGALP0000025373	GA binding protein transcription factor alpha subunit - CGNC Symbol 11756	51.4	5	1 63.5 (M:63.5)	1	2.6	5.5	1366	13.33!	1
441	true	ENSGALP0000022402	galactose mutarotase (aldose 1-epimerase) - CGNC Symbol 10350	38	6.4	1 124.2 (M:124.2)	4	15.4	3.59	1083	1.21!	1
442	true	ENSGALP0000022400	Gallus gallus ABRA C-terminal like (ABRACL) mRNA. - RefSeq mRNA NM_001302176	9	5.6	1 301.0 (M:301.0)	4	35.8	3.79	532	1.16	2
443	true	ENSGALP0000042680	Gallus gallus actin cytoplasmic 2-like (LOC776816) mRNA. - RefSeq mRNA NM_001308613	41.8	5.3	3 4629.9 (M:4629.9)	64	70.7	6.48	2	1.25!	29
444	true	ENSGALP0000035339	Gallus gallus ATP synthase H+ transporting mitochondrial F1 complex beta polypeptide (ATPSB) mRNA	52.9	5.1	1 3004.6 (M:3004.6)	39	50	5.08	5	0.90!	17
445	true	ENSGALP0000002625	Gallus gallus ATPase H+ transporting lysosomal 56/58kDa V1 subunit B2 (ATP6V1B2) mRNA. - RefSeq mRNA NM_001302177	55.8	5.5	1 352.8 (M:352.8)	9	18.8	6.41	443	2.54	2
446	true	ENSGALP00000020185	Gallus gallus chromosome 5 open reading frame human C14orf166 (C14ORF166) mRNA. - RefSeq mRNA NM_001308613	27.4	5.8	1 282.6 (M:282.6)	6	23	3.93	577	0.7	4
447	true	ENSGALP0000022816	Gallus gallus cytochrome b5 reductase 3 (CYB5R3) mRNA. - RefSeq mRNA NM_001291805	34.1	8.7	1 164.3 (M:164.3)	4	10.6	5.58	912	0.52!	1
448	true	ENSGALP0000039796	Gallus gallus DEAD (Asp-Glu-Ala-Asp) box helicase 6 (DDX6) transcript variant 1 mRNA. - RefSeq mRNA NM_001308613	54.4	8.9	1 557.3 (M:557.3)	16	25.3	10.4	267	0.78!	6
449	true	ENSGALP0000019758	Gallus gallus diazepam binding inhibitor (GABA receptor modulator acyl-CoA binding protein) (DBI) mRNA	9.6	7.9	1 149.8 (M:149.8)	2	20.9	0.17	968	1.2	1
450	true	ENSGALP0000042627	Gallus gallus granulin (GNLY) mRNA. - RefSeq mRNA NM_001044680	15.2	5.9	1 148.7 (M:148.7)	3	27.1	11.99	972	0.95!	1
451	true	ENSGALP0000040653	Gallus gallus H2A histone family member J (H2AFJ) mRNA. - RefSeq mRNA NM_00130753	13.9	10.9	2 769.3 (M:769.3)	12	35.7	6.37	159	0.30!	6
452	true	ENSGALP0000038904	Gallus gallus hemoglobin alpha 1 (HBAA) mRNA. - RefSeq mRNA NM_001004376	15.4	8.5	1 1148.8 (M:1148.8)	17	66.2	5.15	79	1.20!	9
453	true	ENSGALP00000041526	Gallus gallus histone cluster 1 H4-VI germinal H4 (similar to human histone cluster 1 class H4 genes) (H4) mRNA	11.4	11.4	1 1735.9 (M:1735.9)	31	61.2	7.24	32	0.38!	14
454	true	ENSGALP0000009829	Gallus gallus hypoxanthine phosphoribosyltransferase 1 (HPRT1) mRNA. - RefSeq mRNA NM_204848	23.7	8.3	1 79.3 (M:79.3)	1	5.3	13.3	1294		
455	true	ENSGALP0000009505	Gallus gallus immunoglobulin lambda-like polypeptide 1 (IGLL1) mRNA. - RefSeq mRNA NM_00127854	24.3	6.3	1 99.4 (M:99.4)	1	8.7	6.61	1209		
456	true	ENSGALP0000012772	Gallus gallus interleukin 18 (IL18) mRNA. - RefSeq mRNA NM_204608	22.7	5.3	1 50.9 (M:50.9)	2	12.2	16.74	1419		
457	true	ENSGALP0000012348	Gallus gallus LIM domain binding 1 (LDB1) mRNA. - RefSeq mRNA NM_205070	46.6	6.6	1 94.8 (M:94.8)	3	5.1	7.35	1231	0.47!	1
458	true	ENSGALP0000010214	Gallus gallus macrophage migration inhibitory factor (MIF) mRNA. - RefSeq mRNA NM_00130753	12.5	6.9	1 290.2 (M:290.2)	4	31.3	12.73	555	0.73	3
459	true	ENSGALP0000017367	Gallus gallus mago-nashi homolog 2 (MAGOH2) transcript variant 1 mRNA. - RefSeq mRNA NM_001308613	17.1	6	1 114.0 (M:114.0)	4	24.7	9.53	1137	0.77	2
460	true	ENSGALP0000004974	Gallus gallus NCK-associated protein 1-like (NCKAP1L) mRNA. - RefSeq mRNA NM_001031339	126.7	6.1	1 51.3 (M:51.3)	2	2.5	17.69	1416		
461	true	ENSGALP0000002426	Gallus gallus nuclear transport factor 2 (NTUF2) transcript variant 2 mRNA. - RefSeq mRNA NM_00130753	14.4	5.9	1 107.0 (M:107.0)	3	26.8	4.09	1171	0.84!	1
462	true	ENSGALP0000002711	Gallus gallus PCI domain containing 2 (PCID2) mRNA. - RefSeq mRNA NM_001006266	53.5	8.7	1 181.6 (M:181.6)	5	9.1	3.24	862	0.98!	1
463	true	ENSGALP00000005078	Gallus gallus polymerase (DNA-directed) delta interacting protein 2 (POLDIP2) mRNA. - RefSeq mRNA NM_001308613	42.7	8.6	1 114.1 (M:114.1)	3	6.7	2.21	1135	1.12!	1
464	true	ENSGALP00000000468	Gallus gallus proteasome (prosome macropain) 26S subunit ATPase 5 (PSMC5) mRNA. - RefSeq mRNA NM_001305057	46.2	7.1	1 254.8 (M:254.8)	6	12.1	6.57	638	0.79!	3
465	true	ENSGALP00000012883	Gallus gallus recombination activating gene 2 (RAG2) mRNA. - RefSeq mRNA NM_001305057	59.1	5.6	1 227.7 (M:227.7)	6	9.8	11.03	704	1.17!	3
466	true	ENSGALP0000001978	Gallus gallus replication factor C (activator 1) 2 40kDa (RFC2) mRNA. - RefSeq mRNA NM_205530	39.7	5.7	2 69.1 (M:69.1)	1	4.7	4.87	1332		
467	true	ENSGALP00000025165	Gallus gallus ribosomal protein L7 (RPL7) mRNA. - RefSeq mRNA NM_001006345	28.7	10.8	1 840.8 (M:840.8)	20	54.3	7.64	134	0.73!	10
468	true	ENSGALP00000022626	Gallus gallus ribosomal protein S12 (RPS12) mRNA. - RefSeq mRNA NM_001277911	14.5	6.8	1 394.9 (M:394.9)	8	44.7	6.22	394	1.24!	4
469	true	ENSGALP00000022671	Gallus gallus S100 calcium binding protein A9 (S100A9) mRNA. - RefSeq mRNA NM_001305151	14.1	6.4	2 76.9 (M:76.9)	2	16.8	17.69	1306	0.9	2
470	true	ENSGALP0000005535	Gallus gallus serine peptidase inhibitor Kazal type 7 (putative) (SPINK7) transcript variant 1 mRNA. - RefSeq mRNA NM_001305151	44.3	5.6	1 260.3 (M:260.3)	5	20.7	12.44	624		

471	true	ENSGALP000000000726	Gallus gallus SH3 domain binding glutamate-rich protein like 3 (SH3BGLR3) mRNA. - RefSeq mRNA NM_001293	10.5	5.1	1 211.3 (M:211.3)	4	24.7	1.57	759	0.38	2	103.38
472	true	ENSGALP000000031725	Gallus gallus SH3 domain binding glutamic acid-rich protein like (SH3BGLR) mRNA. - RefSeq mRNA NM_001293	12.9	4.8	1 166.1 (M:166.1)	3	26.3	8.32	908	0.44!	1	
473	true	ENSGALP00000002508	Gallus gallus SIN3 transcription regulator family member A (SIN3A) mRNA. - RefSeq mRNA NM_001293	145.5	6.9	1 191.5 (M:191.5)	7	5.7	8.51	822	1.05!	3	1.91
474	true	ENSGALP00000004369	Gallus gallus small nuclear ribonucleoprotein polypeptide C (SNRPC) mRNA. - RefSeq mRNA NM_001293	17.4	9.7	1 183.7 (M:183.7)	2	11.3	1.25	851	0.51	1	
475	true	ENSGALP000000039728	Gallus gallus small nuclear ribonucleoprotein polypeptide G (SNRPG) mRNA. - RefSeq mRNA NM_001293	8.5	9	1 203.0 (M:203.0)	6	42.1	4.04	787	1.13!	3	117.68
476	true	ENSGALP000000023081	Gallus gallus suppressor of Ty 5 homolog (S. cerevisiae) (SUPT5H) mRNA. - RefSeq mRNA NM_0010313	119.9	5	1 211.3 (M:211.3)	6	5.7	5.17	760	0.38!	2	68.34
477	true	ENSGALP00000001635	Gallus gallus syntaxin binding protein 1 (STXBP1) mRNA. - RefSeq mRNA NM_001305648	67.4	6.2	1 155.0 (M:155.0)	5	7.8	16.86	951	1.23!	3	29.97
478	true	ENSGALP000000041224	Gallus gallus translocase of inner mitochondrial membrane 13 homolog (yeast) (TIMM13) mRNA. - RefSeq mRNA NM_001113744	11	8.4	1 28.4 (M:28.4)	1	7.9	0.69	1474	0.58	1	
479	true	ENSGALP000000021405	Gallus gallus YKT6 v-SNARE homolog (S. cerevisiae) (YKT6) mRNA. - RefSeq mRNA NM_001113744	22.4	5.5	1 119.5 (M:119.5)	3	15.7	5.59	1104			
480	true	ENSGALP000000034419	GATA zinc finger domain containing 2A - CGNC Symbol 2116	61.8	9.8	2 152.2 (M:152.2)	4	7.2	3.82	960	0.30!	1	
481	true	ENSGALP000000042641	GATA zinc finger domain containing 2B - HGNC:30778	62.9	9.8	1 224.2 (M:224.2)	3	5.4	4.02	718	0.30!	1	
482	true	ENSGALP000000011775	GCN1 eIF2 alpha kinase activator homolog - CGNC Symbol 5500	293.6	7	1 293.4 (M:293.4)	7	3.3	8.37	549	0.83!	3	10.81
483	true	ENSGALP000000013267	GDP dissociation inhibitor 2 - CGNC Symbol 49512	50.7	5.3	1 1707.6 (M:1707.6)	26	42.4	8.47	34	0.78!	13	30.9
484	true	ENSGALP000000042001	GDP-D-glucose phosphorylase 1 - CGNC Symbol 64926	40	5.9	1 73.4 (M:73.4)	1	4.1	4.88	1316			
485	true	ENSGALP000000020915	GDP-mannose 4-6-dehydratase - CGNC Symbol 9729	38.7	6.6	1 59.1 (M:59.1)	1	5.6	13.46	1379			
486	true	ENSGALP00000002197	gelsolin - CGNC Symbol 49472	85.8	6	1 247.6 (M:247.6)	5	5.1	8.37	652	5.14!	2	18.6
487	true	ENSGALP000000041554	GEM interacting protein - HGNC:24852	111.9	5.7	1 135.5 (M:135.5)	5	5.3	9.58	1036	1.05!	2	33.31
488	true	ENSGALP000000007934	glucose-6-phosphate isomerase - CGNC Symbol 3683	62.1	7.8	1 676.6 (M:676.6)	14	15.9	5.04	197	1.19!	6	27.35
489	true	ENSGALP00000003139	glutamate dehydrogenase 1 - CGNC Symbol 52002	47.6	8.3	1 337.1 (M:337.1)	5	9.4	5.8	463	0.81!	2	1.35
490	true	ENSGALP000000026270	glutamate-cysteine ligase catalytic subunit - CGNC Symbol 12202	66.8	5.5	1 88.6 (M:88.6)	3	3.7	6.52	1256	0.61!	1	
491	true	ENSGALP00000012086	glutamic-oxaloacetic transaminase 1 soluble - CGNC Symbol 5645	45.9	8.2	1 270.7 (M:270.7)	6	15.8	2.15	602	0.92!	4	17.07
492	true	ENSGALP00000003646	glutamic-oxaloacetic transaminase 2 - CGNC Symbol 1656	47.3	9.4	1 1073.2 (M:1073.2)	20	30.5	7.24	88	0.94!	9	34.45
493	true	ENSGALP00000012199	glutaminase - CGNC Symbol 5698	69.9	8.5	1 124.0 (M:124.0)	3	4.4	8.68	1084	2.87!	1	
494	true	ENSGALP00000011071	glutaminyl-tRNA synthetase - CGNC Symbol 5185	86.9	6.5	1 290.5 (M:290.5)	7	7.8	10.21	554	0.96!	3	37.91
495	true	ENSGALP00000015623	glutamyl-prolyl-tRNA synthetase - CGNC Symbol 7307	179.8	7.9	2 776.2 (M:776.2)	16	7.9	7.49	157	0.84!	6	41.78
496	true	ENSGALP00000017016	glutaredoxin 3 - CGNC Symbol 7961	37.3	5.5	1 232.5 (M:232.5)	3	12.7	4.33	690			
497	true	ENSGALP00000018029	glutaredoxin 5 - CGNC Symbol 8413	17.4	7.8	1 191.7 (M:191.7)	2	11.7	11.27	821	0.44	1	
498	true	ENSGALP00000041423	glutathione peroxidase 1 - CGNC Symbol 65881	17.9	6.4	1 527.1 (M:527.1)	9	35.7	10.35	285	1.02	5	72.24
499	true	ENSGALP00000042929	glutathione reductase - HGNC:4623	45.2	6.4	1 105.2 (M:105.2)	2	5.8	4.51	1175			
500	true	ENSGALP00000013682	glutathione S-transferase omega 1 - CGNC Symbol 52072	27.2	7	1 68.2 (M:68.2)	2	10	6.01	1338	1.16!	1	
501	true	ENSGALP00000010240	glutathione S-transferase theta 1 - CGNC Symbol 4772	29.8	6.6	1 58.3 (M:58.3)	1	5.7	2.16	1383			
502	true	ENSGALP00000008341	glutathione S-transferase theta 1-like - CGNC Symbol 55583	29.9	8.6	1 322.3 (M:322.3)	5	20.4	5.63	493	0.25!	2	241.75
503	true	ENSGALP00000005180	glutathione synthetase - CGNC Symbol 2381	52.3	5.7	1 250.2 (M:250.2)	6	11.6	7.95	649	0.9	3	37.56
504	true	ENSGALP00000023278	glyceraldehyde-3-phosphate dehydrogenase - CGNC Symbol 49077	34.9	8.5	1 1632.5 (M:1632.5)	24	42.5	4.7	39	0.81!	9	82.33
505	true	ENSGALP00000018695	glycerol-3-phosphate dehydrogenase 1-like - CGNC Symbol 8724	38.6	6.6	2 318.9 (M:318.9)	7	17.3	8.49	500	0.49!	3	40.16
506	true	ENSGALP00000009121	glycyl-tRNA synthetase - CGNC Symbol 4244	77.5	6.1	1 720.7 (M:720.7)	15	17.7	8.14	177	1.50!	5	93.62
507	true	ENSGALP00000007667	glyoxalase domain containing 4 - HGNC:14111	51.2	9.1	1 195.7 (M:195.7)	3	6.3	15.86	810	3.29!	2	69.95
508	true	ENSGALP00000002822	glyoxylate reductase 1 homolog - CGNC Symbol 52955	60.4	9.3	1 144.8 (M:144.8)	3	5.6	7.87	986	0.53!	1	
509	true	ENSGALP00000004317	golgi glycoprotein 1 - CGNC Symbol 1981	119	6.2	1 246.5 (M:246.5)	3	1.6	11.99	655	0.90!	1	
510	true	ENSGALP00000015596	golgi reassembly stacking protein 2 55kDa - CGNC Symbol 7296	44.3	4.8	1 101.9 (M:101.9)	1	2.9	1.48	1197			
511	true	ENSGALP00000023990	golgi-associated PDZ and coiled-coil motif containing - CGNC Symbol 11060	43	5.7	1 34.0 (M:34.0)	1	3.3	3.75	1464			
512	true	ENSGALP00000015897	golgin B1 - CGNC Symbol 7433	369.4	4.9	1 422.2 (M:422.2)	7	2.3	13.89	365			
513	true	ENSGALP00000019667	GRB2-related adaptor protein 2 - CGNC Symbol 9140	37.7	6.7	1 444.6 (M:444.6)	8	27.1	7.47	341	0.23!	2	0.92
514	true	ENSGALP00000018939	group-specific component (vitamin D binding protein) - CGNC Symbol 8824	53.7	6.5	1 150.1 (M:150.1)	3	9.3	10.02	967			
515	true	ENSGALP00000012993	growth factor receptor bound protein 2 - CGNC Symbol 6067	25.2	5.8	1 323.4 (M:323.4)	8	21.2	6.9	490	1.31!	4	12.46
516	true	ENSGALP00000025020	GrpE like 1 mitochondrial - CGNC Symbol 51840	24.8	7	1 85.3 (M:85.3)	1	8.1	6.96	1266	0.55	1	
517	true	ENSGALP00000006604	GTPase activating protein (SH3 domain) binding protein 1 - CGNC Symbol 50211	52.4	5.1	2 672.3 (M:672.3)	10	19.7	6.84	200	0.93!	4	35.78
518	true	ENSGALP00000038576	GTPase IMAP family member 7-like - CGNC Symbol 53739	25.3	7.8	3 425.5 (M:425.5)	8	26.4	7.96	360	0.94!	3	14.61
519	true	ENSGALP00000026664	GTPase very large interferon inducible 1 - CGNC Symbol 53425	278.8	6.2	1 447.1 (M:447.1)	9	3.7	10.44	339	1.46!	1	
520	true	ENSGALP00000024386	guanine deaminase - CGNC Symbol 11266	50.2	5.5	1 51.7 (M:51.7)	1	4	0.32	1414			
521	true	ENSGALP00000041749	guanine nucleotide binding protein (G protein) alpha 13 - CGNC Symbol 3014	43.7	7.6	1 151.7 (M:151.7)	3	7.4	6.97	962	0.58!	1	
522	true	ENSGALP00000007379	guanine nucleotide binding protein (G protein) alpha inhibiting activity polypeptide 2 - CGNC Symbol 4	39	5.5	5 883.1 (M:883.1)	16	35.3	8.81	126	0.65!	7	23.65
523	true	ENSGALP00000039575	guanine nucleotide binding protein (G protein) beta polypeptide 1 - CGNC Symbol 50984	37.3	5.6	2 271.0 (M:271.0)	6	16.2	6.21	601	0.88!	3	31.13
524	true	ENSGALP00000014596	guanine nucleotide binding protein (G protein) beta polypeptide 4 - CGNC Symbol 6824	37.5	5.8	1 322.3 (M:322.3)	5	14.1	6.66	494	0.50!	2	35.04
525	true	ENSGALP00000042788	guanine nucleotide binding protein (G protein) gamma 7 - CGNC Symbol 64142	7.6	8.7	1 44.9 (M:44.9)	1	20.6	1.68	1434			
526	true	ENSGALP00000042552	guanylate binding protein - CGNC Symbol 49284	65.6	5.6	1 852.1 (M:852.1)	16	31.4	4.68	131	1.54!	4	99.07
527	true	ENSGALP00000042357	H2A histone family member X - HGNC:4739	15	10.9	1 321.7 (M:321.7)	7	23.8	4.66	495	0.82!	4	17.62
528	true	ENSGALP00000010267	H2A histone family member Y - CGNC Symbol 4787	39.2	9.8	3 153.7 (M:153.7)	4	13.6	7.37	956	0.86!	2	38.34
529	true	ENSGALP00000028277	H2A histone family member Z - CGNC Symbol 52762	13.6	10.6	2 464.4 (M:464.4)	8	31.2	5.52	323	0.41!	3	54.43

530	true	ENSGALP00000003584	H3 histone family 3B - CGNC Symbol 49711	15.3	11.3	2 571.1 (M:571.1)	11	28.7	9.11	259	0.26!	4	31.55
531	true	ENSGALP00000005905	HAUS augmin like complex subunit 8 - CGNC Symbol 51188	38.6	6.6	1 54.1 (M:54.1)	1	4.1	18.04	1403		2	0.23
532	true	ENSGALP0000022592	HBS1 like translational GTPase - CGNC Symbol 10439	76	6	1 204.9 (M:204.9)	3	3.6	15.48	778	1.12!	1	
533	true	ENSGALP0000023911	HD domain containing 2 - CGNC Symbol 11010	22.8	5.6	1 83.4 (M:83.4)	4	16.1	13.52	1279	1.98!	7	47.69
534	true	ENSGALP0000027534	heat shock 105kDa/110kDa protein 1 - CGNC Symbol 12826	111.2	5.8	1 603.9 (M:603.9)	14	10.8	5.69	235	1.43!	5	20.75
535	true	ENSGALP0000014746	heat shock 10kDa protein 1 - CGNC Symbol 49569	12.1	8.6	2 586.2 (M:586.2)	12	57.7	7.63	250	1.53!	13	63.32
536	true	ENSGALP0000019120	heat shock 70kDa protein 2 - CGNC Symbol 51984	69.9	5.7	1 2036.4 (M:2036.4)	28	27.3	6	21	1.39!	11	73.87
537	true	ENSGALP0000011770	heat shock 70kDa protein 4 - CGNC Symbol 5498	100.6	5.5	1 905.3 (M:905.3)	20	18.8	7.43	115	1.11!	9	22.16
538	true	ENSGALP0000016536	heat shock 70kDa protein 4-like - CGNC Symbol 51755	94.7	5.4	1 1345.6 (M:1345.6)	28	25	5.95	63	2.29!	30	93.42
539	true	ENSGALP0000014747	heat shock 70kDa protein 5 (glucose-regulated protein 78kDa) - CGNC Symbol 667	72	5.1	1 2099.0 (M:2099.0)	30	33.3	5.75	19	2.32!	21	52.01
540	true	ENSGALP0000010510	heat shock 70kDa protein 8 - CGNC Symbol 49511	70.8	5.4	1 3985.0 (M:3985.0)	57	49.8	5.93	4	1.03!	10	88.44
541	true	ENSGALP0000018498	heat shock protein 90kDa alpha (cytosolic) class A member 1 - CGNC Symbol 51974	83.2	5.1	1 2749.3 (M:2749.3)	46	36.9	7.15	7	1.17!	25	30.76
542	true	ENSGALP0000016523	heat shock protein 90kDa alpha (cytosolic) class B member 1 - CGNC Symbol 49691	83.4	5	1 1460.4 (M:1460.4)	27	20	7.9	53	1.19!	1	
543	true	ENSGALP0000020747	heat shock protein 90kDa beta (Grp94) member 1 - CGNC Symbol 49067	91.5	4.8	1 1160.1 (M:1160.1)	25	25.5	9.9	77	1.46!	10	
544	true	ENSGALP0000003717	heat shock protein family A (Hsp70) member 9 - CGNC Symbol 1687	73.1	6.1	1 957.3 (M:957.3)	16	19.3	4.56	105	1.73!	5	48.42
545	true	ENSGALP0000013122	heat shock protein family D (Hsp60) member 1 - CGNC Symbol 6130	60.9	5.7	1 1381.4 (M:1381.4)	17	24.6	4.9	58	1.54!	8	59.25
546	true	ENSGALP0000012919	hematological and neurological expressed 1 - CGNC Symbol 6027	16.1	4.8	1 308.2 (M:308.2)	6	37.2	5.03	519	0.69!	2	6.99
547	true	ENSGALP0000015204	hematological and neurological expressed 1-like - CGNC Symbol 50339	12.9	9.5	1 92.5 (M:92.5)	2	25.2	13.85	1242			
548	true	ENSGALP0000015886	hematopoietic cell-specific Lyn substrate 1 - CGNC Symbol 7430	57.2	4.7	1 715.1 (M:715.1)	13	25.6	5.69	181	0.64!	7	37.75
549	true	ENSGALP0000019231	heme binding protein 1 - CGNC Symbol 8945	21.1	6.4	1 73.3 (M:73.3)	1	11.6	2.38	1317			
550	true	ENSGALP0000012344	heme oxygenase 2 - CGNC Symbol 5763	35.3	5.2	1 83.9 (M:83.9)	3	10.2	4.57	1274	0.36	1	
551	true	ENSGALP00000035593	Hemoglobin subunit beta - UP P02112	16.5	8.8	4 1352.6 (M:1352.6)	21	72.1	5.15	62	1.52!	10	158.71
552	true	ENSGALP0000035386	hemopexin - CGNC Symbol 15517	45.4	5.1	1 170.3 (M:170.3)	3	7.6	10.68	897			
553	true	ENSGALP0000035370	hepatoma-derived growth factor - CGNC Symbol 58434	26.2	5.1	3 218.7 (M:218.7)	5	21.6	7.58	739	0.45!	3	119.76
554	true	ENSGALP0000016363	heterochromatin protein 1 binding protein 3 - CGNC Symbol 7661	61.8	9.4	1 663.7 (M:663.7)	12	17.5	12.36	201	0.41!	5	95.57
555	true	ENSGALP0000023188	heterogeneous nuclear ribonucleoprotein A/B - CGNC Symbol 49727	24.6	9.7	1 515.1 (M:515.1)	8	25.1	8.22	293	0.59!	3	31.15
556	true	ENSGALP0000009933	heterogeneous nuclear ribonucleoprotein A0 - CGNC Symbol 4621	33	9.6	1 300.1 (M:300.1)	5	11.9	5.64	533	0.49	3	28.53
557	true	ENSGALP0000037924	heterogeneous nuclear ribonucleoprotein A1 - CGNC Symbol 7027	40.8	9.3	1 1710.7 (M:1710.7)	27	42.8	7.07	33	0.88!	16	117.19
558	true	ENSGALP0000017954	heterogeneous nuclear ribonucleoprotein A2/B1 - CGNC Symbol 51306	37	8.7	1 2243.8 (M:2243.8)	28	55.3	3.89	14	0.52!	13	47.87
559	true	ENSGALP0000037222	heterogeneous nuclear ribonucleoprotein D-like - CGNC Symbol 51783	33.4	6.9	2 272.4 (M:272.4)	5	10.3	16.44	599	0.99	3	38.23
560	true	ENSGALP0000039530	heterogeneous nuclear ribonucleoprotein H1 (H) - CGNC Symbol 49193	56.5	5.5	1 1459.2 (M:1459.2)	17	29.5	6.43	54	0.56!	7	48.14
561	true	ENSGALP0000006284	heterogeneous nuclear ribonucleoprotein H3 (2H9) - CGNC Symbol 52025	36.6	6.6	1 1836.5 (M:1836.5)	24	58.2	8.9	30	0.98!	11	67.92
562	true	ENSGALP0000020534	heterogeneous nuclear ribonucleoprotein K-like - CGNC Symbol 53093	47.1	6.1	2 1360.3 (M:1360.3)	22	34.3	7.19	61	0.73!	13	61.28
563	true	ENSGALP0000013837	heterogeneous nuclear ribonucleoprotein L-like - CGNC Symbol 6450	50.6	9	1 163.6 (M:163.6)	4	8.1	10.85	915	0.55!	1	
564	true	ENSGALP0000000509	heterogeneous nuclear ribonucleoprotein M - CGNC Symbol 51167	76	8.9	1 1936.3 (M:1936.3)	39	35.1	5.17	27	0.54!	19	41.92
565	true	ENSGALP0000001183	heterogeneous nuclear ribonucleoprotein R - CGNC Symbol 51033	71	8.4	2 656.3 (M:656.3)	16	23.2	8.4	205	0.54!	5	13.47
566	true	ENSGALP0000017341	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A) - CGNC Symbol 8107	74.9	9.4	1 688.7 (M:688.7)	13	11.6	8.55	191	0.50!	7	72.89
567	true	ENSGALP0000006708	hexokinase 1 - CGNC Symbol 3101	102.7	6.3	1 263.0 (M:263.0)	4	5.7	12.87	619	0.71!	1	
568	true	ENSGALP0000024040	hexosaminidase B (beta polypeptide) - CGNC Symbol 11085	63.4	6	1 296.0 (M:296.0)	5	8.9	7.28	545	0.76!	2	32.5
569	true	ENSGALP0000009341	high density lipoprotein binding protein - CGNC Symbol 4348	141.5	6.4	1 263.8 (M:263.8)	7	4.8	3.51	616	0.83!	2	79.48
570	true	ENSGALP0000027541	high mobility group box 1 - CGNC Symbol 49444	24.9	5.6	1 1282.5 (M:1282.5)	17	35.3	4.95	69	0.46!	11	95.43
571	true	ENSGALP0000017462	high mobility group box 2 - CGNC Symbol 8169	23.8	8.5	1 1446.7 (M:1446.7)	26	36.7	4	55	0.39!	11	97.42
572	true	ENSGALP0000000503	high mobility group nucleosomal binding domain 2 - CGNC Symbol 54659	9.4	10	1 54.2 (M:54.2)	1	20	15.17	1401			
573	true	ENSGALP0000015159	high mobility group nucleosome binding domain 5 - CGNC Symbol 51685	20.2	9.9	1 169.9 (M:169.9)	2	8.4	15.36	900	0.56	1	
574	true	ENSGALP0000005647	hippocalcin - CGNC Symbol 2609	22.1	4.9	3 131.8 (M:131.8)	2	3.6	4.77	1059	0.56!	1	
575	true	ENSGALP0000000583	histidine triad nucleotide binding protein 1 - CGNC Symbol 49312	13.8	6.3	2 116.8 (M:116.8)	3	20.6	13.78	1114	0.71	2	31.8
576	true	ENSGALP0000001150	histidyl-tRNA synthetase - CGNC Symbol 50172	56.6	5.8	2 180.0 (M:180.0)	3	3.4	2.31	867	1.20!	2	25.05
577	true	ENSGALP0000023099	histocompatibility (minor) HA-1 - CGNC Symbol 51181	103.3	8.2	1 334.5 (M:334.5)	9	7.7	4.54	467	0.48!	3	88.79
578	true	ENSGALP0000015492	histone acetyltransferase 1 - CGNC Symbol 7250	47.9	5.3	1 329.2 (M:329.2)	4	8.6	13.14	477	0.55!	1	
579	true	ENSGALP0000037266	histone cluster 1 H1.11L (similar to human histone cluster 1 class H1 genes) - CGNC Symbol 53220	22.5	11	2 765.2 (M:765.2)	9	22.2	5.37	161	0.44!	6	101.55
580	true	ENSGALP0000037260	histone cluster 1 H2B-V (similar to human histone cluster 1 class H2B) - CGNC Symbol 50635	13.9	10.3	3 1431.9 (M:1431.9)	23	46	6.1	56	0.35!	11	61.03
581	true	ENSGALP0000005212	histone deacetylase 1 - CGNC Symbol 2394	54.9	5.3	1 404.3 (M:404.3)	12	18.5	6.81	382	0.67!	5	47.19
582	true	ENSGALP0000024133	histone deacetylase 2 - CGNC Symbol 11140	55.3	5.6	1 458.9 (M:458.9)	13	16	6.06	332	0.73!	5	51.06
583	true	ENSGALP0000010190	histone deacetylase 7 - CGNC Symbol 4743	103.4	7	2 131.1 (M:131.1)	1	1.9	2.07	1064			
584	true	ENSGALP0000019163	histone H1 - CGNC Symbol 53214	24.8	11.1	1 696.2 (M:696.2)	9	18.6	5.81	188	0.43!	6	106.12
585	true	ENSGALP00000021743	histone H2B - CGNC Symbol 52653	13.5	10	1 968.1 (M:968.1)	15	41.8	4.74	102	0.46!	5	88.6
586	true	ENSGALP00000015722	histone PARylation factor 1 - HGNC:26051	39.7	8	1 73.5 (M:73.5)	3	10.3	5.11	1315	0.58!	1	
587	true	ENSGALP0000010334	HIV-1 Tat specific factor 1 - CGNC Symbol 51672	51	5	1 18.4 (M:18.4)	1	2.4	9.31	1478			
588	true	ENSGALP00000040785	Hsap of 16: DDB1 and CUL4 associated factor 8-like 1 - HGNC:31810	43.7	4.8	1 183.2 (M:183.2)	3	8.3	3.66	852	1.22!	2	72.55

589	true	ENSGALP0000014480	Hsap of 16: GIMAP1-GIMAP5 readthrough - HGNC:51257		33.1	8.2	1 81.7 (M:81.7)	2	4.7	15.83	1284	0.93	1
590	true	ENSGALP00000030998	Hsap of 16: glutathione S-transferase alpha 1 - HGNC:4626		25.2	7.8	2 171.3 (M:171.3)	4	14	9.15	890	0.86!	1
591	true	ENSGALP00000028993	Hsap of 1: ADP-ribosyltransferase 1 - HGNC:723		31.9	8.7	1 219.7 (M:219.7)	4	15.3	12.91	736	0.84!	3
592	true	ENSGALP00000004985	Hsap of 1: AT-rich interaction domain 1A - HGNC:11110		204.6	6.7	1 175.0 (M:175.0)	4	3.5	10.52	883	0.83!	1
593	true	ENSGALP0000038795	Hsap of 1: ATP synthase H+ transporting mitochondrial F1 complex alpha subunit 1 cardiac muscle - HC	60	9	2 1482.0 (M:1482.0)	25	33.8	10.95	52	0.76!	10	48.65
594	true	ENSGALP0000042254	Hsap of 1: bridging integrator 2 - HGNC:1053		28.4	4.3	1 62.7 (M:62.7)	1	6.5	5.1	1369		
595	true	ENSGALP0000041510	Hsap of 1: calreticulin - HGNC:1455		21.6	4.6	1 143.7 (M:143.7)	4	16.5	7.41	994	2.86	2
596	true	ENSGALP0000041109	Hsap of 1: capping actin protein gelsolin like - HGNC:1474		72.4	8.3	1 254.0 (M:254.0)	7	11.7	9.51	640	0.38!	2
597	true	ENSGALP0000041873	Hsap of 1: chaperonin containing TCP1 subunit 3 - HGNC:1616		16.2	6.4	1 234.3 (M:234.3)	6	27.8	4.34	686	0.67!	3
598	true	ENSGALP0000041574	Hsap of 1: chaperonin containing TCP1 subunit 3 - HGNC:1616		25.9	7	1 136.3 (M:136.3)	2	5.3	3.2	1029	1.02!	1
599	true	ENSGALP0000040011	Hsap of 1: DEAD-box helicase 21 - HGNC:2744		54.1	9.1	1 102.8 (M:102.8)	2	2.6	9.67	1190	0.70!	1
600	true	ENSGALP0000043386	Hsap of 1: dynamin 2 - HGNC:2974		64.8	9.3	1 424.4 (M:424.4)	8	10.3	5.82	361	0.74!	4
601	true	ENSGALP00000291944	Hsap of 1: ETHE1 persulfide dioxygenase - HGNC:23287		11.7	7	1 230.6 (M:230.6)	3	29	2.27	695	0.32!	1
602	true	ENSGALP0000039954	Hsap of 1: formin like 1 - HGNC:1212		52.9	6.9	1 251.1 (M:251.1)	6	8.2	5.81	645	0.88!	3
603	true	ENSGALP0000041179	Hsap of 1: glucosamine-6-phosphate deaminase 1 - HGNC:4417		31.1	6.1	1 94.3 (M:94.3)	3	9.7	3.55	1233	0.6	1
604	true	ENSGALP0000042553	Hsap of 1: Hepatoma-derived growth factor-related protein 2 - UP Q7Z4V5		72.1	6.2	1 186.8 (M:186.8)	5	6.8	13.47	839	0.23!	3
605	true	ENSGALP0000004322	Hsap of 1: high mobility group 20A - HGNC:5001		21.4	6.4	2 88.0 (M:88.0)	3	13	1.18	1260	0.31	2
606	true	ENSGALP0000040966	Hsap of 1: hydroxysteroid 17-beta dehydrogenase 10 - HGNC:4800		13.2	6.7	1 233.2 (M:233.2)	6	55.6	11.46	688	0.73!	2
607	true	ENSGALP0000041633	Hsap of 1: ilvB (bacterial acetolactate synthase)-like - HGNC:6041		25	9.9	1 35.9 (M:35.9)	1	4.3	22.84	1458	3.92	1
608	true	ENSGALP0000043134	Hsap of 1: integrator complex subunit 3 - HGNC:26153		64.1	7.2	1 163.3 (M:163.3)	3	4.1	15.38	917	1.02!	1
609	true	ENSGALP0000038278	Hsap of 1: NAC alpha domain containing - HGNC:22196		137.6	4	1 26.4 (M:26.4)	1	1	9.43	1476		
610	true	ENSGALP0000005807	Hsap of 1: regulator of G-protein signaling like 1 - HGNC:18636		103.8	8.6	1 48.9 (M:48.9)	1	1.4	15.41	1428		
611	true	ENSGALP0000042855	Hsap of 1: ribosomal protein L10 like - HGNC:17976		12.1	9.6	1 213.1 (M:213.1)	4	13.3	4.98	750	0.78!	2
612	true	ENSGALP0000042059	Hsap of 1: RNA binding motif protein 39 - HGNC:15923		34.1	5.9	2 314.3 (M:314.3)	5	11	5.83	509	0.51!	2
613	true	ENSGALP0000010447	Hsap of 1: S-phase kinase-associated protein 1 - HGNC:10899		18.6	4.4	1 114.4 (M:114.4)	2	7.4	6.68	1132	1.65	1
614	true	ENSGALP0000038155	Hsap of 1: serine and arginine rich splicing factor 7 - HGNC:10789		28.7	11.9	3 409.4 (M:409.4)	8	24.8	5.92	376	0.67!	4
615	true	ENSGALP0000005495	Hsap of 1: small nuclear ribonucleoprotein US subunit 200 - HGNC:30859		44.6	5.7	1 177.9 (M:177.9)	6	12.1	10.66	877	0.44!	1
616	true	ENSGALP0000041393	Hsap of 1: SON DNA binding protein - HGNC:11183		30.3	9.5	1 76.5 (M:76.5)	1	10.2	14.73	1307		
617	true	ENSGALP0000042543	Hsap of 1: src kinase associated phosphoprotein 1 - HGNC:15605		20.5	5.1	1 67.5 (M:67.5)	1	6.2	7.17	1345		
618	true	ENSGALP0000042479	Hsap of 1: stress induced phosphoprotein 1 - HGNC:11387		34.1	5.5	1 672.6 (M:672.6)	13	32.1	5.18	199	0.93!	5
619	true	ENSGALP0000042153	Hsap of 1: translocase of inner mitochondrial membrane 50 - HGNC:23656		27.1	6.5	1 55.4 (M:55.4)	2	4.2	2.26	1395	0.93	1
620	true	ENSGALP0000011160	Hsap of 1: ATP synthase H+ transporting mitochondrial Fo complex subunit G - HGNC:14247		11.7	9.9	1 55.5 (M:55.5)	1	8.5	13.31	1394		
621	true	ENSGALP0000042837	Hsap of 4: heterogeneous nuclear ribonucleoprotein A1-like 2 - HGNC:27067		25.5	9.1	1 813.6 (M:813.6)	14	32.5	6.38	142	0.68!	7
622	true	ENSGALP0000041533	Hsap of 4: heterogeneous nuclear ribonucleoprotein L - HGNC:5045		23	7.6	1 132.7 (M:132.7)	3	13.2	8.79	1056	1.13	2
623	true	ENSGALP0000013273	Hsap of 4: methylthioadenosine phosphorylase - HGNC:7413		30.8	6.1	1 98.6 (M:98.6)	2	3.2	4.6	1213	0.32	1
624	true	ENSGALP0000023926	Hsap of 4: myosin light chain 12B - HGNC:29827		19.9	4.6	3 620.7 (M:620.7)	11	41.3	7.43	219	1.00!	5
625	true	ENSGALP0000000669	Hsap of 4: nascent polypeptide-associated complex alpha subunit - HGNC:7629		21.4	9.2	1 282.5 (M:282.5)	5	13.5	6.36	578	1.45!	2
626	true	ENSGALP0000042329	Hsap of 4: nipssnap homolog 3A - HGNC:23619		28.1	9.5	1 96.2 (M:96.2)	2	2.8	0.92	1223	0.66	1
627	true	ENSGALP0000021708	Hsap of 4: poly(rC) binding protein 2 - HGNC:8648		47.5	8	3 738.1 (M:738.1)	12	18.2	8.1	168	0.82!	7
628	true	ENSGALP0000011990	Hsap of 4: proteoglycan 2 bone marrow (natural killer cell activator eosinophil granule major basic prot		17.3	9.7	1 117.6 (M:117.6)	2	18.4	6.53	1112	0.16!	1
629	true	ENSGALP0000000293	Hsap of 4: signal recognition particle 19kDa - HGNC:11300		16.3	9.9	1 96.6 (M:96.6)	2	9.6	3.29	1222	1.25	1
630	true	ENSGALP0000037564	Hsap of 4: solute carrier family 25 member 10 - HGNC:10980		43.2	9.4	1 182.8 (M:182.8)	2	3	4.61	855	0.49!	1
631	true	ENSGALP0000015415	Hsap of 4: sterile alpha motif domain containing 9 - HGNC:1348		182.1	6.8	1 49.9 (M:49.9)	1	0.8	6.97	1425		
632	true	ENSGALP0000002154	Hsap of 4: ubiquitin conjugating enzyme E2 L5 pseudogene - HGNC:13477		17.2	6.9	1 229.2 (M:229.2)	2	14.9	3.36	700	0.91	1
633	true	ENSGALP0000038829	Hsap of 9: DEAD-box helicase 19A - HGNC:25628		53.9	5.8	1 89.5 (M:89.5)	2	4.2	9.56	1253	0.99	2
634	true	ENSGALP0000029322	Hsap of 9: RBM14-RBM4 readthrough - HGNC:38840		27.6	6.1	1 401.0 (M:401.0)	7	28.4	8.16	387	0.67	5
635	true	ENSGALP0000007927	Hsap of 9: ribosomal protein L36a - HGNC:10359		13.2	10.8	1 160.9 (M:160.9)	4	15.8	8.15	925	0.86	3
636	true	ENSGALP0000041195	Hsap of 9: toll like receptor adaptor molecule 2 - HGNC:21354		25	5.5	1 154.9 (M:154.9)	3	10.4	4.03	953	0.73!	1
637	true	ENSGALP0000041511	HSPA (heat shock 70kDa) binding protein cytoplasmic cochaperone 1 - CGNC Symbol 64131		26	5.6	1 284.0 (M:284.0)	7	21.1	3.24	573	0.71!	2
638	true	ENSGALP0000025929	hydroxyacyl-CoA dehydrogenase - CGNC Symbol 12053		34.4	8.7	1 404.0 (M:404.0)	7	17.1	6.69	383	0.72!	3
639	true	ENSGALP0000026633	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein) ε		85.7	9.3	1 870.7 (M:870.7)	16	13.8	9.01	127	0.78!	7
640	true	ENSGALP0000026663	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein) t		50.8	9.4	1 343.4 (M:343.4)	6	13.9	6.59	454	1.32!	3
641	true	ENSGALP0000008657	hydroxyacylglutathione hydrolase - CGNC Symbol 4019		34.2	7.7	1 82.5 (M:82.5)	1	3.9	6.2	1282		
642	true	ENSGALP0000039757	hypoxia up-regulated 1 - CGNC Symbol 53307		108.3	5.1	1 452.9 (M:452.9)	12	9.4	6.33	336	1.84!	3
643	true	ENSGALP0000021333	IKAROS family zinc finger 1 (Ikaros) - CGNC Symbol 49585		57.6	6.1	1 287.3 (M:287.3)	5	7.1	3.74	560	0.35!	3
644	true	ENSGALP0000039156	IKAROS family zinc finger 2 (Helios) - CGNC Symbol 2272		59.2	6.2	2 195.3 (M:195.3)	3	4	3.05	812	0.48!	2
645	true	ENSGALP00000021927	IKAROS family zinc finger 3 (Aiolos) - CGNC Symbol 49403		55.5	6.2	1 637.4 (M:637.4)	14	27.7	6.83	211	0.39!	7
646	true	ENSGALP0000027238	importin 5 - CGNC Symbol 50851		125.1	4.9	1 328.1 (M:328.1)	7	7.6	10.06	480	0.66!	2
647	true	ENSGALP0000009312	importin 7 - CGNC Symbol 4333		116.2	4.7	1 236.6 (M:236.6)	4	4.3	7.76	677	0.87!	1

648	true	ENSGALP00000025404	inner membrane mitochondrial protein - CGNC Symbol 11773	79.2	5.7	1 358.1 (M:358.1)	6	6.8	4.63	436	0.82!	3	24.55
649	true	ENSGALP00000005130	inosine triphosphatase - CGNC Symbol 2361	22.2	5.8	1 99.0 (M:99.0)	2	5.5	2.82	1210	1.27!	1	
650	true	ENSGALP0000013491	inositol 1 4 5-triphosphate receptor type 1 - CGNC Symbol 49305	310.4	5.8	2 275.0 (M:275.0)	4	1.8	12.61	590	1.60!	2	32.99
651	true	ENSGALP0000040662	inositol monophosphatase 1 - HGNC:6050	36.7	6.6	1 312.5 (M:312.5)	6	17.1	7.4	513	0.96!	3	73.99
652	true	ENSGALP0000002409	inositol polyphosphate-5-phosphatase 145kDa - CGNC Symbol 52250	137	7.6	1 398.1 (M:398.1)	8	5.7	4.31	391	0.69!	3	26.33
653	true	ENSGALP0000011103	insulin degrading enzyme - HGNC:5381	118.1	6.1	2 256.0 (M:256.0)	5	5.3	1.88	636	0.86!	2	4.28
654	true	ENSGALP0000017819	insulin-like growth factor 2 mRNA binding protein 3 - CGNC Symbol 51304	64.3	9	2 354.0 (M:354.0)	8	14.4	4.46	442	1.70!	2	6.38
655	true	ENSGALP0000006522	integral membrane protein 2A - CGNC Symbol 3012	28.3	5.1	1 58.3 (M:58.3)	1	5.6	16.75	1382			
656	true	ENSGALP0000008442	integrator complex subunit 2 - CGNC Symbol 3921	132.8	5.6	1 67.7 (M:67.7)	1	1.5	5.11	1343			
657	true	ENSGALP0000015986	integrator complex subunit 7 - CGNC Symbol 7478	116.7	9.2	1 176.0 (M:176.0)	3	2.5	2.94	879	0.57!	1	
658	true	ENSGALP0000042736	integrator complex subunit 9 - CGNC Symbol 12464	73.7	5.9	2 63.5 (M:63.5)	2	4.9	12.4	1367			
659	true	ENSGALP0000012130	integrin beta 2 (complement component 3 receptor 3 and 4 subunit) - CGNC Symbol 49690	85.4	5.5	1 415.7 (M:415.7)	7	10.2	5.69	368	0.50!	3	23.81
660	true	ENSGALP0000011044	inter-alpha-trypsin inhibitor heavy chain 2 - CGNC Symbol 5157	112.6	6.6	1 130.7 (M:130.7)	1	1.5	3.34	1067			
661	true	ENSGALP0000002604	inter-alpha-trypsin inhibitor heavy chain 3 - CGNC Symbol 50111	100.5	5.8	1 110.5 (M:110.5)	1	1.5	2.21	1154			
662	true	ENSGALP0000005345	interferon gamma-inducible protein 30 - CGNC Symbol 2468	27.8	5.6	1 301.3 (M:301.3)	5	12.1	1.92	531	3.32	2	10.69
663	true	ENSGALP0000036413	interferon regulatory factor 4 - CGNC Symbol 9722	47.5	6.4	2 81.5 (M:81.5)	2	6.6	7.02	1285			
664	true	ENSGALP0000001014	interferon-induced guanylate-binding protein 1-like - CGNC Symbol 51030	79.3	5.7	1 231.9 (M:231.9)	6	8.8	4.86	693	0.99!	2	3.06
665	true	ENSGALP0000010303	interleukin 16 - CGNC Symbol 4808	157.8	8.2	1 173.0 (M:173.0)	5	3.3	8.92	886	1.06!	2	50.49
666	true	ENSGALP0000018849	interleukin enhancer binding factor 2 - CGNC Symbol 8794	42.9	5.3	1 189.2 (M:189.2)	6	14.9	5.33	829	0.84!	2	29.39
667	true	ENSGALP0000013987	IQ motif containing GTPase activating protein 1 - CGNC Symbol 6526	159.5	5.9	1 702.4 (M:702.4)	15	9.2	7.38	186	0.78!	6	15.52
668	true	ENSGALP0000024116	IQ motif containing GTPase activating protein 2 - CGNC Symbol 11128	181	6	1 571.3 (M:571.3)	11	5.7	7.9	257	1.15!	4	60.35
669	true	ENSGALP0000026444	isoamyl acetate-hydrolyzing esterase 1 homolog - CGNC Symbol 12296	27.6	5.7	1 212.9 (M:212.9)	5	21.3	10.18	752	2.56!	2	17.95
670	true	ENSGALP0000014317	isocitrate dehydrogenase 1 (NADP+) soluble - CGNC Symbol 6693	46.9	8.3	1 402.2 (M:402.2)	10	18.7	9.82	385	0.55!	5	147.72
671	true	ENSGALP0000035366	isocitrate dehydrogenase 2 (NADP+) mitochondrial - CGNC Symbol 54127	50.4	9	1 718.1 (M:718.1)	14	20.4	6.13	178	0.37!	7	143.52
672	true	ENSGALP0000042526	isocitrate dehydrogenase 3 (NAD(+)) beta - HGNC:5385	44.8	8.2	1 150.5 (M:150.5)	4	4.7	11.36	966	0.94	2	23.09
673	true	ENSGALP0000005224	isocitrate dehydrogenase 3 (NAD+) alpha - CGNC Symbol 2399	39.3	7.7	2 161.2 (M:161.2)	6	10.3	5.39	924	1.19!	3	12.87
674	true	ENSGALP0000042302	isocitrate dehydrogenase 3 (NAD+) gamma - CGNC Symbol 63782	12.2	7.9	1 42.5 (M:42.5)	1	21.4	2.88	1440			
675	true	ENSGALP0000008013	ISY1 splicing factor homolog (S. cerevisiae) - CGNC Symbol 3725	37.3	5.4	1 341.1 (M:341.1)	3	9.9	5.23	456	0.71!	2	2.55
676	true	ENSGALP0000005662	karyopherin alpha 2 (RAG cohort 1 importin alpha 1) - CGNC Symbol 50505	58	5.3	1 226.5 (M:226.5)	3	6.6	13.97	709	2.84!	1	
677	true	ENSGALP0000015528	karyopherin alpha 4 (importin alpha 3) - CGNC Symbol 52315	55.2	4.7	1 123.3 (M:123.3)	2	2.6	4.53	1085	1.87!	1	
678	true	ENSGALP0000000615	karyopherin subunit beta 1 - HGNC:6400	83.9	4.6	1 888.9 (M:888.9)	14	15	7.44	122	0.74!	6	27.1
679	true	ENSGALP0000016631	keratin 5 - CGNC Symbol 49888	62.4	8.5	1 193.7 (M:193.7)	5	5.7	8.27	817	0.80!	2	47.87
680	true	ENSGALP0000003695	keratin 6A - Refseq NP_001001313	57	8.5	1 112.7 (M:112.7)	3	6.7	14.6	1145			
681	true	P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	58.8	5.1	43 639.1 (M:639.1)	15	16.8	7.74	210	1.83	5	60.12
682	true	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	62	5.1	2 401.6 (M:401.6)	8	10	5.06	386	0.61!	4	41.5
683	true	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	66	8.2	3 1087.5 (M:1087.5)	12	17.5	12.69	86	1.26!	6	19.17
684	true	P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	65.4	8.1	1 540.8 (M:540.8)	10	15.2	9.86	275	0.90!	3	47.16
685	true	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	60	8.1	11 314.2 (M:314.2)	9	11.9	10.49	510	1.48!	2	11.44
686	true	ENSGALP0000020654	KIAA1033 - CGNC Symbol 9617	136	7	1 131.7 (M:131.7)	3	1.5	3.41	1060	0.91!	1	
687	true	ENSGALP0000025680	KIAA1429 - CGNC Symbol 11918	202.8	4.8	1 157.7 (M:157.7)	3	1.8	12.55	937	0.85!	1	
688	true	ENSGALP0000004515	KRAB-A domain-containing protein 2 - CGNC Symbol 49788	17.2	10.6	1 424.1 (M:424.1)	12	38.6	10.7	362	0.82!	7	27.45
689	true	ENSGALP0000006364	La ribonucleoprotein domain family member 1 - CGNC Symbol 2939	106.7	9.1	1 52.3 (M:52.3)	1	1.2	12.44	1410			
690	true	ENSGALP0000038626	lactate dehydrogenase A - CGNC Symbol 49707	36.5	7.8	1 235.3 (M:235.3)	5	13	7.74	680	1.14!	1	
691	true	ENSGALP0000021618	lactate dehydrogenase B - CGNC Symbol 10005	36.3	7.1	1 829.7 (M:829.7)	15	26.7	5.3	135	1.20!	7	64.59
692	true	ENSGALP0000015128	lamin B receptor - CGNC Symbol 49736	73.3	9.2	1 617.2 (M:617.2)	11	13.5	4.2	224	0.51!	7	120.39
693	true	ENSGALP0000023635	lamin B1 - CGNC Symbol 10893	73.6	5.5	1 491.9 (M:491.9)	15	22.9	9.14	305	0.41!	6	60.49
694	true	ENSGALP0000000639	lamin B2 - CGNC Symbol 49708	67.9	5.2	1 1505.0 (M:1505.0)	33	41.2	4.86	50	0.50!	16	80.18
695	true	ENSGALP0000041464	late endosomal/lysosomal adaptor MAPK and MTOR activator 1 - CGNC Symbol 65815	12.2	6.3	1 36.9 (M:36.9)	1	11.9	4.44	1457			
696	true	ENSGALP0000016671	latent transforming growth factor beta binding protein 2 - CGNC Symbol 53503	181.2	5.1	1 114.6 (M:114.6)	2	1.1	10.91	1131			
697	true	ENSGALP000000634	LCK proto-oncogene Src family tyrosine kinase - HGNC:6524	58.2	5.1	15 226.2 (M:226.2)	5	11.6	6.21	710			
698	true	ENSGALP0000020275	lectin galactoside-binding soluble 1 - CGNC Symbol 49833	15.1	6.6	1 122.5 (M:122.5)	3	16.3	3.46	1088	0.87	2	36.01
699	true	ENSGALP0000005081	lectin galactoside-binding soluble 2 - CGNC Symbol 2336	14.8	6.6	1 135.9 (M:135.9)	3	17.8	9.97	1031	1.38	1	
700	true	ENSGALP0000041057	lectin mannose binding 2 - CGNC Symbol 63471	38.3	6.4	1 244.5 (M:244.5)	3	7.6	6.88	659	0.71!	1	
701	true	ENSGALP0000017556	legumain - CGNC Symbol 8216	49.2	5.9	1 279.1 (M:279.1)	7	15.5	8.92	582	1.85!	2	65.78
702	true	ENSGALP0000007469	LEO1 homolog Paf1/RNA polymerase II complex component - CGNC Symbol 55225	71.6	4.4	1 101.3 (M:101.3)	2	2.1	4.65	1201	0.93	1	
703	true	ENSGALP0000028055	leucine aminopeptidase 3 - CGNC Symbol 4763	56.3	8.5	1 170.8 (M:170.8)	4	7.5	9.16	893	1.4	2	62.92
704	true	ENSGALP00000016182	leucine rich pentatricopeptide repeat containing - CGNC Symbol 7574	155.5	6.6	1 541.2 (M:541.2)	11	5.8	8.06	274	0.65!	5	30.34
705	true	ENSGALP0000001446	leucine rich repeat containing 47 - CGNC Symbol 649	61.6	8.6	1 56.8 (M:56.8)	2	5.6	13.37	1390	16.09!	1	
706	true	ENSGALP0000012427	leucine rich repeat containing 59 - CGNC Symbol 5794	38.7	9.4	1 147.7 (M:147.7)	2	6.2	3.31	979	1.58!	1	

707	true	ENSGALP00000012100	leucyl-tRNA synthetase - CGNC Symbol 5654	134.2	6.5	1 143.5 (M:143.5)	2	0.8	1.65	996	0.52!	1
708	true	ENSGALP00000010210	leukocyte cell derived chemotaxin 2 - CGNC Symbol 4754	35.2	9.1	1 794.6 (M:794.6)	13	36.3	5.68	147	1.62!	6
709	true	ENSGALP00000033366	leukocyte ribonuclease A-2 - CGNC Symbol 52020	15.9	10	1 296.9 (M:296.9)	5	24.5	2.65	541	2.8	2
710	true	ENSGALP00000018616	leukotriene A4 hydrolase - CGNC Symbol 8686	69.3	6.5	1 357.6 (M:357.6)	8	9.3	8.48	437	0.84!	3
711	true	ENSGALP00000032039	leupaxin - CGNC Symbol 14208	35.9	6.3	1 321.4 (M:321.4)	6	15.5	1.96	496	0.37!	2
712	true	ENSGALP0000002513	LIM and SH3 protein 1 - CGNC Symbol 1150	27.2	6.4	1 208.4 (M:208.4)	6	13.6	2.73	766	0.61	3
713	true	ENSGALP00000039699	LIM domain containing 2 - CGNC Symbol 327	14.3	9.1	1 73.2 (M:73.2)	3	11.7	13.81	1318	0.75!	1
714	true	ENSGALP00000000670	Ion peptidase 1 mitochondrial - CGNC Symbol 300	95.1	5.8	1 102.6 (M:102.6)	2	2.1	10.65	1191	1.55!	1
715	true	ENSGALP0000005122	LSM1 homolog mRNA degradation associated - CGNC Symbol 2356	15.2	5.2	1 82.6 (M:82.6)	2	12	18.69	1281	1.09	1
716	true	ENSGALP0000007884	LSM14A mRNA processing body assembly factor - CGNC Symbol 50074	50.5	9.6	1 109.1 (M:109.1)	3	4.8	14.13	1159	0.36!	1
717	true	ENSGALP0000012171	LUC7-like (S. cerevisiae) - CGNC Symbol 5684	43.6	10.2	1 340.8 (M:340.8)	7	16.8	4.35	457	0.67!	3
718	true	ENSGALP0000019318	LUC7-like 2 (S. cerevisiae) - CGNC Symbol 8987	47.2	10.1	1 494.5 (M:494.5)	9	17.3	5.48	304	0.91!	4
719	true	ENSGALP0000037522	LUC7-like 3 pre-mRNA splicing factor - CGNC Symbol 53432	51.4	9.8	1 229.8 (M:229.8)	3	7.9	11.84	699	0.38!	2
720	true	ENSGALP0000018165	lymphocyte antigen 75 - CGNC Symbol 8470	199.5	6.4	1 201.7 (M:201.7)	5	2.7	11.51	793	0.88!	2
721	true	ENSGALP0000027391	lymphocyte cytosolic protein 1 (L-plastin) - CGNC Symbol 12749	69.7	5.2	2 2696.7 (M:2696.7)	46	51.6	5.92	8	1.12!	21
722	true	ENSGALP0000003296	lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) - CGNC Symbol 151	59.5	5.9	1 184.4 (M:184.4)	3	5.3	8.62	848	0.54!	1
723	true	ENSGALP0000010618	lymphocyte-specific protein 1 - CGNC Symbol 4964	41.6	4.7	2 715.5 (M:715.5)	10	32.9	8.18	180	0.79!	4
724	true	ENSGALP0000017123	lymphoid enhancer binding factor 1 - CGNC Symbol 7997	40.8	6.7	1 323.9 (M:323.9)	6	20.6	6.87	488	0.56!	1
725	true	ENSGALP0000012399	lysine (K)-specific demethylase 3B - CGNC Symbol 66092	189.8	6.9	1 155.9 (M:155.9)	4	2	10.01	944	0.79!	1
726	true	ENSGALP0000023450	lysophosphatidylcholine acyltransferase 3 - CGNC Symbol 10817	54.1	9.1	1 50.3 (M:50.3)	1	2.8	1.69	1421	0.69	1
727	true	ENSGALP0000006365	lysophospholipase II - CGNC Symbol 2940	25.1	7.1	1 105.9 (M:105.9)	2	3.4	4.94	1172	0.52	1
728	true	ENSGALP0000027011	lysosome g-like - CGNC Symbol 50830	21.7	8.4	1 39.7 (M:39.7)	1	6.6	1.99	1450		
729	true	ENSGALP0000027012	lysosome G-like 2 - CGNC Symbol 49435	23.3	9.6	1 88.9 (M:88.9)	1	8.5	2.65	1255		
730	true	ENSGALP0000001332	lysyl-tRNA synthetase - CGNC Symbol 602	67.8	5.8	1 745.4 (M:745.4)	16	19	7.1	167	0.91!	7
731	true	ENSGALP0000041782	M-phase phosphoprotein 8 - CGNC Symbol 12877	95.7	5.5	2 134.6 (M:134.6)	1	1.6	10.54	1041	0.54!	1
732	true	ENSGALP0000008911	Major histocompatibility complex class II beta chain BLB1 - CGNC Symbol 54366	25.3	5.8	1 319.8 (M:319.8)	6	29	4.17	498	1.43!	4
733	true	ENSGALP0000000316	major vault protein - CGNC Symbol 136	93.7	5.3	1 954.7 (M:954.7)	18	17.3	7.78	107	0.91!	8
734	true	ENSGALP0000014374	malate dehydrogenase 1 - CGNC Symbol 6725	36.5	6.9	1 581.8 (M:581.8)	10	21	6.69	253	0.66!	4
735	true	ENSGALP0000003012	malate dehydrogenase 2 - CGNC Symbol 1378	35.6	8.8	1 1651.5 (M:1651.5)	22	49.9	6.98	38	1.20!	10
736	true	ENSGALP0000003934	mannose-1-phosphate guanylyltransferase beta - Refseq NP_001280244	39.4	6.8	1 134.1 (M:134.1)	3	6.4	7.04	1046		
737	true	ENSGALP0000023961	mannosidase alpha class 1A member 1 - CGNC Symbol 11043	53.6	5.8	1 54.7 (M:54.7)	1	3.2	15.41	1399	0.57	1
738	true	ENSGALP0000010097	MAP7 domain containing 3 - CGNC Symbol 4697	81.3	8.9	1 110.1 (M:110.1)	3	3.3	4.41	1156	1.79!	1
739	true	ENSGALP0000039948	MARCKS-like 1 - CGNC Symbol 14646	21.2	4.7	1 322.5 (M:322.5)	4	24.4	8.6	492	5.26!	1
740	true	ENSGALP0000041817	marginal zone B and B1 cell specific protein - CGNC Symbol 63940	20.9	6.4	1 221.6 (M:221.6)	5	21.8	5.76	727	1.42	3
741	true	ENSGALP0000043196	marker of proliferation Ki-67 - CGNC Symbol 16321	270.7	9.5	1 705.8 (M:705.8)	10	3.8	6.4	183	0.36!	4
742	true	ENSGALP000003898	matrin 3 - CGNC Symbol 1772	100.7	5.8	1 1530.6 (M:1530.6)	29	23.7	6.35	49	0.66!	17
743	true	ENSGALP0000046487	MAU2 sister chromatid cohesion factor - CGNC Symbol 2145	72.4	7	1 120.4 (M:120.4)	3	5.1	8.28	1101		
744	true	ENSGALP0000025327	MDN1 midasin homolog (yeast) - CGNC Symbol 11734	632.3	5.4	1 369.8 (M:369.8)	8	1.6	10.37	421	0.79!	3
745	true	ENSGALP0000010367	mediator complex subunit 15 - CGNC Symbol 4845	85.9	10.1	1 103.9 (M:103.9)	2	3.7	12.01	1184	0.75!	1
746	true	ENSGALP0000017268	mediator of cell motility 1 - CGNC Symbol 8068	33.3	6.5	1 132.8 (M:132.8)	5	22.2	4.89	1054	1.11!	2
747	true	ENSGALP0000003715	mesencephalic astrocyte derived neurotrophic factor - HGNC:15461	18.8	8.8	1 112.9 (M:112.9)	2	16.2	20.64	1143		
748	true	ENSGALP0000041764	mesoderm development candidate 2 - CGNC Symbol 4821	24.5	6.9	2 63.9 (M:63.9)	2	2.7	4.38	1363	1.48	1
749	true	ENSGALP0000042113	Metallothionein - UP P68497	6.5	8.4	1 102.2 (M:102.2)	1	33.3	7.05	1193		
750	true	ENSGALP0000023519	metallothionein 3 - CGNC Symbol 56142	6.3	8.5	1 94.1 (M:94.1)	1	33.3	4.91	1234		
751	true	ENSGALP0000016118	metastasis associated 1 family member 3 - CGNC Symbol 7538	86.1	9.2	2 257.4 (M:257.4)	4	3.5	3.32	631	0.50!	1
752	true	ENSGALP0000019961	methionyl aminopeptidase 1 - CGNC Symbol 9297	39.1	7.4	2 133.4 (M:133.4)	3	14.4	12.82	1051	0.56!	1
753	true	ENSGALP0000019224	methylene tetrahydrofolate dehydrogenase (NADP+ dependent) 1 methenyltetrahydrofolate cyclohydr	100.2	8.7	1 611.4 (M:611.4)	12	13.7	5.59	227	1.09!	3
754	true	ENSGALP0000020258	methylene tetrahydrofolate dehydrogenase (NADP+ dependent) 1-like - CGNC Symbol 9427	100.9	8.3	1 158.8 (M:158.8)	4	2.5	6.9	932	1.13	2
755	true	ENSGALP0000041134	microfibrillar associated protein 1 - CGNC Symbol 6322	51.9	4.9	1 188.1 (M:188.1)	3	8.4	6.82	834	0.59!	1
756	true	ENSGALP0000021353	microsomal glutathione S-transferase 1 - CGNC Symbol 9903	17.3	9.7	1 118.3 (M:118.3)	4	21.9	3.22	1108	0.75	1
757	true	ENSGALP000005448	microsomal glutathione S-transferase 3 - CGNC Symbol 2512	17.2	9.3	1 164.7 (M:164.7)	4	12.8	1.48	911	0.53	2
758	true	ENSGALP0000030734	microtubule associated monooxygenase calponin and LIM domain containing 1 - CGNC Symbol 25636	127.9	5.1	1 213.4 (M:213.4)	3	2.5	6.98	749	0.43!	1
759	true	ENSGALP0000010754	microtubule-associated protein RP/EB family member 1 - CGNC Symbol 50961	29.1	5	1 178.4 (M:178.4)	3	21.3	5.41	874	0.55!	2
760	true	ENSGALP000000885	microtubule-associated protein tau - CGNC Symbol 389	36.3	9.7	1 79.2 (M:79.2)	1	4.3	7.45	1295		
761	true	ENSGALP0000037974	minichromosome maintenance complex binding protein - CGNC Symbol 7190	67.6	5.1	1 98.0 (M:98.0)	2	1.7	2.61	1215	0.96	1
762	true	ENSGALP0000009709	minichromosome maintenance complex component 2 - CGNC Symbol 4524	100.2	5.2	1 1274.3 (M:1274.3)	23	19.4	9.52	71	0.68!	11
763	true	ENSGALP0000026858	minichromosome maintenance complex component 3 - CGNC Symbol 12496	91.3	5.5	2 822.9 (M:822.9)	17	17.4	7.03	136	0.82!	8
764	true	ENSGALP0000042281	minichromosome maintenance complex component 3 associated protein - CGNC Symbol 3212	133.4	8.2	1 182.1 (M:182.1)	4	1.7	13.7	857	0.62!	3
765	true	ENSGALP0000021034	minichromosome maintenance complex component 4 - CGNC Symbol 9780	96.8	7	1 1114.2 (M:1114.2)	20	18.9	6.44	83	0.55!	10

766	true	ENSGALP00000020463	minichromosome maintenance complex component 5 - CGNC Symbol 9524	82.4	8.6	1 1082.6 (M:1082.6)	17	16.5	10.29	87	0.63!	7	23.34
767	true	ENSGALP00000032274	minichromosome maintenance complex component 6 - CGNC Symbol 9378	93.2	5.3	2 799.0 (M:799.0)	17	16.7	5.05	145	0.52!	8	43.75
768	true	ENSGALP00000002491	MIS12 kinetochore complex component - CGNC Symbol 1136	24.7	5.6	1 68.0 (M:68.0)	1	6.2	17.07	1339			
769	true	ENSGALP00000025726	mitochondrial antiviral signaling protein - CGNC Symbol 51863	67.6	5	1 50.5 (M:50.5)	1	2.7	9.53	1420			
770	true	ENSGALP00000008279	mitochondrial carrier 2 - CGNC Symbol 3845	33.1	9.4	1 256.0 (M:256.0)	6	19.7	6.47	635	0.67!	2	23.9
771	true	ENSGALP00000024854	mitochondrial pyruvate carrier 2 - CGNC Symbol 11506	15.1	10.1	1 72.0 (M:72.0)	1	7.5	9.02	1321	0.51	1	
772	true	ENSGALP00000016732	mitochondrial ribosomal protein S18A - CGNC Symbol 7834	21.7	10.1	1 63.6 (M:63.6)	2	13.7	9.97	1365			
773	true	ENSGALP00000002172	mitochondrial trans-2-enoyl-CoA reductase - CGNC Symbol 981	39	8.9	1 108.5 (M:108.5)	3	12.6	7.52	1165	0.47	1	
774	true	ENSGALP00000002278	mitogen-activated protein kinase 1 - CGNC Symbol 48975	37.3	6.7	1 314.9 (M:314.9)	7	19.4	7.47	506	2.25!	2	71.55
775	true	ENSGALP0000001201	mitogen-activated protein kinase 14 - CGNC Symbol 13975	41.7	5.3	1 262.1 (M:262.1)	4	11	7.9	621	0.94	3	40.93
776	true	ENSGALP00000015741	mitotic checkpoint protein BUB3 - Refseq NP_001006506	44	7.8	1 373.9 (M:373.9)	9	24	13.33	415	0.60!	5	67.89
777	true	ENSGALP00000012231	MM519 homolog cytosolic iron-sulfur assembly component - CGNC Symbol 5715	111.8	5.6	1 192.1 (M:192.1)	3	4.3	3.94	820			
778	true	ENSGALP00000013177	MOB family member 4 phoein - CGNC Symbol 53535	26	5.6	1 48.8 (M:48.8)	1	6.7	11.82	1429			
779	true	ENSGALP00000018856	MOB kinase activator 1B - CGNC Symbol 8797	25.3	6.3	2 65.5 (M:65.5)	2	5.5	1.84	1355	0.72	1	
780	true	ENSGALP00000007490	moesin - HGNC:7373	68.5	6	1 2352.8 (M:2352.8)	45	35.1	8.31	12	1.21!	18	85.45
781	true	ENSGALP00000025794	MORC family CW-type zinc finger 3 - CGNC Symbol 11977	105.2	5.4	1 100.9 (M:100.9)	3	3.2	16.92	1204	0.80!	1	
782	true	ENSGALP00000002366	Mov10 Moloney leukemia virus 10 homolog (mouse) - CGNC Symbol 51112	109.2	9	1 462.8 (M:462.8)	9	10.2	6.1	326	1.06!	2	59.48
783	true	ENSGALP00000043298	muscleblind-like splicing regulator 1 - CGNC Symbol 52321	41.6	9.2	12 139.9 (M:139.9)	4	7.2	5.95	1014	0.91	3	21.49
784	true	ENSGALP00000014557	mutS homolog 2 - CGNC Symbol 6808	95.2	5.5	1 205.8 (M:205.8)	4	3.9	7.14	775	0.57	3	23.75
785	true	ENSGALP00000038835	mutS homolog 6 - CGNC Symbol 6804	149.8	5.9	1 201.9 (M:201.9)	5	3.9	10.54	791	0.59!	1	
786	true	ENSGALP00000007833	myelin expression factor 2 - CGNC Symbol 49981	65.7	9.1	2 223.5 (M:223.5)	6	9.9	6.64	722	0.51!	3	99.14
787	true	ENSGALP00000042597	myeloid differentiation primary response 88 - CGNC Symbol 4445	33.8	5.9	2 83.7 (M:83.7)	2	5	15.97	1276	0.94!	1	
788	true	ENSGALP00000006768	myeloid-derived growth factor - CGNC Symbol 3135	18.5	5.4	1 110.3 (M:110.3)	2	5.4	6.05	1155	3.13!	1	
789	true	ENSGALP00000001480	myeloperoxidase - CGNC Symbol 50519	82.6	9.4	1 334.1 (M:334.1)	7	10.9	4.66	469	0.67!	3	18.02
790	true	ENSGALP00000006242	myopalladin - CGNC Symbol 2877	147	5.9	2 209.8 (M:209.8)	4	1.9	10.07	763	1.84!	1	
791	true	ENSGALP00000023352	myosin heavy chain 10 non-muscle - CGNC Symbol 49817	228.9	5.4	2 1579.6 (M:1579.6)	31	9.1	5.33	46	0.62!	14	84.38
792	true	ENSGALP00000020445	myosin heavy chain 9 non-muscle - CGNC Symbol 49820	226.5	5.5	11 6191.1 (M:6191.1)	97	33	5.99	1	0.79!	47	53.65
793	true	ENSGALP00000002385	myosin IF - CGNC Symbol 1089	126.1	9.2	1 144.7 (M:144.7)	4	2.6	4.1	987	0.56!	2	69.58
794	true	ENSGALP00000009037	myosin Ig - CGNC Symbol 51252	115	9	1 902.9 (M:902.9)	15	14	7.6	117	0.51!	6	52.7
795	true	ENSGALP000000040101	myosin IXB - CGNC Symbol 2718	233.3	8.3	1 462.7 (M:462.7)	4	1.6	6.22	327	0.85!	2	1.55
796	true	ENSGALP00000008730	myosin light chain 3 alkali ventricular skeletal slow - CGNC Symbol 49636	21.9	5.1	3 222.5 (M:222.5)	3	8.2	3.61	724	0.91!	1	
797	true	ENSGALP000000042167	myotrophin - Refseq NP_990217	16.1	5.1	1 34.5 (M:34.5)	1	11.5	9.42	1461	3.9	1	
798	true	ENSGALP00000016147	MYST histone acetyltransferase 2 - CGNC Symbol 52487	70.5	9	1 68.6 (M:68.6)	1	1.5	8.34	1335	0.46!	1	
799	true	ENSGALP0000015892	N(alpha)-acetyltransferase 15 Nata auxiliary subunit - CGNC Symbol 7432	95.3	6.3	2 187.8 (M:187.8)	5	3.6	6.63	836	0.81!	4	10.92
800	true	ENSGALP00000024681	N-acetylglycosaminidase - CGNC Symbol 11406	40.1	7.1	1 131.4 (M:131.4)	2	2.8	2.22	1062	0.59!	1	
801	true	ENSGALP00000037111	N-acylethanolamine acid amidase - CGNC Symbol 8761	40.4	7.1	1 39.5 (M:39.5)	1	2.2	9.29	1451			
802	true	ENSGALP00000001579	N-ethylmaleimide sensitive factor - CGNC Symbol 715	82.1	6.4	1 203.0 (M:203.0)	4	3.5	13.42	788	1.56!	1	
803	true	ENSGALP00000013516	N-ethylmaleimide-sensitive factor attachment protein beta - CGNC Symbol 6300	33.3	5.4	1 171.1 (M:171.1)	4	15.5	10.46	891	0.95!	1	
804	true	ENSGALP00000018418	N-glycanase 1 - CGNC Symbol 8593	74	8.1	1 101.0 (M:101.0)	2	4	7.64	1203			
805	true	ENSGALP0000001254	N-myristoyltransferase 1 - CGNC Symbol 561	56.8	8.7	1 66.6 (M:66.6)	1	3.8	7.87	1351			
806	true	ENSGALP00000041318	NADH dehydrogenase - Refseq NP_001289036	9.5	9.6	1 84.3 (M:84.3)	3	22	4.2	1269	0.84	2	49.46
807	true	ENSGALP00000013999	NADH:ubiquinone oxidoreductase core subunit S1 - CGNC Symbol 6532	79.5	6.5	1 286.6 (M:286.6)	5	6.7	7.2	563	0.89!	3	84.38
808	true	ENSGALP00000042023	NADH:ubiquinone oxidoreductase core subunit S2 - CGNC Symbol 66024	14.1	7.8	1 84.8 (M:84.8)	2	9.4	7.51	1268	1.05	1	
809	true	ENSGALP00000030898	NADH:ubiquinone oxidoreductase subunit A10 - CGNC Symbol 3165	41.4	5.9	1 57.9 (M:57.9)	2	11.1	8.32	1385			
810	true	ENSGALP00000018456	NADH:ubiquinone oxidoreductase subunit A12 - CGNC Symbol 8606	16.9	9.8	1 108.9 (M:108.9)	2	24	3.44	1162	0.41!	1	
811	true	ENSGALP00000014321	NADH:ubiquinone oxidoreductase subunit A5 - CGNC Symbol 50588	13.4	6.6	1 80.0 (M:80.0)	2	8.6	13.01	1289	0.65!	1	
812	true	ENSGALP00000034255	NADH:ubiquinone oxidoreductase subunit A8 - CGNC Symbol 929	20.1	8.4	1 100.7 (M:100.7)	2	6.4	12.07	1206	2.26	1	
813	true	ENSGALP00000008764	NADH:ubiquinone oxidoreductase subunit B10 - CGNC Symbol 4071	20.5	6	1 144.6 (M:144.6)	4	16.6	2.29	988	0.97	3	43.79
814	true	ENSGALP00000026301	NADH:ubiquinone oxidoreductase subunit B9 - CGNC Symbol 12221	21.9	8.9	1 135.1 (M:135.1)	4	15.6	6.5	1038	1.03!	2	18.67
815	true	ENSGALP00000005729	NADH:ubiquinone oxidoreductase subunit S5 - CGNC Symbol 2647	12.6	8.4	1 204.6 (M:204.6)	2	17	3.6	780	0.48	1	
816	true	ENSGALP00000021519	NADH:ubiquinone oxidoreductase subunit S6 - CGNC Symbol 9959	14	9.2	1 38.9 (M:38.9)	1	11.7	16.9	1452			
817	true	ENSGALP00000017172	nardilysin convertase - CGNC Symbol 8022	126.8	5	1 108.9 (M:108.9)	3	2.3	16.96	1163	1.15	1	
818	true	ENSGALP00000008356	NEDD8 activating enzyme E1 subunit 1 - CGNC Symbol 50078	60.4	5.4	1 201.8 (M:201.8)	2	3.2	5.85	792	0.47!	1	
819	true	ENSGALP00000027504	neurobeachin - CGNC Symbol 12814	330.2	5.8	1 75.2 (M:75.2)	2	0.8	14.1	1309			
820	true	ENSGALP00000005033	NHP2 ribonucleoprotein - CGNC Symbol 17192	16.6	8.2	1 181.8 (M:181.8)	4	29.1	8.08	859	0.8	3	5.62
821	true	ENSGALP00000040722	nicotinamide nucleotide adenylyltransferase 1 - HGNC:17877	32.2	8.8	1 51.7 (M:51.7)	1	2.8	9.12	1415	0.95!	1	
822	true	ENSGALP000000023944	nicotinamide nucleotide transhydrogenase - CGNC Symbol 11035	113.7	7	1 194.2 (M:194.2)	5	5.4	8.88	816	0.59!	2	58.12
823	true	ENSGALP00000001685	NIMA-related kinase 6 - CGNC Symbol 759	36.3	7.2	1 63.3 (M:63.3)	2	3.8	10.27	1368	1.57	1	
824	true	ENSGALP00000024244	ninjurin 1 - CGNC Symbol 3885	16.4	6.8	1 32.9 (M:32.9)	1	7.3	5.4	1469			

825	true	ENSGALP00000034078	NME/NM23 nucleoside diphosphate kinase 2 - CGNC Symbol 49549	17.3	7.7	4 1145.6 (M:1145.6)	18	73.9	4.14	80	1.13!		10	62.45
826	true	ENSGALP00000012689	Nmra-like family domain containing 1 - CGNC Symbol 5919	32.7	7.8	1 40.6 (M:40.6)	1	3.7	2.58	1447	0.99		1	
827	true	ENSGALP00000040638	no description available	164.1	6.1	1 631.0 (M:631.0)	13	9.3	4.86	212	0.53!		7	30.56
828	true	ENSGALP00000015665	no description available	32.6	5.7	3 614.1 (M:614.1)	11	39.8	6.81	226	0.16!		3	35.48
829	true	ENSGALP00000030678	no description available	68.2	6.5	1 276.8 (M:276.8)	5	5.6	5.27	586	0.81!		2	18.27
830	true	ENSGALP00000039237	no description available	182.2	5.8	1 159.9 (M:159.9)	5	3.6	10.02	928	0.75!		2	46.46
831	true	ENSGALP00000021785	no description available	27.8	8.8	1 127.9 (M:127.9)	3	11.1	3.89	1071	0.36!		1	
832	true	ENSGALP00000033554	no description available	38.2	9.1	1 93.5 (M:93.5)	1	6.5	4.95	1237				
833	true	ENSGALP00000041100	no description available	16.8	12.3	1 87.5 (M:87.5)	3	13.1	4.16	1263	0.44		2	44.16
834	true	ENSGALP00000009052	no description available	122.5	5.8	1 63.8 (M:63.8)	1	1.8	4.47	1364				
835	true	ENSGALP00000008824	non-POU domain containing octamer-binding - CGNC Symbol 4102	54	8.9	1 1344.3 (M:1344.3)	24	37	5.37	64	0.54!		10	38.62
836	true	ENSGALP00000023274	non-SMC condensin I complex subunit D2 - CGNC Symbol 50724	157.6	5.5	1 327.6 (M:327.6)	7	5.9	5.66	481	0.45!		2	26.78
837	true	ENSGALP00000023257	non-SMC condensin I complex subunit G - CGNC Symbol 10729	117.3	5.4	1 105.6 (M:105.6)	2	2.5	9.32	1173				
838	true	ENSGALP00000023281	NOP2 nucleolar protein - CGNC Symbol 10744	71.5	8.6	1 69.0 (M:69.0)	2	3	12.41	1334				
839	true	ENSGALP00000021294	NOP2/Sun RNA methyltransferase family member 2 - CGNC Symbol 9878	90.5	6.3	1 385.1 (M:385.1)	4	7.4	7.03	403	0.43!		2	32.02
840	true	ENSGALP00000023364	NOP56 ribonucleoprotein - CGNC Symbol 10777	52.2	9.3	1 430.6 (M:430.6)	8	10.1	2.3	353	0.41		4	35.58
841	true	ENSGALP00000013761	NOP58 ribonucleoprotein - CGNC Symbol 52126	61.6	8.8	1 135.3 (M:135.3)	4	8.7	9.76	1037	0.78!		3	110.71
842	true	ENSGALP00000009964	NSFL1 (p97) cofactor (p47) - CGNC Symbol 50955	40.6	5	2 454.9 (M:454.9)	8	24.7	8.56	335	0.69!		4	21.25
843	true	ENSGALP00000016660	nuclear autoantigenic sperm protein (histone-binding) - CGNC Symbol 7802	80.2	4.4	1 274.6 (M:274.6)	6	7.5	5	592	0.68!		2	6.75
844	true	ENSGALP00000003250	nuclear cap binding protein subunit 1 - CGNC Symbol 53067	92.5	5.9	1 92.7 (M:92.7)	2	1.5	0.8	1239	0.96		1	
845	true	ENSGALP0000001002	nuclear casein kinase and cyclin-dependent kinase substrate 1 - CGNC Symbol 448	32	5.1	1 268.2 (M:268.2)	4	7	2.31	609	0.92		2	11.49
846	true	ENSGALP00000012917	nuclear factor of activated T-cells cytoplasmic calcineurin-dependent 2 - CGNC Symbol 6025	101.2	6.7	1 200.2 (M:200.2)	2	3.9	5.81	800	0.51!		1	
847	true	ENSGALP00000043213	nuclear mitotic apparatus protein 1 - CGNC Symbol 859	241.2	5.9	2 603.3 (M:603.3)	12	6.2	10.87	236	0.84!		3	16.58
848	true	ENSGALP00000031109	nuclear receptor coactivator 7 - CGNC Symbol 51536	107.9	5.4	1 142.7 (M:142.7)	3	5	8.1	999	0.61!		1	
849	true	ENSGALP00000004924	nuclear receptor corepressor 2 - CGNC Symbol 2259	274.4	8	1 237.8 (M:237.8)	7	2.8	9.78	673	0.88!		3	94.73
850	true	ENSGALP00000038782	nucleobindin 2 - CGNC Symbol 51883	53.8	5	1 227.1 (M:227.1)	5	7.7	8.35	707	0.98!		2	21.81
851	true	ENSGALP00000026477	nucleolar protein 10 - CGNC Symbol 12312	80.4	8.6	1 137.5 (M:137.5)	4	5.4	10.23	1024	0.72!		1	
852	true	ENSGALP00000030436	nucleolar protein 7 - CGNC Symbol 9631	25.4	10.2	1 108.4 (M:108.4)	3	13.7	0.78	1166	0.60!		1	
853	true	ENSGALP00000043475	nucleolar protein 9 - CGNC Symbol 55846	36	6.4	1 68.0 (M:68.0)	1	7.5	6	1340	0.36		1	
854	true	ENSGALP00000019016	nucleolar protein interacting with the FHA domain of MKI67 - CGNC Symbol 8852	31.4	10.3	1 199.0 (M:199.0)	3	10.1	7.37	803	0.73		2	18.14
855	true	ENSGALP00000032625	nucleolin - CGNC Symbol 5823	67.2	4.7	2 1596.9 (M:1596.9)	25	26	8.99	44	0.91!		12	87.02
856	true	ENSGALP00000003431	nucleophosmin (nucleolar phosphoprotein B23 numatrin) - CGNC Symbol 49698	30.3	4.7	1 967.9 (M:967.9)	14	28.7	8.57	103	0.92!		6	41.36
857	true	ENSGALP00000020737	nucleoporin 153kDa - CGNC Symbol 9650	146.7	8.6	1 200.5 (M:200.5)	5	3.9	12.02	799	1.25!		2	20.11
858	true	ENSGALP00000005832	nucleoporin 155kDa - CGNC Symbol 2697	154.7	5.8	1 220.1 (M:220.1)	7	4.7	2.42	734	0.48!		3	44.21
859	true	ENSGALP0000000613	nucleoporin 160kDa - CGNC Symbol 54143	100.1	5.3	1 202.6 (M:202.6)	4	3.9	4.76	789	0.56!		2	7.17
860	true	ENSGALP00000019040	nucleoporin 205kDa - CGNC Symbol 8864	228.2	5.7	1 299.4 (M:299.4)	8	3.8	12.79	534	0.99!		3	31.16
861	true	ENSGALP00000008128	nucleoporin 210kDa - CGNC Symbol 3777	195.4	6.1	1 692.0 (M:692.0)	14	7.2	7.73	190	1.03!		5	39.69
862	true	ENSGALP00000017873	nucleoporin 54kDa - CGNC Symbol 8743	58.8	6.3	1 53.8 (M:53.8)	1	3.2	3.31	1405				
863	true	ENSGALP00000027595	nucleoporin 58kDa - CGNC Symbol 12853	60.5	9.4	1 155.0 (M:155.0)	3	4.2	4.34	952	0.51!		1	
864	true	ENSGALP00000007743	nucleoporin 62kDa - CGNC Symbol 3605	57.4	5.5	1 75.2 (M:75.2)	2	3	2.11	1310	0.55		1	
865	true	ENSGALP00000004745	nucleoporin 93kDa - CGNC Symbol 2176	93.5	5.9	1 318.6 (M:318.6)	8	10.3	8.34	502	0.61!		2	24.66
866	true	ENSGALP00000022023	nucleoporin 98kDa - CGNC Symbol 10169	195.3	5.7	1 239.8 (M:239.8)	7	2.7	11.32	666	2.11!		2	7.39
867	true	ENSGALP00000017923	nucleotide-triphosphatase cancer-related - CGNC Symbol 8371	20.8	9.2	1 94.7 (M:94.7)	2	6.8	20.67	1232	1.01		1	
868	true	ENSGALP00000016623	nucleosome assembly protein 1-like 1 - CGNC Symbol 50609	45.3	4.3	1 521.1 (M:521.1)	10	16.5	7.86	291	0.48!		5	71.57
869	true	ENSGALP00000010387	nucleosome assembly protein 1-like 4 - CGNC Symbol 51885	42.9	4.5	1 368.8 (M:368.8)	8	10.1	13.28	424	0.44!		4	53.35
870	true	ENSGALP00000011700	nucleotide binding protein 1 - CGNC Symbol 5471	34.5	5.2	1 181.7 (M:181.7)	2	11.1	3.12	861	0.64!		1	
871	true	ENSGALP000000025900	NudC domain containing 1 - HGNC:24306	77.9	6.2	1 113.6 (M:113.6)	3	3.5	5.86	1139	0.54!		1	
872	true	ENSGALP00000022856	NudC domain containing 3 - CGNC Symbol 10553	39.7	5	1 33.3 (M:33.3)	1	4.8	3.71	1467				
873	true	ENSGALP00000001315	nudC nuclear distribution protein - CGNC Symbol 591	39.2	5.3	1 212.9 (M:212.9)	6	17.3	6.53	751	1.28!		2	30.89
874	true	ENSGALP00000041772	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1 - CGNC Symbol 20168	33.8	5.7	1 981.1 (M:981.1)	18	35.6	4.99	100	0.74!		11	56.34
875	true	ENSGALP00000004866	nudix hydrolase 21 - CGNC Symbol 66135	26.4	8.9	1 219.8 (M:219.8)	4	24.9	10.55	735	0.36!		2	79.33
876	true	ENSGALP00000028424	O-6-methylguanine-DNA methyltransferase - HGNC:7059	28.1	9.4	1 108.9 (M:108.9)	3	12.8	8.19	1161	1.14!		2	19.61
877	true	ENSGALP00000008699	O-linked N-acetylglucosamine (GlcNAc) transferase - CGNC Symbol 4043	18.5	5.6	1 66.3 (M:66.3)	2	19.2	7.47	1353				
878	true	ENSGALP00000015171	Obg-like ATPase 1 - CGNC Symbol 7087	44.8	8.1	1 140.5 (M:140.5)	3	11.1	4.55	1011				
879	true	ENSGALP00000037866	ornithine aminotransferase - CGNC Symbol 52788	48.3	7.1	1 148.6 (M:148.6)	3	9.3	10.65	974				
880	true	ENSGALP00000028084	osteoclast stimulating factor 1 - CGNC Symbol 13080	23.6	5.3	1 216.9 (M:216.9)	5	12.6	2.76	744	1.39!		2	11.61
881	true	ENSGALP00000041974	OTU deubiquitinase ubiquitin aldehyde binding 1 - CGNC Symbol 58812	38.5	5.8	1 737.8 (M:737.8)	14	36.3	6.81	169	0.85!		6	48.71
882	true	ENSGALP00000009933	outer mitochondrial membrane cytochrome b5 - CGNC Symbol 50102	16.2	5	1 282.9 (M:282.9)	7	27.8	7.51	576	0.77!		3	14.27
883	true	ENSGALP00000028857	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) - CGNC Symbol 52787	115.1	6.6	1 270.6 (M:270.6)	6	4.4	4.67	603	1.05!		2	0.76

884	true	ENSGALP0000012564	oxysterol binding protein 2 - CGNC Symbol 5865	89.5	6.7	1 86.3 (M:86.3)	4	6.8	17.05	1264	0.84	2	51.28
885	true	ENSGALP0000019672	oxysterol binding protein-like 11 - CGNC Symbol 9142	78.7	6.2	2 170.5 (M:170.5)	5	5.2	10.01	895		3	23.79
886	true	ENSGALP0000010358	p21 protein (Cdc42/Rac)-activated kinase 2 - CGNC Symbol 4842	57.5	5.6	2 418.3 (M:418.3)	8	18	10.39	367	0.35!	1	
887	true	ENSGALP0000042900	PAF1 homolog Paf1/RNA polymerase II complex component - CGNC Symbol 64966	58.9	4.7	1 130.9 (M:130.9)	2	4	2.81	1065	0.57!	2	
888	true	ENSGALP000006259	palmitoyl-protein thioesterase 1 - CGNC Symbol 2887	33.8	7.1	1 224.2 (M:224.2)	4	7	2.76	719	0.93!	2	36.77
889	true	ENSGALP0000035658	paraspeckle component 1 - CGNC Symbol 50884	58.4	6.3	1 821.1 (M:821.1)	15	18.5	6.21	139	0.62!	8	32.45
890	true	ENSGALP0000041756	Parkinsonism associated deglycase - HGNC:16369	19.9	6.3	1 394.7 (M:394.7)	9	41.3	5.25	395	0.89!	3	24.18
891	true	ENSGALP0000007472	PDGFA associated protein 1 - CGNC Symbol 3481	20.6	7.8	1 124.3 (M:124.3)	4	20.6	7.21	1082	1.76!	2	11.54
892	true	ENSGALP0000023059	PDSS regulator of cohesion maintenance homolog A (<i>S. cerevisiae</i>) - CGNC Symbol 10643	150	8	1 792.0 (M:792.0)	18	11.7	6.3	149	0.73!	6	86.69
893	true	ENSGALP0000027519	PDSS regulator of cohesion maintenance homolog B (<i>S. cerevisiae</i>) - CGNC Symbol 12819	164.6	8.5	1 727.1 (M:727.1)	17	10.9	12.31	175	0.54!	7	38.45
894	true	ENSGALP000005084	penta-EF-hand domain containing 1 - CGNC Symbol 2337	24.3	5.4	1 95.7 (M:95.7)	3	8.5	5.06	1228	0.46	1	
895	true	ENSGALP000007493	pentatricopeptide repeat domain 1 - CGNC Symbol 3492	83.8	8.6	1 251.1 (M:251.1)	3	3.1	6.26	646	0.74!	2	33.94
896	true	ENSGALP0000007819	peptidase D - CGNC Symbol 3636	55.3	6.2	1 505.4 (M:505.4)	10	22.1	8.65	301	2.64!	4	126.1
897	true	ENSGALP000003014	peptidase mitochondrial processing alpha subunit - CGNC Symbol 1379	57.5	6.7	1 111.6 (M:111.6)	2	3.5	3.9	1147			
898	true	ENSGALP0000041690	peptidyl-prolyl cis-trans isomerase A - Refseq NP_001159798	15.9	9	1 1598.8 (M:1598.8)	23	65.3	6.45	43	1.02!	12	55.4
899	true	ENSGALP000006157	peptidyl-prolyl cis/trans isomerase NIMA-interacting 4 - CGNC Symbol 2839	13.2	9.7	1 198.3 (M:198.3)	3	16	12.54	804	1.09!	2	44.19
900	true	ENSGALP0000003455	peptidylprolyl isomerase B (cyclophilin B) - CGNC Symbol 1580	16.2	9.2	1 580.6 (M:580.6)	9	31.3	12.28	255	2.86!	2	74.49
901	true	ENSGALP0000015366	peptidylprolyl isomerase D - CGNC Symbol 7186	40.5	6	1 169.9 (M:169.9)	4	10	4.75	899	1.23!	2	15.05
902	true	ENSGALP000007666	peptidylprolyl isomerase F - CGNC Symbol 52036	21.7	9.2	1 138.8 (M:138.8)	2	21.6	20.96	1019			
903	true	ENSGALP0000015979	peptidylprolyl isomerase G (cyclophilin G) - CGNC Symbol 7474	88.1	10.6	1 146.1 (M:146.1)	4	4.5	13.4	982	0.21!	1	
904	true	ENSGALP0000016629	peroxiredoxin 1 - CGNC Symbol 7794	22.3	8.2	1 904.3 (M:904.3)	17	59.3	5.08	116	0.77!	9	38.48
905	true	ENSGALP0000015246	peroxiredoxin 3 - CGNC Symbol 7123	28	8.8	1 565.5 (M:565.5)	8	18.7	4.63	261	0.68!	4	16.36
906	true	ENSGALP0000026337	peroxiredoxin 4 - CGNC Symbol 12239	32.1	8.6	1 532.0 (M:532.0)	9	21.5	3.47	284	1.13!	2	55.26
907	true	ENSGALP0000004817	peroxiredoxin 6 - CGNC Symbol 2214	25.1	6	1 594.4 (M:594.4)	11	33	9.16	241	0.84!	5	28.2
908	true	ENSGALP0000012605	pescadillo ribosomal biogenesis factor 1 - CGNC Symbol 5881	65	6.3	1 194.5 (M:194.5)	6	7.2	3.05	813	0.77!	3	30.49
909	true	ENSGALP0000008273	PHD finger protein 2 - CGNC Symbol 3843	118.3	9.3	1 157.2 (M:157.2)	5	5.5	10.55	938	1.26!	2	11.73
910	true	ENSGALP0000019471	PHD finger protein 5A - CGNC Symbol 9062	13.1	8.4	1 331.2 (M:331.2)	6	45.3	5.93	473	0.60!	3	71.48
911	true	ENSGALP0000009819	PHD finger protein 6 - CGNC Symbol 4572	41	8.9	1 41.3 (M:41.3)	1	3.8	6.06	1443			
912	true	ENSGALP0000008398	phenylalanyl-tRNA synthetase beta subunit - CGNC Symbol 3896	65.9	6	1 310.6 (M:310.6)	7	7	11.59	516	1.00!	3	31.83
913	true	ENSGALP0000019561	phosphatidylethanolamine binding protein 1 - CGNC Symbol 5589	20.9	7	1 608.1 (M:608.1)	11	51.9	10.42	229	0.43!	2	30.22
914	true	ENSGALP0000004385	phosphatidylinositol transfer protein alpha - CGNC Symbol 63402	31.8	5.8	2 74.6 (M:74.6)	2	5.9	16.16	1312	0.91!	1	
915	true	ENSGALP0000004061	phosphatidylinositol-4 5-bisphosphate 3-kinase catalytic subunit delta - CGNC Symbol 1859	120.2	6.9	1 82.9 (M:82.9)	2	2.2	10.5	1280	1.12!	1	
916	true	ENSGALP0000042061	phosphatidylinositol-5-phosphate 4-kinase type II alpha - CGNC Symbol 5959	38.4	5.8	2 270.1 (M:270.1)	6	17.1	10.21	606	0.55!	4	66.39
917	true	ENSGALP0000009004	phosphodiesterase 12 - CGNC Symbol 50135	64.4	6.9	1 112.9 (M:112.9)	2	4.5	3.79	1144	0.38!	2	2.85
918	true	ENSGALP0000011232	phosphofructokinase platelet - CGNC Symbol 53359	61.2	6.3	1 909.4 (M:909.4)	15	22.7	8.72	114	1.90!	5	48.97
919	true	ENSGALP0000017926	phosphoglucomutase 1 - CGNC Symbol 8372	66.4	9	1 214.3 (M:214.3)	6	6.3	4.25	748	0.65	4	78.73
920	true	ENSGALP0000000666	phosphoglucomutase 2 - CGNC Symbol 52790	67.9	6.9	1 406.4 (M:406.4)	11	11.5	5.24	379	0.72!	5	17.5
921	true	ENSGALP0000004417	phosphogluconate dehydrogenase - CGNC Symbol 2017	53.3	6.5	1 543.1 (M:543.1)	7	12	4.82	272	1.96!	4	19.39
922	true	ENSGALP0000012878	phosphoglycerate kinase 1 - CGNC Symbol 49503	44.6	8.3	1 1227.2 (M:1227.2)	18	32.4	6.88	73	1.65!	9	49.04
923	true	ENSGALP0000038677	phosphoglycerate mutase 1 (brain) - CGNC Symbol 53524	23.7	7.1	1 887.2 (M:887.2)	18	51.4	5.43	124	1.01!	6	31.85
924	true	ENSGALP0000033594	phosphohistidine phosphatase 1 - CGNC Symbol 14487	13.9	5.7	1 144.5 (M:144.5)	2	15.1	10.66	989	0.72	1	
925	true	ENSGALP0000008107	phospholipase A2 group IVA - CGNC Symbol 3767	84.9	5.1	1 65.0 (M:65.0)	1	2	14.03	1357			
926	true	ENSGALP0000005944	phospholipase C gamma 1 - CGNC Symbol 50935	146.9	5.7	1 411.4 (M:411.4)	12	10	6.57	372	0.79!	7	29.95
927	true	ENSGALP000007780	phosphopantethenoylcysteine synthetase - CGNC Symbol 66161	35.2	6.6	1 399.4 (M:399.4)	7	19.7	7	390	0.74!	3	19.2
928	true	ENSGALP000007837	phosphoribosyl pyrophosphate synthetase 1 - CGNC Symbol 51649	35.4	6.4	2 428.1 (M:428.1)	9	21.4	6.04	355	0.81!	4	50.98
929	true	ENSGALP000008105	phosphoribosyl pyrophosphate synthetase-associated protein 2 - CGNC Symbol 50275	40.7	6.7	2 651.3 (M:651.3)	13	26.8	6.85	208	0.86!	6	31.92
930	true	ENSGALP0000022269	phosphoribosylaminoimidazole carboxylase phosphoribosylaminoimidazolesuccinocarboxamide synthetase - CGNC Symbol 4811	48.1	8.5	1 361.1 (M:361.1)	6	9.9	6.2	431	0.86	4	48.28
931	true	ENSGALP0000035973	phosphoribosylglycinamide formyltransferase phosphoribosylglycinamide synthetase phosphoribosyla	106.5	7.5	1 361.4 (M:361.4)	8	7.9	7.48	430	0.53!	3	26.25
932	true	ENSGALP0000020169	phosphorylase glycogen liver - CGNC Symbol 49139	87.4	5.6	1 380.5 (M:380.5)	6	5.5	10.06	409	1.01!	3	5.9
933	true	ENSGALP0000014828	PIT54 protein precursor - Refseq NP_997063	54.8	4.6	1 249.1 (M:249.1)	4	9.1	4.59	651			
934	true	ENSGALP0000011372	pitrilysin metallopeptidase 1 - CGNC Symbol 5310	117.2	6.5	1 120.1 (M:120.1)	4	4.4	10.96	1102	2.32!	1	
935	true	ENSGALP0000006818	plasminogen - CGNC Symbol 51506	90.7	7.9	1 55.2 (M:55.2)	1	1.5	4.73	1397			
936	true	ENSGALP0000009354	platelet activating factor acetylhydrolase 1b regulatory subunit 1 - CGNC Symbol 4356	46.6	7	1 351.2 (M:351.2)	5	10.7	5.08	447	0.95!	2	34.24
937	true	ENSGALP0000014229	pleckstrin - CGNC Symbol 6647	40.3	8.7	1 254.5 (M:254.5)	8	13	2.25	639	0.56!	3	44.04
938	true	ENSGALP0000015051	pleiotropic regulator 1 - CGNC Symbol 7032	57.1	9	1 126.4 (M:126.4)	3	5.4	13.07	1074	0.77!	1	
939	true	ENSGALP0000015000	poly (ADP-ribose) polymerase 1 - CGNC Symbol 7010	103.7	8.8	2 750.2 (M:750.2)	14	11.8	9.5	164	0.76!	6	47.68
940	true	ENSGALP0000019695	poly (ADP-ribose) polymerase family member 14 - CGNC Symbol 9152	187.2	6.1	1 228.3 (M:228.3)	5	3.4	6.31	702	0.60!	2	44.21
941	true	ENSGALP0000023288	poly(A) binding protein cytoplasmic 1 - CGNC Symbol 54111	63.7	9.6	1 814.0 (M:814.0)	17	20.2	6.03	141	1.16!	8	39.27
942	true	ENSGALP000006555	poly(A) binding protein cytoplasmic 1-like - CGNC Symbol 3026	70.1	9.5	1 330.1 (M:330.1)	5	6.2	7.5	475	0.51!	2	48.21

943	true	ENSGALP00000006018	poly(A) binding protein cytoplasmic 4 (inducible form) - CGNC Symbol 2781	70.1	9.6	1 660.0 (M:660.0)	10	12.3	8.75	203 1.27!	4	28.3
944	true	ENSGALP00000023942	poly(A) binding protein interacting protein 1 - CGNC Symbol 53015	52.3	4.6	1 95.8 (M:95.8)	2	5.9	2.41	1227 1.32!	1	
945	true	ENSGALP0000022772	poly(U) binding splicing factor 60KDa - CGNC Symbol 52777	50.3	5.2	1 438.6 (M:438.6)	7	13.3	4.51	346 0.61!	3	57.26
946	true	ENSGALP0000035738	poly(U) binding splicing factor 60KDa - CGNC Symbol 52777	38.9	8.5	1 379.1 (M:379.1)	5	14.8	7.21	411 0.40!	2	6.93
947	true	ENSGALP0000005619	polyamine oxidase (exo-N4-amino) - CGNC Symbol 65340	54.9	5	1 59.0 (M:59.0)	1	2.4	4.16	1380 0.29	1	
948	true	ENSGALP0000039553	polymerase (DNA directed) epsilon 3 accessory subunit - CGNC Symbol 6738	16.3	4.6	1 66.2 (M:66.2)	2	24.5	18.61	1354 1.59	1	
949	true	ENSGALP0000005963	polymerase (DNA) beta - CGNC Symbol 2752	38.5	8.9	1 51.1 (M:51.1)	1	4.5	21.67	1418		
950	true	ENSGALP0000016829	polymerase (RNA) I subunit C - CGNC Symbol 7876	40	5.4	1 50.0 (M:50.0)	1	5.1	7.74	1424		
951	true	ENSGALP0000037170	polymerase (RNA) II (DNA directed) polypeptide B 140kDa - CGNC Symbol 8655	133.7	6.5	1 426.5 (M:426.5)	11	9.3	7.71	358 0.66!	5	18.78
952	true	ENSGALP0000024243	polymerase (RNA) II subunit I - HGNC:9196	14.4	5	1 158.4 (M:158.4)	4	31.2	11.81	934 2.52!	1	
953	true	ENSGALP0000003035	polypyrimidine tract binding protein 1 - CGNC Symbol 1388	60	9.3	1 1049.0 (M:1049.0)	16	26.3	6.08	94 0.61!	8	34.57
954	true	ENSGALP0000008892	polypyrimidine tract binding protein 2 - CGNC Symbol 52202	64.7	8.8	1 114.7 (M:114.7)	2	5.8	7.91	1129		
955	true	ENSGALP0000001105	potassium voltage-gated channel shaker-related subfamily beta member 2 - CGNC Symbol 606	38.6	9	1 64.3 (M:64.3)	2	5.5	16.74	1360 0.41	1	
956	true	ENSGALP0000001788	potassium voltage-gated channel subfamily J member 5 - HGNC:6266	47.8	5	1 29.8 (M:29.8)	1	3.3	22.28	1473 0.73	1	
957	true	ENSGALP0000039818	pre-mRNA processing factor 3 - CGNC Symbol 52857	77.3	9.5	1 59.8 (M:59.8)	2	4.8	4.52	1374		
958	true	ENSGALP0000003060	pre-mRNA processing factor 38B - CGNC Symbol 1397	64.9	10.6	1 222.6 (M:222.6)	6	9.3	7.3	723 0.49!	2	11.75
959	true	ENSGALP0000020349	pre-mRNA processing factor 39 - HGNC:20314	81	4.9	1 337.0 (M:337.0)	7	10.4	8.19	464 0.64!	3	6.92
960	true	ENSGALP0000014372	pre-mRNA processing factor 4 - CGNC Symbol 6724	59.9	8.3	1 239.2 (M:239.2)	6	13.8	3.05	668 0.96!	1	
961	true	ENSGALP0000020874	pre-mRNA processing factor 4B - CGNC Symbol 9712	126.7	10.3	1 161.8 (M:161.8)	2	2.5	4.34	921 1.00!	1	
962	true	ENSGALP0000009642	pre-mRNA processing factor 6 - CGNC Symbol 4493	106.7	8.2	1 212.8 (M:212.8)	3	4.3	5.25	753 1.15!	2	5.86
963	true	ENSGALP0000004641	pre-mRNA processing factor 8 - CGNC Symbol 2126	273.5	8.9	1 965.9 (M:965.9)	22	9.2	7.12	104 0.70!	10	52.73
964	true	ENSGALP0000022525	pre-mRNA-processing factor 19 - Refseq NP_001034420	40.5	6.3	1 148.0 (M:148.0)	3	8.2	8.57	976 0.55!	2	29.23
965	true	ENSGALP0000026194	primase (DNA) subunit 2 - CGNC Symbol 12170	58.7	8.5	1 119.4 (M:119.4)	2	3.5	3.84	1106 0.55	1	
966	true	ENSGALP0000038130	profilin-2 - Refseq NP_001073228	10.3	9	1 238.6 (M:238.6)	5	38.5	1.58	671 1.17!	2	14.2
967	true	ENSGALP0000016583	progesterone receptor membrane component 2 - CGNC Symbol 7765	21.6	5.2	1 263.6 (M:263.6)	4	20	4.52	617 0.64!	2	86.65
968	true	ENSGALP0000013431	programmed cell death 11 - CGNC Symbol 6260	206	8.8	1 211.9 (M:211.9)	4	3.3	7.61	757		
969	true	ENSGALP0000007391	programmed cell death 5 - CGNC Symbol 3442	14.2	5.5	1 224.2 (M:224.2)	5	27	14.11	717 0.79	1	
970	true	ENSGALP0000021816	programmed cell death 6 - CGNC Symbol 10082	21.6	5.4	1 134.2 (M:134.2)	4	16	18.68	1044 0.72!	2	15.08
971	true	ENSGALP0000019634	programmed cell death 6 interacting protein - CGNC Symbol 9128	97.3	6	1 363.1 (M:363.1)	7	8	5.25	426 0.55!	4	52.46
972	true	ENSGALP0000001750	prohibitin - CGNC Symbol 51144	29.9	5.6	2 274.0 (M:274.0)	8	17.3	12.89	596 0.67	4	30.51
973	true	ENSGALP0000023446	prohibitin 2 - CGNC Symbol 10814	30.6	9.8	1 512.2 (M:512.2)	8	24.5	9.53	296 0.84!	4	26.71
974	true	ENSGALP0000000224	proliferating cell nuclear antigen - CGNC Symbol 92	28.9	4.6	1 574.4 (M:574.4)	14	29	5.89	256 1.14!	6	30.58
975	true	ENSGALP0000009605	proliferation-associated 2G4 38kDa - CGNC Symbol 4474	38.1	8.1	1 681.0 (M:681.0)	14	27.6	9.91	194 1.02!	5	60.36
976	true	ENSGALP0000004889	proline synthetase co-transcribed homolog (bacterial) - CGNC Symbol 2245	30.1	8.4	1 214.4 (M:214.4)	5	13	7.68	747 0.60!	2	54.84
977	true	ENSGALP0000011689	prolyl 4-hydroxylase beta polypeptide - CGNC Symbol 5464	55.8	4.8	1 435.4 (M:435.4)	8	10.6	6.02	349 0.85!	3	45.99
978	true	ENSGALP0000024803	prolyl endopeptidase - CGNC Symbol 11476	80.8	5.7	1 629.1 (M:629.1)	11	13.2	5.6	214 0.84!	4	26.95
979	true	ENSGALP00000027828	prolylcarboxypeptidase (angiotensinase C) - CGNC Symbol 12960	54.1	5.8	1 114.9 (M:114.9)	3	4.4	8.26	1128 0.40!	1	
980	true	ENSGALP0000025278	prostaglandin reductase 1 - CGNC Symbol 11711	35.9	8.8	1 118.7 (M:118.7)	2	6.7	11.2	1107 0.69	2	68.81
981	true	ENSGALP0000043088	proteasome (prosome macropain) 26S subunit non-ATPase 4 - CGNC Symbol 59257	39.8	4.7	2 156.5 (M:156.5)	3	8.9	3.71	942 0.63!	1	
982	true	ENSGALP0000029711	proteasome (prosome macropain) assembly chaperone 1 - CGNC Symbol 11998	31.5	4.9	1 38.0 (M:38.0)	1	4.6	11.58	1456		
983	true	ENSGALP000001655	proteasome (prosome macropain) subunit beta type 7 - CGNC Symbol 49143	28.1	6	1 155.4 (M:155.4)	3	5.4	8.79	947 1.37!	1	
984	true	ENSGALP0000017347	proteasome 26S subunit ATPase 1 - CGNC Symbol 8111	47.5	5.8	1 121.7 (M:121.7)	5	13.5	12.14	1095 0.48!	3	55.49
985	true	ENSGALP0000037708	proteasome 26S subunit ATPase 3 - CGNC Symbol 6143	47.2	5.1	1 183.9 (M:183.9)	4	14.2	6.95	849 0.99!	1	
986	true	ENSGALP0000036405	proteasome 26S subunit ATPase 6 - CGNC Symbol 9424	44.1	6.7	2 175.2 (M:175.2)	5	15.7	11.89	882 1.1	4	68.47
987	true	ENSGALP0000012405	proteasome 26S subunit non-ATPase 1 - CGNC Symbol 5786	88.2	6.6	1 136.1 (M:136.1)	3	3.8	13.72	1030 0.41!	1	
988	true	ENSGALP0000039552	proteasome 26S subunit non-ATPase 13 - CGNC Symbol 51869	42.7	5.4	1 143.4 (M:143.4)	4	5.9	6.1	997 0.68!	2	20.28
989	true	ENSGALP0000018120	proteasome 26S subunit non-ATPase 14 - CGNC Symbol 8450	34.5	6	1 134.4 (M:134.4)	4	6.8	4.48	1043 1.03!	1	
990	true	ENSGALP0000010153	proteasome 26S subunit non-ATPase 2 - CGNC Symbol 4727	100	5.1	2 545.5 (M:545.5)	16	14.4	5.64	271 0.86!	8	65.37
991	true	ENSGALP0000029109	proteasome 26S subunit non-ATPase 3 - CGNC Symbol 15224	53.2	9.1	1 439.6 (M:439.6)	11	16.9	7.29	345 0.63!	5	35.5
992	true	ENSGALP0000002497	proteasome 26S subunit non-ATPase 5 - CGNC Symbol 1140	55.7	5.2	1 326.1 (M:326.1)	9	17.5	5.43	484 0.60!	4	24.31
993	true	ENSGALP0000011822	proteasome 26S subunit non-ATPase 6 - CGNC Symbol 5531	45.5	5.9	1 369.5 (M:369.5)	9	18.3	4.75	422 0.56!	4	37.84
994	true	ENSGALP0000000338	proteasome inhibitor subunit 1 - CGNC Symbol 152	29.1	5.2	1 101.7 (M:101.7)	4	17	18.02	1198 0.48!	1	
995	true	ENSGALP0000019629	proteasome subunit alpha 3 - CGNC Symbol 9125	28.5	4.9	1 274.1 (M:274.1)	7	26.3	4.04	595 1.14!	4	25.74
996	true	ENSGALP0000016334	proteasome subunit alpha 6 - CGNC Symbol 7649	27.7	6.1	1 361.9 (M:361.9)	6	13.7	2.47	429 1.05	3	19.37
997	true	ENSGALP0000009681	Proteasome subunit alpha type - UniProtKB/TrEMBL B4DEV8 - CGNC Symbol 4513	29.3	6.1	1 291.1 (M:291.1)	8	24.5	4.83	552 1.30!	2	33.36
998	true	ENSGALP0000000088	proteasome subunit alpha type-5 - Refseq NP_001026578	25.3	4.8	1 134.6 (M:134.6)	2	12.5	4.21	1040 1.66	2	6.15
999	true	ENSGALP00000042455	proteasome subunit alpha type-7 - Refseq NP_989944	24.5	8.8	1 235.1 (M:235.1)	4	18	2.87	683 0.73!	1	
1000	true	ENSGALP0000018195	proteasome subunit beta 1 - CGNC Symbol 8487	26	6.4	1 274.9 (M:274.9)	6	13.9	5.01	591 1.66	3	18.9
1001	true	ENSGALP00000042988	proteasome subunit beta 2 - HGNC:9539	22.7	6.1	1 257.2 (M:257.2)	7	20.4	6.93	632 0.90!	3	90.81

1002	true	ENSGALP00000002420	proteasome subunit beta 3 - CGNC Symbol 1108	23.1	5.3	1 276.0 (M:276.0)	5	20.5	13.31	587	0.4	2	30.12
1003	true	ENSGALP00000013574	protein disulfide isomerase family A member 3 - CGNC Symbol 6325	56.1	5.8	1 1965.2 (M:1965.2)	31	37.2	6.03	24 1.47!		18	52.87
1004	true	ENSGALP00000020268	protein disulfide isomerase family A member 4 - CGNC Symbol 9429	71	5	1 463.5 (M:463.5)	13	17.1	7.03	325 3.25!		4	22.32
1005	true	ENSGALP00000026487	protein disulfide isomerase family A member 6 - CGNC Symbol 12314	48.8	5	1 605.4 (M:605.4)	12	24.6	7.62	233	1.85	4	37.1
1006	true	ENSGALP0000006278	protein kinase C alpha - CGNC Symbol 50506	76.8	6.4	3 181.0 (M:181.0)	5	7.4	11.1	863 0.52!		1	
1007	true	ENSGALP00000035514	protein kinase C delta - CGNC Symbol 50113	78.4	8.4	2 132.2 (M:132.2)	4	5.3	11.1	1058			
1008	true	ENSGALP00000039316	protein kinase C theta - CGNC Symbol 57974	81.8	6.9	1 121.5 (M:121.5)	2	3.9	9.17	1099 0.51!		1	
1009	true	ENSGALP00000041979	protein kinase cAMP-dependent catalytic beta - CGNC Symbol 66476	39.1	8.7	1 285.0 (M:285.0)	6	13.7	6.28	566 0.52!		1	
1010	true	ENSGALP00000039315	protein kinase cAMP-dependent regulatory type I alpha - CGNC Symbol 3113	43.3	5.3	2 518.8 (M:518.8)	10	15.4	5.68	292 0.44!		4	27.3
1011	true	ENSGALP0000007458	protein kinase N3 - CGNC Symbol 50459	148.8	8.8	1 228.3 (M:228.3)	3	2.3	13.33	703 0.63!		1	
1012	true	ENSGALP00000039734	Protein LOC105369241 - UniProtKB/TrEMBL A0A0B4J2C8 - CGNC Symbol 51059	104.6	9.4	1 284.7 (M:284.7)	6	4.7	2.82	569 1.00!		4	25.77
1013	true	ENSGALP00000038505	protein O-fucosyltransferase 1 - CGNC Symbol 4973	32	8.1	2 93.0 (M:93.0)	2	5.7	9.52	1238	0.59	1	
1014	true	ENSGALP00000031272	protein phosphatase 1 catalytic subunit beta isozyme - CGNC Symbol 49609	37.2	5.8	1 990.4 (M:990.4)	15	31.5	5.89	99 0.89!		7	74.94
1015	true	ENSGALP00000007265	protein phosphatase 1 catalytic subunit gamma isozyme - CGNC Symbol 50363	37	6.1	1 1069.6 (M:1069.6)	18	41.8	5.47	90 0.77!		8	77.38
1016	true	ENSGALP00000016789	protein phosphatase 1 regulatory subunit 12A - CGNC Symbol 49610	120.9	5.5	1 138.9 (M:138.9)	5	4.7	5.92	1018 0.71!		1	
1017	true	ENSGALP00000009351	protein phosphatase 1 regulatory subunit 7 - CGNC Symbol 4354	34.3	5.1	1 467.7 (M:467.7)	8	23.6	6.91	320 0.95!		4	62.22
1018	true	ENSGALP00000001030	protein phosphatase 1 regulatory subunit 8 - CGNC Symbol 463	38.7	6.3	1 96.2 (M:96.2)	2	9.6	4	1224			
1019	true	ENSGALP00000010423	protein phosphatase 2 catalytic subunit alpha isozyme - CGNC Symbol 4870	35.5	5.3	2 606.9 (M:606.9)	9	25.9	7.22	231 0.37!		4	73.88
1020	true	ENSGALP00000030863	protein phosphatase 2 regulatory subunit B alpha - CGNC Symbol 51022	52.6	5.8	1 56.1 (M:56.1)	1	3.5	3.35	1392			
1021	true	ENSGALP00000015963	protein phosphatase 2 regulatory subunit B' alpha - CGNC Symbol 7467	56.8	8.1	1 114.0 (M:114.0)	2	2.4	3.03	1136	0.53	1	
1022	true	ENSGALP00000013883	protein phosphatase 2 regulatory subunit B' delta - CGNC Symbol 6469	70.7	7	3 144.8 (M:144.8)	2	3.4	17.42	985 0.43!		1	
1023	true	ENSGALP00000032688	protein phosphatase 4 regulatory subunit 2 - CGNC Symbol 5906	40.8	4.5	1 138.4 (M:138.4)	2	7.9	15.79	1020 0.55!		1	
1024	true	ENSGALP00000017444	protein phosphatase 4 regulatory subunit 3A - CGNC Symbol 8158	93.9	4.8	1 71.4 (M:71.4)	1	2.2	7.46	1324			
1025	true	ENSGALP0000001493	protein phosphatase 6 catalytic subunit - CGNC Symbol 57480	35.1	5.4	1 227.2 (M:227.2)	5	14.1	6.32	706 0.53!		1	
1026	true	ENSGALP00000021949	protein phosphatase 6 regulatory subunit 2 - CGNC Symbol 10141	107.2	4.5	1 374.6 (M:374.6)	8	7.7	5.14	413 0.30!		1	
1027	true	ENSGALP00000026595	protein phosphatase Mg2+/Mn2+ dependent 1G - CGNC Symbol 12369	60.8	4.3	1 74.8 (M:74.8)	2	1.4	11.53	1311	1.12	1	
1028	true	ENSGALP00000002238	protein PML-like - CGNC Symbol 65465	86.3	5.4	1 212.0 (M:212.0)	3	2.3	4.88	756	1.21	1	
1029	true	ENSGALP0000003092	protein prune homolog - CGNC Symbol 65719	45.8	5.1	1 186.2 (M:186.2)	4	7.6	12.29	844	0.49	2	4.33
1030	true	ENSGALP00000012986	protein tyrosine phosphatase non-receptor type 1 - CGNC Symbol 6062	50.3	5.7	2 240.5 (M:240.5)	5	11.3	5.68	665 0.51!		3	31.71
1031	true	ENSGALP00000023439	protein tyrosine phosphatase non-receptor type 6 - CGNC Symbol 10812	68.3	7.9	1 770.2 (M:770.2)	15	16.4	7.27	158 0.60!		7	59.51
1032	true	ENSGALP00000000837	protein tyrosine phosphatase non-receptor type 7 - CGNC Symbol 371	40.7	7.2	1 73.9 (M:73.9)	1	2.2	0.42	1313	1.71	1	
1033	true	ENSGALP00000003423	protein tyrosine phosphatase receptor type C - CGNC Symbol 1563	139.3	5.5	1 696.7 (M:696.7)	13	8.9	3.94	187 0.43!		6	30.83
1034	true	ENSGALP00000040869	protein-lysine 6-oxidase precursor - Refseq NP_990812	47.8	9.3	1 34.1 (M:34.1)	1	2.2	5	1463			
1035	true	ENSGALP00000036952	PRP40 pre-mRNA processing factor 40 homolog A (<i>S. cerevisiae</i>) - CGNC Symbol 48984	84.7	5.4	2 115.2 (M:115.2)	2	1.9	3.67	1123	1.07	1	
1036	true	ENSGALP0000003706	pseudouridylate synthase 1 - CGNC Symbol 1681	45.2	8.5	1 28.0 (M:28.0)	1	2.7	4.95	1475			
1037	true	ENSGALP0000013183	pseudouridylate synthase 7 (putative) - CGNC Symbol 6164	73.9	6.2	1 127.7 (M:127.7)	1	1.7	9.77	1072 0.66!		1	
1038	true	ENSGALP00000016527	pumilio RNA binding family member 3 - CGNC Symbol 7739	73	9.6	1 95.7 (M:95.7)	2	3.4	7.86	1229	1.21	2	8.15
1039	true	ENSGALP00000034555	pumilio RNA-binding family member 1 - CGNC Symbol 369	116.3	6.4	2 95.0 (M:95.0)	3	2.2	14.71	1230 0.91!		1	
1040	true	ENSGALP00000042475	purine-rich element binding protein A - CGNC Symbol 15180	27.7	9.1	1 298.2 (M:298.2)	4	16.5	12.09	537 0.53!		1	
1041	true	ENSGALP00000026307	Putative eukaryotic translation initiation factor 2 subunit 3-like protein - UP Q2VIR3 - CGNC Symbol 501	51.1	8.5	1 374.1 (M:374.1)	7	11.2	6.48	414 0.88!		4	37.71
1042	true	ENSGALP00000026076	pyridoxal (pyridoxine vitamin B6) kinase - CGNC Symbol 12115	35.6	6.1	1 186.5 (M:186.5)	5	15.8	7.23	841 1.24!		2	40.69
1043	true	ENSGALP00000004190	pyroglutamyl-peptidase I - CGNC Symbol 17204	22.7	5.4	1 167.4 (M:167.4)	3	26.9	7.15	906			
1044	true	ENSGALP0000007055	pyrophosphatase (inorganic) 1 - CGNC Symbol 3275	34	5.7	1 483.5 (M:483.5)	11	29.7	5.48	311 1.23!		3	18.38
1045	true	ENSGALP0000017202	pyrophosphatase (inorganic) 2 - CGNC Symbol 8036	34.5	5.5	1 119.5 (M:119.5)	2	4.9	2.41	1105	1.53	1	
1046	true	ENSGALP00000026457	pyruvate dehydrogenase (lipoamide) alpha 1 - CGNC Symbol 50805	44.4	8.2	1 156.5 (M:156.5)	5	10	5.6	941	0.73	2	49.3
1047	true	ENSGALP0000011491	pyruvate dehydrogenase (lipoamide) beta - CGNC Symbol 5364	39	6.1	1 204.9 (M:204.9)	4	10	14.7	777 0.74!		2	6.67
1048	true	ENSGALP00000034108	pyruvate kinase muscle - CGNC Symbol 1412	57.8	8	2 1956.4 (M:1956.4)	33	45.7	6.37	26 1.86!		14	46.51
1049	true	ENSGALP00000036002	RAB10 member RAS oncogene family - CGNC Symbol 12382	18.7	8.4	1 312.7 (M:312.7)	4	18.9	4.09	512 2.65!		2	67.46
1050	true	ENSGALP0000000864	RAB11B member RAS oncogene family - CGNC Symbol 51171	24.5	5.6	3 221.5 (M:221.5)	5	12.4	1.72	728 0.67!		2	32.09
1051	true	ENSGALP0000002234	RAB14 member RAS oncogene family - CGNC Symbol 1018	23.9	5.9	11 385.6 (M:385.6)	6	38.1	9.22	402 1.10!		3	20.53
1052	true	ENSGALP00000014265	RAB1A member RAS oncogene family - CGNC Symbol 6666	22.7	5.9	1 186.6 (M:186.6)	2	7.8	4.61	840 1.30!		1	
1053	true	ENSGALP00000024868	RAB2A member RAS oncogene family - CGNC Symbol 49674	23.5	6	1 236.2 (M:236.2)	5	9.9	7.83	678 0.77!		4	5.35
1054	true	ENSGALP00000005302	RAB5C member RAS oncogene family - CGNC Symbol 2444	23.5	8.6	3 115.1 (M:115.1)	3	10.2	8.82	1124	0.82	1	
1055	true	ENSGALP0000009481	RAB7A member RAS oncogene family - CGNC Symbol 4408	23.5	6.4	1 187.2 (M:187.2)	4	14.5	5.51	837 0.82!		2	0.26
1056	true	ENSGALP0000005505	RAB8B member RAS oncogene family - CGNC Symbol 2544	23.6	9.1	1 325.7 (M:325.7)	2	6.8	4.63	485 0.59!		1	
1057	true	ENSGALP00000039547	rabaptin RAB GTPase binding effector protein 1 - CGNC Symbol 49558	99.3	4.9	1 122.4 (M:122.4)	1	1.3	24.11	1090			
1058	true	ENSGALP00000010376	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 - CGNC Symbol 4852	86.9	6	1 204.8 (M:204.8)	6	10.7	5.37	779 0.31!		1	
1059	true	ENSGALP00000025921	RAD21 cohesin complex component - CGNC Symbol 12049	72	4.6	1 132.7 (M:132.7)	3	5.7	11.24	1055 0.40!		1	
1060	true	ENSGALP00000025005	RAD23 homolog B (<i>S. cerevisiae</i>) - CGNC Symbol 11587	43.1	4.7	1 224.5 (M:224.5)	5	8.9	7.08	716 0.54!		3	15.5

1061	true	ENSGALP0000021028	radixin - CGNC Symbol 49356	68.4	5.9	1 1171.6 (M:1171.6)	21	18.7	7.93	76	1.35!	9	61.61
1062	true	ENSGALP0000018309	raftin lipid raft linker 1 - CGNC Symbol 8540	65.6	5.3	1 229.1 (M:229.1)	8	13.8	8.22	701	0.79!	5	73.6
1063	true	ENSGALP0000003284	RAN binding protein 1 - CGNC Symbol 50345	24.2	5.2	1 145.4 (M:145.4)	3	15.4	12.96	984	0.67!	2	3.68
1064	true	ENSGALP0000035780	RAN binding protein 2 - CGNC Symbol 50838	334.3	5.7	1 372.1 (M:372.1)	7	2.7	10.97	417	0.76!	3	11.19
1065	true	ENSGALP000000805	RAN binding protein 3 - CGNC Symbol 357	59.6	4.7	1 66.9 (M:66.9)	2	3.2	6.49	1350	0.34!	1	
1066	true	ENSGALP000004046	RAN member RAS oncogene family - CGNC Symbol 1850	24.4	7.7	1 786.5 (M:786.5)	16	31.5	4.47	151	0.74!	8	70.23
1067	true	ENSGALP0000042497	RAR-related orphan receptor C - CGNC Symbol 58847	55.6	9.7	1 179.9 (M:179.9)	3	8.6	8.06	868			
1068	true	ENSGALP000001221	Ras association domain family member 5 - CGNC Symbol 541	28.9	8.3	1 142.4 (M:142.4)	2	4.3	4.55	1001	0.29	1	
1069	true	ENSGALP0000033584	ras homolog family member A - CGNC Symbol 49322	21.8	5.8	2 204.1 (M:204.1)	6	26.4	8.48	785	1.94!	2	38.14
1070	true	ENSGALP0000027098	RAS p21 protein activator 3 - CGNC Symbol 12617	96.2	7.9	1 117.9 (M:117.9)	3	3.7	5.85	1110			
1071	true	ENSGALP0000042240	RAS protein activator like 3 - CGNC Symbol 52700	46.6	8.7	1 50.1 (M:50.1)	2	6.2	7.65	1423			
1072	true	ENSGALP0000037001	ras-related C3 botulinum toxin substrate 2 (rho family small GTP binding protein Rac2) - CGNC Symbol	21.4	8.1	6 682.4 (M:682.4)	14	38.5	7.47	193	0.60!	7	25.17
1073	true	ENSGALP0000012233	Ras-related GTP binding B - CGNC Symbol 5717	40.8	8.6	1 100.1 (M:100.1)	2	2.8	2.95	1208	0.58	1	
1074	true	ENSGALP0000002254	Ras-related GTP binding C - CGNC Symbol 1028	44.9	4.9	2 140.6 (M:140.6)	4	6.1	13.2	1008	1	2	22.81
1075	true	ENSGALP0000030639	Ras-related protein Rab-6A - UP Q1KME6	23.5	5.4	1 188.8 (M:188.8)	4	19.7	10.94	831	2.41!	1	
1076	true	ENSGALP0000041790	Ras-related protein Rab-8A - UP Q5F470	23.5	9.2	1 218.6 (M:218.6)	1	6.8	5.5	740			
1077	true	ENSGALP0000016120	Ras-related protein Rap-1b-like protein - CGNC Symbol 50604	20.8	5.6	2 469.1 (M:469.1)	7	13.6	4.19	318	0.88!	3	28.68
1078	true	ENSGALP0000018575	RCD1 required for cell differentiation1 homolog (S. pombe) - CGNC Symbol 8665	26.7	7.2	1 151.9 (M:151.9)	2	7.6	10.91	961	0.47!	1	
1079	true	ENSGALP0000037103	receptor accessory protein 5 - CGNC Symbol 16088	21.5	6.8	1 98.7 (M:98.7)	2	5.3	6.3	1212	1.46	1	
1080	true	ENSGALP0000000170	receptor for activated C kinase 1 - CGNC Symbol 61	35.1	7.6	1 1055.4 (M:1055.4)	18	49.5	7.5	92	0.64!	5	70.16
1081	true	ENSGALP0000010965	regulation of nuclear pre-mRNA domain containing 1B - CGNC Symbol 50965	44.2	9.3	1 69.4 (M:69.4)	1	3.8	0.94	1330	0.51	1	
1082	true	ENSGALP0000023574	regulation of nuclear pre-mRNA domain containing 2 - CGNC Symbol 52333	136.5	6.1	1 296.5 (M:296.5)	6	5.1	6.2	543	0.51!	2	25.63
1083	true	ENSGALP0000042317	regulator of chromosome condensation 1 - HGNC:1913	44.5	6.8	1 565.1 (M:565.1)	12	26.1	4.85	262	0.83!	5	23.15
1084	true	ENSGALP0000039872	regulator of chromosome condensation 2 - CGNC Symbol 287	49.3	8.7	1 1039.0 (M:1039.0)	17	41	8.82	95	0.34!	4	68.51
1085	true	ENSGALP0000007102	regulator of microtubule dynamics 3 - CGNC Symbol 3296	52.6	5	1 57.5 (M:57.5)	1	2.1	16.58	1386			
1086	true	ENSGALP0000023075	replication factor C subunit 1 - CGNC Symbol 51823	128.4	9.4	1 143.5 (M:143.5)	3	1.9	4.2	995	0.93!	1	
1087	true	ENSGALP0000004840	replication protein A1 - CGNC Symbol 2225	68	8.1	1 115.4 (M:115.4)	3	7	12.4	1121	1.20!	2	15.12
1088	true	ENSGALP0000001048	replication protein A2 32kDa - CGNC Symbol 51031	28.8	5.9	1 190.7 (M:190.7)	2	6	5.28	826	0.86	1	
1089	true	ENSGALP0000017383	replication protein A3 - CGNC Symbol 8130	13.5	5	1 274.3 (M:274.3)	4	25.6	4.57	594	0.85!	2	3.21
1090	true	ENSGALP0000004476	reticulocalbin 2 - CGNC Symbol 2050	35.7	4.4	1 139.3 (M:139.3)	4	13.9	16.18	1015	1.09!	2	105.36
1091	true	ENSGALP0000005565	retinoblastoma binding protein 4 - CGNC Symbol 2572	47.6	4.7	2 542.8 (M:542.8)	11	16.2	7.82	273	0.78!	5	45.31
1092	true	ENSGALP0000033974	RGD motif leucine rich repeats tropomodulin domain and proline-rich containing - CGNC Symbol 1280	155.5	7.1	1 244.5 (M:244.5)	2	2.2	16.44	658			
1093	true	ENSGALP0000013738	Rho GDP dissociation inhibitor (GDI) alpha - CGNC Symbol 55089	23.2	5	1 609.4 (M:609.4)	13	21.1	6.72	228	1.64!	6	129.11
1094	true	ENSGALP0000029933	Rho GDP dissociation inhibitor (GDI) beta - CGNC Symbol 8920	23.2	5.1	1 422.8 (M:422.8)	8	42.4	5.07	364	0.52!	3	23.74
1095	true	ENSGALP0000036056	Rho-associated coiled-coil containing protein kinase 1 - CGNC Symbol 11078	158.6	5.7	2 362.1 (M:362.1)	6	2.2	8.14	428	0.93!	3	53.03
1096	true	ENSGALP0000005645	Rho/Rac guanine nucleotide exchange factor (GEF) 18 - CGNC Symbol 2608	130.6	6.7	1 171.0 (M:171.0)	3	2.8	10.79	892	0.72!	1	
1097	true	ENSGALP00000020863	ribonuclease P/MRP 40kDa subunit - CGNC Symbol 9707	41.3	6.5	1 56.9 (M:56.9)	2	3.3	4.24	1389	0.78!	1	
1098	true	ENSGALP0000011167	ribonuclease/angiogenin inhibitor 1 - CGNC Symbol 5211	49.8	4.9	1 298.2 (M:298.2)	5	11.4	10.77	538	0.77!	2	29.12
1099	true	ENSGALP0000012383	ribonucleic acid export 1 - CGNC Symbol 5777	47.4	9.2	1 247.0 (M:247.0)	6	14.7	2.61	654	0.66!	3	42.73
1100	true	ENSGALP0000027981	ribonucleotide reductase catalytic subunit M1 - CGNC Symbol 13036	90	6.8	1 287.1 (M:287.1)	8	11.4	8.81	561	0.73!	3	33.27
1101	true	ENSGALP0000025808	ribonucleotide reductase M2 B (TP53 inducible) - CGNC Symbol 11989	40.4	5	2 188.9 (M:188.9)	3	9.4	9.06	830	0.23!	1	
1102	true	ENSGALP0000009487	ribophorin I - CGNC Symbol 4413	60.6	6.4	1 368.8 (M:368.8)	6	9.8	8.29	423	1.02!	3	9.92
1103	true	ENSGALP0000006038	ribophorin II - CGNC Symbol 2792	68.8	5.9	1 355.1 (M:355.1)	5	5.5	11.61	441	1.28!	2	40.68
1104	true	ENSGALP0000004521	ribosomal L1 domain containing 1 - CGNC Symbol 2075	49.6	9.9	1 159.2 (M:159.2)	4	6.8	9.89	931	0.73!	1	
1105	true	ENSGALP0000004159	ribosomal protein L10a - CGNC Symbol 51119	24.7	9.9	1 221.4 (M:221.4)	4	11.5	7.54	729	1.31!	2	31.79
1106	true	ENSGALP0000014298	ribosomal protein L12 - CGNC Symbol 50469	17.7	9.5	1 593.3 (M:593.3)	6	27.9	7.06	243	1.01	3	8.5
1107	true	ENSGALP0000009960	ribosomal protein L13 - CGNC Symbol 49509	24.4	11.7	1 321.4 (M:321.4)	8	20.9	8.97	497	0.53!	3	23.06
1108	true	ENSGALP0000018765	ribosomal protein L14 - CGNC Symbol 49056	17.3	10.6	1 465.8 (M:465.8)	10	32.2	8.37	322	0.67!	5	24.02
1109	true	ENSGALP0000041361	ribosomal protein L17 - HGNC:10307	17.1	10.1	3 396.7 (M:396.7)	9	26.7	4.2	392	1.90!	5	61.43
1110	true	ENSGALP0000015964	ribosomal protein L18a - CGNC Symbol 50601	21.2	10.8	1 459.7 (M:459.7)	9	31.3	8.83	331	0.50!	3	93.71
1111	true	ENSGALP0000039326	ribosomal protein L19 - CGNC Symbol 1159	23.2	11.4	1 297.6 (M:297.6)	8	21.1	4.9	539	0.69!	3	11.89
1112	true	ENSGALP0000041993	ribosomal protein L21 - HGNC:10313	18.6	10.5	1 318.9 (M:318.9)	8	28.8	11.42	499	1.24!	4	42.61
1113	true	ENSGALP0000001013	ribosomal protein L22 - CGNC Symbol 48966	14.6	9.2	1 79.4 (M:79.4)	1	10.2	0.77	1291	1.17!	1	
1114	true	ENSGALP0000002493	ribosomal protein L23 - CGNC Symbol 1138	14.9	10.5	1 184.6 (M:184.6)	4	30	9.78	846	1.03!	2	2.11
1115	true	ENSGALP0000006308	ribosomal protein L23a - CGNC Symbol 2910	17.6	10.4	1 195.3 (M:195.3)	5	14.2	15.83	811	0.95!	2	16.04
1116	true	ENSGALP0000024710	ribosomal protein L24 - CGNC Symbol 50756	17.8	11.4	1 259.2 (M:259.2)	6	15.9	11.56	625	0.92!	3	36.11
1117	true	ENSGALP00000038957	ribosomal protein L27 - CGNC Symbol 49733	15.8	10.6	1 285.8 (M:285.8)	6	36	5.48	564	1.13!	2	23.56
1118	true	ENSGALP0000009552	ribosomal protein L27a - CGNC Symbol 55716	16.8	10.9	1 211.4 (M:211.4)	3	17.6	2.27	758	0.77	2	19.82
1119	true	ENSGALP0000029968	ribosomal protein L3 - CGNC Symbol 50654	46.1	10.2	2 737.3 (M:737.3)	17	28.3	9.16	170	0.63!	7	85.95

1120	true	ENSGALP0000013355	ribosomal protein L30 - CGNC Symbol 6224	13.6	9.5	1 304.3 (M:304.3)	5	32	3.12	525	0.84!	3	33.21
1121	true	ENSGALP0000027030	ribosomal protein L31 - CGNC Symbol 50833	14.7	10.5	1 427.7 (M:427.7)	10	31.2	4.63	356	1.30!	4	38.18
1122	true	ENSGALP0000037906	ribosomal protein L35 - CGNC Symbol 49055	12.9	11	1 134.4 (M:134.4)	3	21.1	12.83	1042	0.86!	1	
1123	true	ENSGALP0000012293	ribosomal protein L35a - CGNC Symbol 5744	15.7	11.6	1 285.5 (M:285.5)	9	21.8	5.98	565	1.02!	4	20.43
1124	true	ENSGALP0000012481	ribosomal protein L4 - CGNC Symbol 5828	46.7	11.1	1 956.0 (M:956.0)	17	28.5	3.2	106	0.89!	7	49.55
1125	true	ENSGALP0000009511	ribosomal protein L5 - CGNC Symbol 4424	33.9	9.7	1 806.0 (M:806.0)	17	27	4.86	143	1.79!	8	110.27
1126	true	ENSGALP0000007680	ribosomal protein L6 - CGNC Symbol 48978	33.9	10.7	1 727.0 (M:727.0)	14	22.8	5.68	176	0.44!	6	38.54
1127	true	ENSGALP0000038463	ribosomal protein L7a - CGNC Symbol 50454	29.8	10.5	1 735.3 (M:735.3)	10	21.1	6.83	173	0.77!	7	43.18
1128	true	ENSGALP0000026126	ribosomal protein L8 - CGNC Symbol 12137	28	11	1 522.7 (M:522.7)	13	45.1	4.48	289	0.77!	8	71.33
1129	true	ENSGALP0000017171	ribosomal protein large P0 - CGNC Symbol 49505	34.6	6.5	1 627.6 (M:627.6)	13	24.5	10.11	215	1.22!	7	41.76
1130	true	ENSGALP0000026015	ribosomal protein large P1 - CGNC Symbol 49724	11.5	4.1	1 124.6 (M:124.6)	2	14	13.66	1081	0.21!	1	
1131	true	ENSGALP0000023089	ribosomal protein large P2 - CGNC Symbol 10655	14.2	4.7	1 43.1 (M:43.1)	1	9.7	1.46	1437	1.48	1	
1132	true	ENSGALP0000004437	ribosomal protein S10 - CGNC Symbol 51122	18.9	10.2	1 655.0 (M:655.0)	12	52.1	7.88	206	0.95!	4	11.94
1133	true	ENSGALP0000009821	ribosomal protein S13 - CGNC Symbol 49921	17.2	10.5	1 461.2 (M:461.2)	8	35.8	4.69	328	1.20!	2	71.56
1134	true	ENSGALP0000007287	ribosomal protein S14 - CGNC Symbol 3393	16.3	10.1	1 601.3 (M:601.3)	9	37.7	4.41	238	1.16!	4	59.54
1135	true	ENSGALP0000024468	ribosomal protein S15 - CGNC Symbol 11306	16.9	10.4	1 79.4 (M:79.4)	2	8.3	2.64	1292	1.97	1	
1136	true	ENSGALP0000010942	ribosomal protein S15a - CGNC Symbol 5109	17.3	9.8	1 607.8 (M:607.8)	11	46.7	3.89	230	0.74!	6	22.26
1137	true	ENSGALP0000041159	ribosomal protein S16 - HGNC:10396	16.4	10.2	1 869.1 (M:869.1)	16	54.1	4.19	128	1.20!	8	80.28
1138	true	ENSGALP0000003373	ribosomal protein S17 - CGNC Symbol 49022	9.5	5.8	1 83.9 (M:83.9)	1	26.5	3.93	1275			
1139	true	ENSGALP0000008802	ribosomal protein S2 - CGNC Symbol 50281	30.7	10.3	1 307.6 (M:307.6)	8	19.2	6.32	521	1.15!	3	43.92
1140	true	ENSGALP0000023266	ribosomal protein S20 - HGNC:10405	13.6	9.9	1 449.6 (M:449.6)	7	23.1	5.62	337	0.96	4	68.27
1141	true	ENSGALP0000033411	ribosomal protein S21 - HGNC:10409	9.1	8.7	1 209.9 (M:209.9)	6	42.2	5.49	762	1.02	2	24.82
1142	true	ENSGALP0000025130	ribosomal protein S23 - HGNC:10410	15.8	10.5	1 328.3 (M:328.3)	7	25.2	10.21	479	0.79!	2	17.95
1143	true	ENSGALP0000007763	ribosomal protein S24 - CGNC Symbol 3616	15.6	10.8	1 105.3 (M:105.3)	2	8.1	9.18	1174	1.21!	1	
1144	true	ENSGALP0000013174	ribosomal protein S27a - CGNC Symbol 49483	18	9.7	2 939.6 (M:939.6)	17	58.3	3	111	1.01!	7	50.05
1145	true	ENSGALP0000040484	ribosomal protein S28 - CGNC Symbol 54861	7.8	10.7	1 164.2 (M:164.2)	4	30.4	9.13	914	1.31	2	10.06
1146	true	ENSGALP0000019945	ribosomal protein S29 - CGNC Symbol 9289	7	10.2	1 56.9 (M:56.9)	2	11.7	11.69	1387	1.16	1	
1147	true	ENSGALP0000027953	ribosomal protein S3 - CGNC Symbol 13020	26.7	9.7	1 765.8 (M:765.8)	15	47.7	6.48	160	1.00!	8	23.95
1148	true	ENSGALP0000016361	ribosomal protein S3A - CGNC Symbol 51748	29.8	9.7	1 969.4 (M:969.4)	16	45.5	4.19	101	0.84!	9	85.03
1149	true	ENSGALP0000007705	ribosomal protein S4 X-linked - CGNC Symbol 49597	29.4	10.2	1 747.2 (M:747.2)	13	25.2	6.74	165	1.04!	7	47.1
1150	true	ENSGALP0000024283	ribosomal protein S6 - CGNC Symbol 49670	33.9	11.1	1 258.1 (M:258.1)	3	8	8.21	628	0.82!	1	
1151	true	ENSGALP0000026406	ribosomal protein S6 kinase 90kDa polypeptide 3 - CGNC Symbol 12282	80.6	7	4 411.1 (M:411.1)	9	9.7	9.26	373	0.59!	4	64.44
1152	true	ENSGALP0000026392	ribosomal protein S7 - CGNC Symbol 51562	22.3	10.1	1 182.0 (M:182.0)	4	25	14.94	858	0.96!	1	
1153	true	ENSGALP0000016447	ribosomal protein S8 - CGNC Symbol 52222	24.2	10.3	1 779.8 (M:779.8)	14	45.2	8.01	155	0.69!	7	108.26
1154	true	ENSGALP0000019469	ribosomal protein SA - CGNC Symbol 49202	33	4.8	1 562.0 (M:562.0)	10	22.6	5.51	264	1.67!	5	105.77
1155	true	ENSGALP0000024213	ribosome production factor 2 homolog - CGNC Symbol 11187	35.1	9.9	1 222.4 (M:222.4)	7	17	15.1	726	0.73!	2	39.31
1156	true	ENSGALP0000000742	ring finger protein 113A - CGNC Symbol 51137	37.8	6.2	1 121.7 (M:121.7)	2	9.1	14.84	1097			
1157	true	ENSGALP0000020561	RNA 2' 3'-cyclic phosphate and 5'-OH ligase - CGNC Symbol 9570	55.2	6.8	1 230.2 (M:230.2)	6	12.5	11.76	696	0.68!	2	20.26
1158	true	ENSGALP0000025629	RNA binding motif protein 1B - CGNC Symbol 51213	78.8	9.1	1 190.0 (M:190.0)	5	5.6	10.77	827	0.68!	2	28.82
1159	true	ENSGALP0000021838	RNA binding motif protein 14 - HGNC:14219	58.4	9.6	1 270.3 (M:270.3)	5	7.3	4.91	605	0.28!	2	6.86
1160	true	ENSGALP0000000545	RNA binding motif protein 15 - CGNC Symbol 238	96.9	10.1	1 81.4 (M:81.4)	2	3.7	12.46	1286			
1161	true	ENSGALP0000013474	RNA binding motif protein 19 - CGNC Symbol 6281	107.8	6.7	1 141.3 (M:141.3)	1	1.5	7.9	1004			
1162	true	ENSGALP0000015182	RNA binding motif protein 25 - CGNC Symbol 7094	96.8	5.8	1 278.6 (M:278.6)	5	5.9	10.95	584	1.16!	2	150.44
1163	true	ENSGALP0000007358	RNA binding motif protein 5 - CGNC Symbol 3423	92.3	5.8	1 155.1 (M:155.1)	2	2.5	2.97	950	0.48!	2	49.01
1164	true	ENSGALP0000011338	RNA binding motif protein 7 - CGNC Symbol 5294	31.3	9.4	1 42.7 (M:42.7)	1	3.9	0.21	1438	0.59	1	
1165	true	ENSGALP0000010414	RNA binding motif protein X-linked - CGNC Symbol 51674	41.5	10.1	1 568.4 (M:568.4)	12	20	7.92	260	0.43!	4	34.81
1166	true	ENSGALP0000039645	RNA pseudouridylate synthase domain containing 2 - HGNC:24180	54	6.4	1 178.0 (M:178.0)	5	11.2	11.93	876	0.75!	2	45.37
1167	true	ENSGALP0000025762	runt-related transcription factor 1 - CGNC Symbol 49673	51.1	9.3	1 230.2 (M:230.2)	5	18	8.77	697			
1168	true	ENSGALP0000009528	RuvB like AAA ATPase 1 - CGNC Symbol 4431	50.1	6	1 619.3 (M:619.3)	7	14.9	5	220	0.82!	4	37.68
1169	true	ENSGALP0000014912	S100 calcium binding protein A11 - CGNC Symbol 6970	11.4	6.1	1 140.5 (M:140.5)	2	10.9	21.97	1010	3.39	1	
1170	true	ENSGALP0000040890	Sad1 and UNC84 domain containing 2 - CGNC Symbol 50656	77.4	6.5	1 483.8 (M:483.8)	13	23.2	7.47	310	0.83!	8	29.84
1171	true	ENSGALP0000039758	SAM and SH3 domain containing 3 - CGNC Symbol 2900	41.6	5.1	1 201.2 (M:201.2)	4	13.4	13.01	796	0.30!	1	
1172	true	ENSGALP0000001866	SAM domain and HD domain 1 - CGNC Symbol 839	70.2	6.4	1 250.4 (M:250.4)	4	6.8	7.93	647	1.99!	1	
1173	true	ENSGALP0000022917	SAMM50 sorting and assembly machinery component - CGNC Symbol 10580	52.2	6	1 90.4 (M:90.4)	2	6.8	7.18	1250			
1174	true	ENSGALP0000023543	SAP domain-containing ribonucleoprotein - Refseq NP_001026495	23.4	6.8	1 188.2 (M:188.2)	5	14.3	6.77	833	0.90!	2	79.07
1175	true	ENSGALP0000007043	SAR1 homolog A (<i>S. cerevisiae</i>) - CGNC Symbol 52032	22.4	6.2	2 172.4 (M:172.4)	3	15.7	5.9	888	1.08!	1	
1176	true	ENSGALP00000041108	SATB homeobox 1 - CGNC Symbol 8550	88.1	6.2	4 550.3 (M:550.3)	11	16.4	5.32	270	0.78!	5	58.2
1177	true	ENSGALP0000021769	scaffold attachment factor B - CGNC Symbol 52657	103.7	5.5	1 227.3 (M:227.3)	7	5.8	8.47	705	0.86!	4	12.3
1178	true	ENSGALP0000003011	scaffold attachment factor B2 - CGNC Symbol 52976	105.6	5.5	1 349.3 (M:349.3)	9	9.9	11.08	448	0.95!	3	18.39

1179	true	ENSGALP00000017495	scinderin - CGNC Symbol 8188		80.5	5.5	1 890.0 (M:890.0)	15	20.8	7.05	120	1.29!	5	47.43
1180	true	ENSGALP00000003877	SEC11 homolog A (S. cerevisiae) - CGNC Symbol 1762		20.6	9.5	1 103.3 (M:103.3)	3	8.4	13.16	1188	0.67!	1	
1181	true	ENSGALP0000003718	SEC16 homolog A (S. cerevisiae) - CGNC Symbol 1688		243.9	5.6	1 107.7 (M:107.7)	2	1.3	0.86	1168	1.43!	1	
1182	true	ENSGALP0000041744	SEC22 homolog B vesicle trafficking protein - CGNC Symbol 52179		24.7	8.9	1 197.4 (M:197.4)	4	16.7	8.77	806		1.8	3 111.66
1183	true	ENSGALP0000016481	Sec23 homolog A (S. cerevisiae) - CGNC Symbol 7715		86.1	6.5	1 78.5 (M:78.5)	2	3.4	3.16	1302			
1184	true	ENSGALP0000014280	Sec23 homolog B (S. cerevisiae) - CGNC Symbol 50333		86.2	6.3	1 191.1 (M:191.1)	7	8.3	8.06	823	0.40!	3	23.2
1185	true	ENSGALP0000015396	SEC23 interacting protein - CGNC Symbol 7197		110.1	5.2	1 130.8 (M:130.8)	2	1.5	8.21	1066	0.73!	1	
1186	true	ENSGALP0000010342	SEC24 family member A - CGNC Symbol 4833		120	8.1	3 115.1 (M:115.1)	2	1.2	16.07	1125		0.69	1
1187	true	ENSGALP0000008311	SEC24 family member C - CGNC Symbol 3857		121.6	6.4	1 202.1 (M:202.1)	4	3.1	5.74	790	0.66!	1	
1188	true	ENSGALP0000018179	SEC31 homolog A (S. cerevisiae) - CGNC Symbol 8479		133.2	5.9	2 196.7 (M:196.7)	5	3.5	13.35	808	1.50!	2	38.42
1189	true	ENSGALP0000039343	SEC31 homolog B (S. cerevisiae) - CGNC Symbol 4268		80.7	5.5	1 54.8 (M:54.8)	1	1.9	3.38	1398			
1190	true	ENSGALP0000002580	secretory carrier membrane protein 2 - CGNC Symbol 1178		36.7	8.8	1 126.0 (M:126.0)	4	12	10.91	1076	0.55!	2	16.19
1191	true	ENSGALP0000023456	seleophosphate synthetase 1 - CGNC Symbol 10819		42.9	5.6	1 116.1 (M:116.1)	3	6.4	13.17	1116	0.73!	2	60.74
1192	true	ENSGALP0000018689	septin 11 - CGNC Symbol 8720		50.6	6.4	2 233.0 (M:233.0)	7	10.2	8.59	689	1.21!	2	28.84
1193	true	ENSGALP0000009314	septin 2 - CGNC Symbol 4335		41.6	5.9	1 1155.2 (M:1155.2)	19	44.8	7.94	78	0.76!	9	61.85
1194	true	ENSGALP0000002520	septin 2-like - CGNC Symbol 50343		40.2	6.1	1 592.6 (M:592.6)	12	25.8	6.89	246	1.03!	5	60.29
1195	true	ENSGALP0000029589	septin 6 - CGNC Symbol 51720		48.6	6.5	1 292.1 (M:292.1)	8	12.9	7.08	551	0.92!	3	19
1196	true	ENSGALP0000019801	septin 7 - CGNC Symbol 51333		48.4	8.8	1 1118.2 (M:1118.2)	18	31.3	8.85	82	0.63!	8	77.74
1197	true	ENSGALP0000002525	septin 9 - CGNC Symbol 50494		65.5	8.4	1 527.0 (M:527.0)	13	20.4	8.39	286	0.51!	4	49.6
1198	true	ENSGALP0000009486	sequestosome 1 - CGNC Symbol 4412		49.7	4.8	1 50.2 (M:50.2)	1	2.2	4.19	1422			
1199	true	ENSGALP0000001957	serine and arginine repetitive matrix 1 - CGNC Symbol 876		100.8	11.8	1 147.2 (M:147.2)	2	1.7	15.58	980			
1200	true	ENSGALP0000038262	serine/arginine-rich splicing factor 1 - Refseq NP_001107213		20.7	11	2 466.5 (M:466.5)	11	35.9	9.04	321		1.12	6 100.7
1201	true	ENSGALP0000006566	serine/arginine-rich splicing factor 10 - CGNC Symbol 51061		31.3	11.3	1 194.3 (M:194.3)	5	17.9	7.81	815	0.81!	2	54.47
1202	true	ENSGALP0000027988	Serine/arginine-rich splicing factor 2 - UP P30352		25.5	11.9	1 257.8 (M:257.8)	8	16.7	4.73	630		0.77	4 32.61
1203	true	ENSGALP0000000734	serine/arginine-rich splicing factor 3 - CGNC Symbol 329		19.3	11.6	2 400.9 (M:400.9)	7	28.7	7.55	388	0.70!	3	81.51
1204	true	ENSGALP0000001460	serine/arginine-rich splicing factor 6 - CGNC Symbol 657		40.4	11.6	3 687.8 (M:687.8)	15	19.3	9.81	192	0.81!	7	29.28
1205	true	ENSGALP0000025754	serine/threonine kinase 3 - CGNC Symbol 52437		56.1	5.2	2 296.6 (M:296.6)	5	6.1	9.12	542	0.86!	2	0.32
1206	true	ENSGALP0000021343	serine/threonine kinase receptor associated protein - CGNC Symbol 9899		38.1	5	1 192.7 (M:192.7)	3	14.3	5.1	818	1.45!	1	
1207	true	ENSGALP0000009728	serine/threonine protein kinase MST4 - CGNC Symbol 51666		47	5.9	1 47.2 (M:47.2)	1	2.9	4.93	1430			
1208	true	ENSGALP0000020954	serpin peptidase inhibitor clade B (ovalbumin) member 1 - CGNC Symbol 13903		43.1	5.4	1 212.1 (M:212.1)	5	11.9	8.49	755		1.21	2 49.85
1209	true	ENSGALP0000020953	serpin peptidase inhibitor clade B (ovalbumin) member 6 - CGNC Symbol 51364		43.1	5.2	1 326.8 (M:326.8)	7	13.5	4.94	483	0.92!	3	14.77
1210	true	ENSGALP0000018295	SERPINE1 mRNA binding protein 1 - CGNC Symbol 8530		33	7.3	1 449.2 (M:449.2)	6	12.1	2	338	1.10!	2	8.18
1211	true	ENSGALP0000042163	seryl-tRNA synthetase - CGNC Symbol 332		53.1	6	1 325.4 (M:325.4)	8	14.1	8.07	486	1.61!	4	251.19
1212	true	ENSGALP0000020310	SET binding factor 1 - CGNC Symbol 9447		200.1	7	1 257.9 (M:257.9)	4	3.4	8.1	629			
1213	true	ENSGALP0000007476	SET nuclear oncogene - CGNC Symbol 3483		32.1	4.1	1 224.1 (M:224.1)	8	22.4	8.63	720	0.97!	3	11.18
1214	true	ENSGALP0000001306	SFRS protein kinase 1 - CGNC Symbol 586		83.6	6.4	2 159.5 (M:159.5)	3	2.7	5.06	930	0.91!	1	
1215	true	ENSGALP00000035717	SGT1 homolog MIS12 kinetochore complex assembly cochaperone - CGNC Symbol 12721		37.2	5.5	2 457.9 (M:457.9)	10	26.3	6.39	333	0.69!	3	8.63
1216	true	ENSGALP0000013748	SH2 domain containing 1A - CGNC Symbol 65191		13.9	9.4	1 79.2 (M:79.2)	1	10.2	10.27	1296			
1217	true	ENSGALP0000007174	SH3-domain GRB2-like endophilin B1 - CGNC Symbol 4722		40.8	6	1 88.0 (M:88.0)	2	7.7	14.33	1261		0.42	1
1218	true	ENSGALP0000017599	signal peptidase complex subunit 3 - CGNC Symbol 8235		15.5	5.8	1 119.9 (M:119.9)	3	7.4	6.23	1103		0.58	1
1219	true	ENSGALP0000020852	signal sequence receptor alpha - CGNC Symbol 9701		32.2	4.4	1 83.5 (M:83.5)	1	5.2	8.78	1278	0.60!	1	
1220	true	ENSGALP0000012376	signal transducer and activator of transcription 1 91kDa - CGNC Symbol 52118		86.4	7.8	1 560.1 (M:560.1)	12	17.1	5.05	265	2.00!	5	43.24
1221	true	ENSGALP0000005161	signal transducer and activator of transcription 3 (acute-phase response factor) - CGNC Symbol 2374		88.1	5.9	1 349.3 (M:349.3)	10	12.2	11.75	449		0.98	5 13.15
1222	true	ENSGALP0000005182	signal transducer and activator of transcription 5B - CGNC Symbol 49373		90	5.9	1 596.5 (M:596.5)	12	12.5	5.35	240	0.67!	6	20.12
1223	true	ENSGALP00000042430	signal transducer and activator of transcription 6 - CGNC Symbol 63933		26.9	7.8	1 114.4 (M:114.4)	4	16.2	14.66	1133	0.64!	1	
1224	true	ENSGALP0000017467	Sin3A-associated protein 30kDa - CGNC Symbol 8174		20.3	9.5	1 54.4 (M:54.4)	1	6.5	9.42	1400			
1225	true	ENSGALP0000020973	single-stranded DNA binding protein 1 mitochondrial - CGNC Symbol 9754		17.5	9.5	1 67.1 (M:67.1)	2	9.9	11.28	1348		0.41	1
1226	true	ENSGALP0000015735	Sjogren syndrome antigen B - CGNC Symbol 7359		46.3	8.3	1 443.7 (M:443.7)	9	14.1	8.95	342	0.60!	5	47.37
1227	true	ENSGALP0000023673	Ski-like RNA helicase 2 - CGNC Symbol 10905		133.4	8.4	1 231.1 (M:231.1)	6	5.1	4.01	694	0.65!	3	64.28
1228	true	ENSGALP0000012367	SLC9A3 regulator 1 - CGNC Symbol 51624		35.9	5.8	1 187.9 (M:187.9)	5	15.3	8.25	835	0.81!	3	28.92
1229	true	ENSGALP0000009795	small acidic protein - Refseq NP_990089		19	5.2	1 111.3 (M:111.3)	3	15.7	5.95	1150		1.17	2 108.3
1230	true	ENSGALP0000039979	small ArfGAP2 - CGNC Symbol 51046		43.7	8.8	1 64.0 (M:64.0)	2	6	2.17	1362			
1231	true	ENSGALP0000022734	small glutamine-rich tetratricopeptide repeat-containing protein alpha - Refseq NP_001026550		33.7	4.7	1 315.4 (M:315.4)	6	25.2	5.99	505	0.65!	2	24.43
1232	true	ENSGALP0000019299	small nuclear ribonucleoprotein D1 polypeptide - CGNC Symbol 8976		13.5	11.4	1 148.7 (M:148.7)	3	14	13.97	973		0.49	1
1233	true	ENSGALP0000010633	small nuclear ribonucleoprotein D3 polypeptide - CGNC Symbol 4974		13.9	10.3	1 617.6 (M:617.6)	10	37.3	16.29	223	0.67!	4	27.14
1234	true	ENSGALP0000001598	small nuclear ribonucleoprotein polypeptide A' - CGNC Symbol 50006		28.4	8.8	1 358.7 (M:358.7)	8	23.5	4.97	434	0.81!	3	54.98
1235	true	ENSGALP00000041366	small nuclear ribonucleoprotein polypeptide B2 - HGNC:11155		25.6	9.7	1 252.0 (M:252.0)	5	25.7	4.65	644	0.97!	3	73.62
1236	true	ENSGALP0000000189	small nuclear ribonucleoprotein polypeptide E - CGNC Symbol 49689		10.8	9.5	1 217.9 (M:217.9)	4	12	11.66	742		0.9	2 11.14
1237	true	ENSGALP0000018594	small nuclear ribonucleoprotein polypeptide F - CGNC Symbol 8670		12.4	6.6	1 111.5 (M:111.5)	3	18.8	2.15	1148		0.48	2 15.86

1238	true	ENSGALP00000011718	small nuclear ribonucleoprotein polypeptides B and B1 - CGNC Symbol 49251	47.3	11.7	1 304.5 (M:304.5)	9	12.3	13.54	524	0.61!	4	10.83
1239	true	ENSGALP00000040424	small nuclear ribonucleoprotein U5 subunit 40 - CGNC Symbol 381	41.3	8.3	1 470.1 (M:470.1)	8	21.8	3.7	317	0.61!	4	18.34
1240	true	ENSGALP00000013729	small ubiquitin-like modifier 1 - CGNC Symbol 48961	11.5	5.3	1 206.6 (M:206.6)	6	39.6	9.27	772	1.17!	1	
1241	true	ENSGALP00000033053	SMT3 suppressor of mif two 3 homolog 3 - CGNC Symbol 56110	10.7	5.3	2 115.9 (M:115.9)	2	12.8	9.09	1117	0.65	1	
1242	true	ENSGALP00000003130	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) - CGNC Symbol 1430	57.5	6.7	1 262.5 (M:262.5)	7	13.3	3.9	620	1.33!	3	88.95
1243	true	ENSGALP00000025878	SMYD family member 5 - CGNC Symbol 51866	41.7	4.7	1 66.9 (M:66.9)	3	4.9	11.55	1349	0.42	1	
1244	true	ENSGALP00000019435	SNU13 homolog small nuclear ribonucleoprotein (U4/U6.U5) - CGNC Symbol 9043	14.1	8.4	1 271.6 (M:271.6)	5	30.5	8.53	600	0.79!	3	27.36
1245	true	ENSGALP00000041377	snurportin-1 - Refseq NP_001074347	40.6	5.4	1 30.7 (M:30.7)	1	3.3	0.48	1471	0.96	1	
1246	true	ENSGALP00000017080	SNW domain containing 1 - CGNC Symbol 7983	61.8	9.5	1 103.3 (M:103.3)	1	4.1	7.26	1189			
1247	true	ENSGALP00000005587	solute carrier family 12 (potassium/chloride transporters) member 4 - CGNC Symbol 50057	121.6	6.4	1 141.1 (M:141.1)	3	1.6	13.29	1007	1.22!	1	
1248	true	ENSGALP0000004710	solute carrier family 2 member 6 - HGNC:11011	56.1	9.4	1 61.6 (M:61.6)	2	4.3	10.32	1373	0.34	1	
1249	true	ENSGALP00000015519	solute carrier family 25 (aspartate/glutamate carrier) member 12 - CGNC Symbol 7264	77.3	8.9	1 178.9 (M:178.9)	3	5.7	12.18	871			
1250	true	ENSGALP00000015517	solute carrier family 25 (aspartate/glutamate carrier) member 13 - CGNC Symbol 7395	74.7	8.7	2 275.0 (M:275.0)	5	4.9	9.52	589	1.22!	2	0.98
1251	true	ENSGALP00000014105	solute carrier family 25 (mitochondrial carrier adenine nucleotide translocator) member 5 - CGNC Symk	35	10	2 1035.8 (M:1035.8)	19	42	6.1	96	0.76!	9	31.02
1252	true	ENSGALP00000035815	solute carrier family 25 (mitochondrial carrier adenine nucleotide translocator) member 6 - CGNC Synt	29.1	9.7	1 888.3 (M:888.3)	17	46.8	6.7	123	1.08!	8	113.86
1253	true	ENSGALP0000002996	solute carrier family 25 (mitochondrial carrier phosphate carrier) member 24 - CGNC Symbol 1369	51.9	8.7	1 206.2 (M:206.2)	3	8.4	6.7	774	1.01!	2	1.22
1254	true	ENSGALP00000018750	solute carrier family 25 member 3 - CGNC Symbol 8748	40	9.4	1 512.5 (M:512.5)	14	24.9	6.12	295	1.28!	7	101.3
1255	true	ENSGALP00000024856	solute carrier family 44 (choline transporter) member 1 - CGNC Symbol 53042	72.4	8.7	1 90.4 (M:90.4)	2	2.2	12.17	1249	0.57	1	
1256	true	ENSGALP00000010157	SON DNA binding protein - CGNC Symbol 4729	48.2	9.6	1 67.7 (M:67.7)	1	2.5	0.7	1344			
1257	true	ENSGALP00000014599	sorcin - CGNC Symbol 51278	21.8	5.4	1 253.1 (M:253.1)	6	22.7	3.37	641	0.69!	3	16.19
1258	true	ENSGALP00000008547	sorting nexin 2 - CGNC Symbol 52887	66.5	5.7	1 96.7 (M:96.7)	3	3.2	4.39	1220	2.26!	1	
1259	true	ENSGALP00000016263	sorting nexin 6 - CGNC Symbol 56458	46.4	5.8	1 175.5 (M:175.5)	5	10.1	4.88	881	0.71!	1	
1260	true	ENSGALP00000022252	sorting nexin 9 - CGNC Symbol 10266	67.1	5.4	1 176.4 (M:176.4)	2	5.2	9.86	878			
1261	true	ENSGALP00000001411	sorting nexin family member 27 - CGNC Symbol 636	62.6	5.6	1 77.2 (M:77.2)	2	3.6	15.33	1305			
1262	true	ENSGALP00000015174	Sp3 transcription factor - CGNC Symbol 7089	76.5	5.1	1 117.7 (M:117.7)	2	4.5	4.94	1111			
1263	true	ENSGALP00000037408	spastic paraplegia 11 (autosomal recessive) - CGNC Symbol 50019	275.5	5.6	1 257.1 (M:257.1)	3	1	13.18	633	0.54!	1	
1264	true	ENSGALP00000038979	spectrin alpha non-erythrocytic 1 - CGNC Symbol 3498	285.2	5.2	1 1377.8 (M:1377.8)	25	9.2	9.27	59	0.96!	13	51.03
1265	true	ENSGALP00000042294	spectrin beta non-erythrocytic 1 - CGNC Symbol 6184	273.9	5.4	2 822.0 (M:822.0)	18	7.5	7.29	137	0.70!	9	36.69
1266	true	ENSGALP00000019252	spectrin repeat containing nuclear envelope 2 - CGNC Symbol 8956	803.7	5.1	1 537.0 (M:537.0)	6	0.9	15.57	280			
1267	true	ENSGALP00000005794	spen family transcriptional repressor - CGNC Symbol 2675	397.1	6.9	1 238.0 (M:238.0)	4	1.2	16.68	672	0.65!	2	53.75
1268	true	ENSGALP00000001800	spermatid perinuclear RNA binding protein - CGNC Symbol 50441	73.3	8.9	2 115.7 (M:115.7)	2	2.1	8.65	1119	0.57!	1	
1269	true	ENSGALP00000004799	spermidine synthase - CGNC Symbol 2201	23.6	5	1 164.2 (M:164.2)	3	14.8	7.15	913	0.64!	2	12.83
1270	true	ENSGALP00000014514	sphingomyelin phosphodiesterase 1 - CGNC Symbol 50914	49.6	7	1 77.6 (M:77.6)	1	6.4	11.68	1303			
1271	true	ENSGALP00000010409	sphingomyelin phosphodiesterase 4 - CGNC Symbol 4864	96.2	7.7	1 42.1 (M:42.1)	1	1.8	4.94	1442			
1272	true	ENSGALP00000012879	splicing factor 3a subunit 1 - CGNC Symbol 6003	88.4	5	1 310.2 (M:310.2)	6	7.6	5.31	518	0.49!	2	3
1273	true	ENSGALP0000001205	splicing factor 3a subunit 2 - CGNC Symbol 14678	35.1	9.7	1 111.4 (M:111.4)	4	10.2	5.3	1149	0.59!	2	21.82
1274	true	ENSGALP0000002338	splicing factor 3a subunit 3 - CGNC Symbol 1064	58.9	5.3	1 121.9 (M:121.9)	5	9.6	12.5	1093	0.61!	2	42.92
1275	true	ENSGALP00000013029	splicing factor 3b subunit 1 - CGNC Symbol 6082	145.6	6.6	1 432.8 (M:432.8)	9	8.1	7.28	350	2.00!	3	40.32
1276	true	ENSGALP00000039265	splicing factor 3b subunit 3 - CGNC Symbol 1817	122.7	5.2	2 954.5 (M:954.5)	22	17	6.77	108	0.65!	9	40.79
1277	true	ENSGALP0000003954	splicing factor proline/glutamine-rich - CGNC Symbol 49487	69.5	9.5	1 1668.4 (M:1668.4)	28	30.6	11.16	36	0.57!	13	48.4
1278	true	ENSGALP00000038107	squamous cell carcinoma antigen recognized by T-cells 3 - HGNC:16860	107.7	5.3	1 141.1 (M:141.1)	4	3.2	7.72	1006	1.13!	2	232.13
1279	true	ENSGALP00000025508	SR-related CTD-associated factor 4 - CGNC Symbol 11826	120.8	9.6	2 179.5 (M:179.5)	3	2.6	7.87	869	0.31!	2	10.56
1280	true	ENSGALP00000015177	SRP receptor alpha subunit - CGNC Symbol 713	71.2	9.1	1 145.6 (M:145.6)	5	5.9	12.58	983	1.00!	2	6.38
1281	true	ENSGALP00000022235	stathmin 1 - CGNC Symbol 49630	17.1	6.2	3 540.6 (M:540.6)	9	46.6	10.68	276	0.12!	2	24.55
1282	true	ENSGALP00000013524	STE20-like kinase - CGNC Symbol 6304	143.9	5	1 183.9 (M:183.9)	3	2.1	8.33	850	1.03!	1	
1283	true	ENSGALP00000013808	stromal antigen 2 - CGNC Symbol 51718	145.7	5.3	1 426.4 (M:426.4)	9	4.7	8.5	359	0.41!	5	34.44
1284	true	ENSGALP00000027982	stromal interaction molecule 1 - CGNC Symbol 13037	73	7.2	1 290.6 (M:290.6)	7	11.4	6.92	553	0.90!	3	12.06
1285	true	ENSGALP00000013963	structural maintenance of chromosomes 3 - CGNC Symbol 6512	141.5	6.7	1 821.9 (M:821.9)	14	12.1	5.2	138	0.61!	5	49.72
1286	true	ENSGALP00000032358	structural maintenance of chromosomes 4 - CGNC Symbol 7271	145.6	6	1 191.0 (M:191.0)	4	2.9	6.7	824	0.53!	3	56.14
1287	true	ENSGALP00000023866	structural maintenance of chromosomes flexible hinge domain containing 1 - CGNC Symbol 10985	226.6	7.4	1 357.1 (M:357.1)	8	3.4	8.37	438	0.70!	3	52.66
1288	true	ENSGALP00000012145	structure specific recognition protein 1 - CGNC Symbol 49844	80	6.4	1 318.6 (M:318.6)	8	11.3	4.95	501	0.58!	4	71.69
1289	true	ENSGALP00000018671	STT3B subunit of the oligosaccharyltransferase complex (catalytic) - CGNC Symbol 53366	82.8	9	1 84.0 (M:84.0)	2	3.6	7.61	1272	2.40!	1	
1290	true	ENSGALP00000021475	succinate dehydrogenase complex flavoprotein subunit A - CGNC Symbol 49461	72.9	6.8	1 348.8 (M:348.8)	7	11.6	3.59	450	0.82!	3	44.54
1291	true	ENSGALP0000000693	succinate dehydrogenase complex subunit B iron sulfur (lp) - CGNC Symbol 63429	32.6	9.1	2 306.1 (M:306.1)	9	21.4	5.31	523	1.11!	5	154.03
1292	true	ENSGALP00000031379	succinate-CoA ligase alpha subunit - CGNC Symbol 11915	34.8	9.5	1 95.8 (M:95.8)	1	7.3	3.87	1226			
1293	true	ENSGALP00000008003	SUMO-activating enzyme subunit 2 - Refseq NP_001025742	45.2	6.1	1 142.4 (M:142.4)	3	3.7	4.87	1000	0.93!	1	
1294	true	ENSGALP00000035996	superoxide dismutase 1 soluble - CGNC Symbol 11821	15.7	6.1	1 702.6 (M:702.6)	8	44.8	5.07	185	0.99!	3	38.25
1295	true	ENSGALP00000019039	superoxide dismutase 2 mitochondrial - CGNC Symbol 8863	24.8	8.6	1 108.5 (M:108.5)	4	13.8	9.72	1164	0.87!	1	
1296	true	ENSGALP00000019569	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein) - CGNC Symbol 50650	40.2	5.1	1 375.7 (M:375.7)	5	10	4.56	412	0.62!	2	24.56

1297	true	ENSGALP00000041673	Surfeit locus protein 4 - UP Q800K9	30.6	7.6	1 311.6 (M:311.6)	6	11.5	4.38	515	0.83	3	18.55
1298	true	ENSGALP0000016509	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily a member 2 - CG	176.7	8.2	1 603.0 (M:603.0)	12	8	3.48	237	0.36!	4	38.17
1299	true	ENSGALP0000016102	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily a member 5 - CG	116.6	8.7	3 484.6 (M:484.6)	15	12.3	8.5	309	0.63!	9	109.19
1300	true	ENSGALP0000018696	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily a-like 1 - CGNC S _i	107.6	8.9	1 244.0 (M:244.0)	3	2.1	15.51	661	0.69!	2	14.14
1301	true	ENSGALP0000009608	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily b member 1 - CG	44.5	5.8	1 69.0 (M:69.0)	2	7.5	12.81	1333			
1302	true	ENSGALP0000008082	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily c member 1 - CGI	110.5	5.3	1 402.8 (M:402.8)	9	6.8	8.99	384	0.51!	4	37.22
1303	true	ENSGALP0000006164	SWI/SNF related matrix associated actin dependent regulator of chromatin subfamily e member 1 - CG	46.7	4.9	1 123.0 (M:123.0)	2	5.6	6.57	1086	0.80!	2	33.34
1304	true	ENSGALP0000008955	synaptotagyrin 3 - CGNC Symbol 4162	25.2	4.8	1 31.2 (M:31.2)	1	4.3	15.9	1470			
1305	true	ENSGALP0000025475	synaptotagmin binding cytoplasmic RNA interacting protein - CGNC Symbol 51548	49.7	6.7	1 264.1 (M:264.1)	7	13.4	9.1	614	0.82!	2	24.67
1306	true	ENSGALP0000024853	syndecan binding protein (syntenin) - CGNC Symbol 51422	32	7	1 298.5 (M:298.5)	3	11.6	13.85	536	1.49!	1	
1307	true	ENSGALP0000018987	t-complex 1 - CGNC Symbol 8842	60.4	5.6	1 1069.7 (M:1069.7)	22	25.6	5.97	89	1.07!	11	53.69
1308	true	ENSGALP0000004013	talin 1 - CGNC Symbol 1830	271.7	5.9	1 1737.4 (M:1737.4)	33	12.6	7.5	31	0.84!	15	57.37
1309	true	ENSGALP0000004576	TBC1 domain family protein 1 - CGNC Symbol 2099	44.5	6	2 247.4 (M:247.4)	3	7.2	10.46	653	0.41!	1	
1310	true	ENSGALP0000003005	TBC1 domain family member 2 - CGNC Symbol 1373	90.8	5.6	1 81.1 (M:81.1)	4	5.5	10.52	1287	0.85!	1	
1311	true	ENSGALP0000018335	TBC1 domain family member 5 - CGNC Symbol 8548	91.3	5.8	1 196.8 (M:196.8)	3	3.4	2.44	807	0.18!	1	
1312	true	ENSGALP0000015293	testis derived transcript (3 LIM domains) - CGNC Symbol 7146	47.1	7.6	1 140.6 (M:140.6)	1	4.3	1.96	1009			
1313	true	ENSGALP0000015780	tetratricopeptide repeat protein 38-like - CGNC Symbol 52836	53.2	5.9	2 161.6 (M:161.6)	5	14.8	10.32	923	0.97!	1	
1314	true	ENSGALP0000042374	thimet oligopeptidase 1 - CGNC Symbol 52774	78.3	5.8	1 559.1 (M:559.1)	13	14.6	10.61	266	0.54!	7	61.05
1315	true	ENSGALP0000025280	thioredoxin - CGNC Symbol 49804	11.7	5.1	1 470.5 (M:470.5)	10	43.8	4.95	316	1.78!	5	38.2
1316	true	ENSGALP0000020830	thioredoxin domain containing 5 (endoplasmic reticulum) - CGNC Symbol 51359	46.4	5.7	1 784.7 (M:784.7)	13	22	6.4	152	0.66!	7	85.13
1317	true	ENSGALP0000004651	thioredoxin like 1 - CGNC Symbol 2131	32.3	4.9	1 384.5 (M:384.5)	7	28	3.86	404	1.05!	2	21.2
1318	true	ENSGALP00000040938	thioredoxin related transmembrane protein 4 - CGNC Symbol 6720	35.4	4.4	1 209.7 (M:209.7)	3	9.3	3.63	764	0.37!	1	
1319	true	ENSGALP0000024009	THO complex 1 - CGNC Symbol 11072	73.4	5	1 96.7 (M:96.7)	1	2.3	2.81	1221			
1320	true	ENSGALP0000013843	THO complex 2 - CGNC Symbol 6452	170.8	8.3	1 348.7 (M:348.7)	7	5.4	6.93	451	0.41!	3	90.45
1321	true	ENSGALP0000018083	THO complex 7 - CGNC Symbol 5517	23.9	5.9	1 43.5 (M:43.5)	1	7.8	3.44	1436			
1322	true	ENSGALP0000002322	thymocyte nuclear protein 1 - CGNC Symbol 1055	28	8.3	1 606.7 (M:606.7)	12	31.4	5.11	232	1.34!	6	642.91
1323	true	ENSGALP0000037462	thymopoietin - CGNC Symbol 50621	50.1	8.8	1 779.4 (M:779.4)	13	28.7	6.8	156	0.33!	5	16.84
1324	true	ENSGALP0000028782	thymosin beta 10 - CGNC Symbol 13616	5.2	5	1 44.5 (M:44.5)	1	28.9	3.28	1435			
1325	true	ENSGALP0000040654	thymosin beta 4 Y-linked - HGNC:11882	5	5	1 710.9 (M:710.9)	13	86.4	7.84	182	1.90!	5	44.56
1326	true	ENSGALP0000026127	thyroglobulin - CGNC Symbol 65221	299.7	4.9	1 173.5 (M:173.5)	2	0.5	23.49	885	0.56!	1	
1327	true	ENSGALP0000003357	thyroid hormone receptor associated protein 3 - CGNC Symbol 51043	109.8	10.2	1 618.6 (M:618.6)	14	17.6	7.82	221	1.07!	7	62.73
1328	true	ENSGALP0000004614	thyroid hormone receptor interactor 12 - CGNC Symbol 2117	225.6	8.9	1 97.4 (M:97.4)	3	1.1	13.68	1217	0.38	1	
1329	true	ENSGALP0000015333	TIA1 cytotoxic granule-associated RNA binding protein - CGNC Symbol 56693	42.9	8.1	2 280.8 (M:280.8)	5	12.9	14.36	579	0.72!	3	14.42
1330	true	ENSGALP0000025935	tissue specific transplantation antigen P35B - CGNC Symbol 12057	36.4	6.9	1 130.1 (M:130.1)	2	2.8	1.08	1068	1.22	1	
1331	true	ENSGALP0000018643	TNF alpha induced protein 2 - CGNC Symbol 8698	77.9	8	1 53.6 (M:53.6)	2	4.2	16.78	1406			
1332	true	ENSGALP0000043331	topoisomerase (DNA) I - CGNC Symbol 2691	88.8	9.4	3 506.9 (M:506.9)	12	13.6	6.3	299	0.75!	4	31.43
1333	true	ENSGALP0000039270	topoisomerase (DNA) II alpha 170kDa - CGNC Symbol 49380	167.9	8.9	1 604.0 (M:604.0)	13	6.8	8.95	234	0.89!	6	40.91
1334	true	ENSGALP0000018410	topoisomerase (DNA) II beta 180kDa - CGNC Symbol 8591	183.2	8.5	1 627.4 (M:627.4)	15	8.4	5.67	216	0.56!	5	59.03
1335	true	ENSGALP0000022248	topoisomerase (DNA) III beta - CGNC Symbol 1026	96.6	8.4	1 71.8 (M:71.8)	2	2.9	17.54	1322	0.67!	1	
1336	true	ENSGALP0000012474	trafficking protein particle complex 4 - CGNC Symbol 5825	24.2	6.2	1 115.4 (M:115.4)	2	6.4	13.69	1120	0.49!	1	
1337	true	ENSGALP0000024417	trafficking protein particle complex 8 - CGNC Symbol 11281	160.8	6.4	1 91.3 (M:91.3)	1	1.7	5.16	1245			
1338	true	ENSGALP0000032101	transaldolase - Refseq NP_001026348	37.6	7.1	1 148.8 (M:148.8)	4	12.5	11.09	971	0.78!	3	51.33
1339	true	ENSGALP0000024609	transcription elongation factor A (SII) 1 - CGNC Symbol 51413	32.4	8.8	2 514.3 (M:514.3)	6	19.9	9.37	294	0.52!	3	30.25
1340	true	ENSGALP0000025184	transcription elongation factor B subunit 1 - CGNC Symbol 11667	12.5	4.7	1 64.8 (M:64.8)	2	8.9	13.65	1358	0.85	1	
1341	true	ENSGALP0000012163	transcription elongation regulator 1 - CGNC Symbol 5680	109.9	8.6	1 592.7 (M:592.7)	13	11.7	6.64	245	0.69!	4	68.56
1342	true	ENSGALP0000040388	transcription factor 3 - CGNC Symbol 739	70.3	6.3	2 140.4 (M:140.4)	3	3.3	4.15	1012	0.87!	1	
1343	true	ENSGALP0000004251	transcription factor A mitochondrial - CGNC Symbol 1948	29.9	10.3	1 158.2 (M:158.2)	4	12.6	20.63	935	0.48!	1	
1344	true	ENSGALP0000021770	transducin (beta)-like 1X-linked - CGNC Symbol 52656	56.6	5.4	1 169.5 (M:169.5)	3	5.4	15.49	903	2.15!	1	
1345	true	ENSGALP0000010405	transferrin (ovotransferrin) - CGNC Symbol 49715	77.8	6.8	1 677.5 (M:677.5)	10	20.6	6.03	196	0.44!	4	59.75
1346	true	ENSGALP0000005678	transformation/transcription domain associated protein - CGNC Symbol 2626	433.3	8.5	1 225.9 (M:225.9)	3	1	10.72	711			
1347	true	ENSGALP0000017856	transformer 2 alpha homolog (Drosophila) - CGNC Symbol 51305	32.4	11.2	1 419.8 (M:419.8)	9	27.1	7.25	366	0.51!	3	36.05
1348	true	ENSGALP0000010541	transformer 2 beta homolog (Drosophila) - CGNC Symbol 49299	33.8	11.2	1 405.3 (M:405.3)	8	23.5	8.03	380	0.50!	4	86.96
1349	true	ENSGALP0000042171	transgelin 2 - CGNC Symbol 65718	29	9.6	1 460.7 (M:460.7)	10	26.5	9.43	329	0.88!	4	13.26
1350	true	ENSGALP0000038435	transglutaminase 2 (C polypeptide protein-glutamine-gamma-glutamyltransferase) - CGNC Symbol 498	77.7	4.9	1 583.2 (M:583.2)	11	20.1	10.17	252	2.36!	2	74.72
1351	true	ENSGALP0000027733	transient receptor potential cation channel subfamily C member 6 - CGNC Symbol 12918	108.8	7.5	1 133.2 (M:133.2)	2	2.5	19.62	1052			
1352	true	ENSGALP0000008498	transketolase - CGNC Symbol 3953	68.4	7.3	1 1631.2 (M:1631.2)	28	31.1	6.68	40	0.75!	12	42.24
1353	true	ENSGALP0000042618	Translationally-controlled tumor protein homolog - UP P43347	19.5	4.9	1 159.6 (M:159.6)	5	16.3	6.92	929	1.81	4	242.99
1354	true	ENSGALP0000019018	translin - CGNC Symbol 8854	26	6.2	1 199.8 (M:199.8)	5	22.3	13.29	801	0.56!	3	124.51
1355	true	ENSGALP0000007945	translocase of inner mitochondrial membrane 8 homolog A (yeast) - CGNC Symbol 3689	12.2	7.9	1 194.4 (M:194.4)	4	20	13.09	814	0.59!	2	10.49

1356	true	ENSGALP00000029965	translocase of outer mitochondrial membrane 22 homolog (yeast) - CGNC Symbol 13830	24.7	4.7	1 111.1 (M:111.1)	3	7.7	10.25	1151	0.77	1
1357	true	ENSGALP00000006527	translocase of outer mitochondrial membrane 34 - CGNC Symbol 3015	33.7	9.1	1 136.7 (M:136.7)	3	11.9	14.92	1025	1.57	1
1358	true	ENSGALP00000024624	translocase of outer mitochondrial membrane 70 - CGNC Symbol 11379	72.5	8	1 153.2 (M:153.2)	3	3.7	9.26	958	0.64	2
1359	true	ENSGALP00000008171	translocated promoter region nuclear basket protein - CGNC Symbol 3800	243.4	5.2	1 737.3 (M:737.3)	16	6	4.86	171 0.61!	6	59.61
1360	true	ENSGALP00000042322	translocon-associated protein subunit gamma - Refseq NP_001264404	21.2	9.6	1 78.7 (M:78.7)	2	12.8	17.5	1301 3.58!	1	
1361	true	ENSGALP00000008863	transmembrane 9 superfamily member 3 - CGNC Symbol 4123	68.2	6.8	1 97.7 (M:97.7)	3	3.6	10.28	1216	1.53	2
1362	true	ENSGALP00000041758	transporter 1 ATP-binding cassette sub-family B (MDR/TAP) - CGNC Symbol 53176	62.8	7.7	1 382.3 (M:382.3)	6	11	3.24	408	2.51	2
1363	true	ENSGALP00000024167	transportin 1 - CGNC Symbol 11160	88.5	4.9	1 201.6 (M:201.6)	3	4.5	16.04	794 0.86!	1	
1364	true	ENSGALP00000022392	transportin 3 - CGNC Symbol 10345	96.2	5.4	1 234.0 (M:234.0)	5	6.3	12.33	687		
1365	true	ENSGALP00000024388	transthyretin - CGNC Symbol 49731	16.3	5.1	1 239.2 (M:239.2)	2	30	7.36	667		
1366	true	ENSGALP00000023396	triosephosphate isomerase 1 - CGNC Symbol 49803	26.6	6.7	1 1905.2 (M:1905.2)	27	70.2	5.58	28 0.65!	15	62.32
1367	true	ENSGALP00000004962	tripartite motif containing 25 - CGNC Symbol 2279	75.4	8	1 200.8 (M:200.8)	4	3.6	10.3	798 0.78!	1	
1368	true	ENSGALP00000035601	tripeptidyl peptidase I - CGNC Symbol 15637	30	5.9	1 94.0 (M:94.0)	3	10.7	7.51	1235		
1369	true	ENSGALP0000027194	tripeptidyl peptidase II - CGNC Symbol 12657	144.1	6.1	1 135.8 (M:135.8)	4	3.6	10.72	1033 0.78!	2	73.63
1370	true	ENSGALP00000041514	tRNA methyltransferase 1 like - CGNC Symbol 3801	83.6	5.9	1 138.4 (M:138.4)	5	5.8	8.24	1021 1.12!	2	15.64
1371	true	ENSGALP00000014919	tRNA methyltransferase 6 - CGNC Symbol 6973	54.2	6.2	1 47.0 (M:47.0)	1	2.9	8.37	1431		
1372	true	ENSGALP00000018762	tRNA methyltransferase 61A - CGNC Symbol 8754	33.5	6.2	1 90.9 (M:90.9)	2	5.5	5.56	1246	0.9	1
1373	true	ENSGALP00000027999	tRNA nucleotidyl transferase CCA-adding 1 - CGNC Symbol 13046	41.5	6.3	1 88.2 (M:88.2)	2	8	5.07	1258		
1374	true	ENSGALP00000007492	tropomodulin 3 (ubiquitous) - CGNC Symbol 49978	39.3	5.1	4 104.8 (M:104.8)	3	5.4	8.13	1180 0.56!	1	
1375	true	ENSGALP00000038799	tropomyosin 1 (alpha) - CGNC Symbol 49772	32.9	4.7	1 845.7 (M:845.7)	14	22.2	4.31	133 0.88!	7	89.81
1376	true	ENSGALP00000022004	tropomyosin 3 - HGNC:12012	35.3	4.9	6 901.2 (M:901.2)	14	20.2	6.98	118 0.92!	7	111.08
1377	true	ENSGALP00000018294	tryptophanyl-tRNA synthetase - CGNC Symbol 8529	53.7	6.8	1 115.0 (M:115.0)	2	5.7	3.3	1127	1.03	1
1378	true	ENSGALP00000037524	tubulin alpha 4a - CGNC Symbol 65758	51	4.9	3 2072.9 (M:2072.9)	30	43.7	6.41	20 0.65!	14	131.09
1379	true	ENSGALP00000018454	tubulin alpha 4b - CGNC Symbol 65790	52.2	5.1	1 1585.9 (M:1585.9)	25	38.8	7.14	45 0.56!	11	144.85
1380	true	ENSGALP00000036688	tubulin alpha 8a - CGNC Symbol 262	50.1	5	1 1223.1 (M:1223.1)	17	27.5	6.06	74 0.98!	6	155.34
1381	true	ENSGALP00000036691	tubulin alpha 8b - CGNC Symbol 49796	49.8	4.8	1 1101.9 (M:1101.9)	17	25.8	6.74	84 0.80!	6	225.51
1382	true	ENSGALP00000016978	tubulin alpha-3 chain-like - CGNC Symbol 52325	50	4.9	1 1567.7 (M:1567.7)	20	34.2	5.63	47 0.91!	8	124.55
1383	true	ENSGALP00000020884	tubulin beta 2B class IIb - CGNC Symbol 51362	49.9	4.8	2 2537.2 (M:2537.2)	42	45.4	6.42	11 0.53!	22	81.72
1384	true	ENSGALP00000013964	tubulin beta 4B class IVb - CGNC Symbol 50466	49.8	4.8	2 2779.5 (M:2779.5)	48	50.8	5.71	6 0.60!	27	88.36
1385	true	ENSGALP00000042665	tubulin beta 6 class V - CGNC Symbol 51389	49.9	4.8	1 1560.1 (M:1560.1)	25	28.9	5.68	48 0.58!	13	94.73
1386	true	ENSGALP00000022436	tubulin beta class I - HGNC:20778	43.5	4.8	2 2662.3 (M:2662.3)	45	55.8	5.92	9 0.53!	24	77.65
1387	true	ENSGALP00000006933	tubulin folding cofactor A - CGNC Symbol 3204	12.7	5.4	1 149.1 (M:149.1)	4	16.7	8.03	970 0.51!	2	21.27
1388	true	ENSGALP00000022871	tubulin tyrosine ligase like 12 - CGNC Symbol 10561	72.8	5.1	1 102.0 (M:102.0)	2	4.8	9.79	1195		
1389	true	ENSGALP00000029249	tumor protein D52-like 2 - CGNC Symbol 50951	22.2	5.6	1 68.0 (M:68.0)	2	9.3	10.71	1341		
1390	true	ENSGALP00000026380	tumor suppressing subtransferable candidate 1 - CGNC Symbol 12263	43.7	4.9	1 124.6 (M:124.6)	2	3.6	4.25	1080	0.46	1
1391	true	ENSGALP0000006326	twinfilin actin-binding protein homolog 2 (Drosophila) - CGNC Symbol 50121	39.1	6.1	1 522.4 (M:522.4)	7	19.2	13.92	290 0.71!	4	27.08
1392	true	ENSGALP00000006578	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein beta - CGNC Symbol 5093	27.9	4.8	1 792.8 (M:792.8)	18	26.6	5.42	148 0.79!	9	94.63
1393	true	ENSGALP00000039133	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein epsilon - CGNC Symbol 50	26.6	4.7	1 897.5 (M:897.5)	18	35.9	7.13	119 1.43!	7	74.43
1394	true	ENSGALP00000010888	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein eta - CGNC Symbol 50393	28.3	4.8	2 598.7 (M:598.7)	16	29.6	7.11	239 1.23!	8	96.38
1395	true	ENSGALP00000036122	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein theta - CGNC Symbol 123	27.8	4.7	2 1091.6 (M:1091.6)	20	31.8	8.33	85 0.78!	10	111.2
1396	true	ENSGALP00000028746	tyrosine 3-monoxygenase/tryptophan 5-monoxygenase activation protein zeta - CGNC Symbol 5251	27.8	4.7	1 1422.8 (M:1422.8)	27	51	6.08	57 0.88!	11	89.38
1397	true	ENSGALP00000005633	tyrosyl-tRNA synthetase - CGNC Symbol 2601	59.3	6.2	1 155.6 (M:155.6)	4	6.8	13.26	945 1.00!	2	16.56
1398	true	ENSGALP00000026067	U2 small nuclear RNA auxiliary factor 1 - CGNC Symbol 49287	27.7	9.1	1 212.7 (M:212.7)	6	25.7	5.44	754 0.40!	2	21.73
1399	true	ENSGALP00000004104	U2 snRNP-associated SURP domain containing - CGNC Symbol 52256	109.6	8.4	1 334.2 (M:334.2)	9	6.9	7.17	468 1.14!	5	105.31
1400	true	ENSGALP00000020520	ubiquilin 1 - CGNC Symbol 9551	62.8	5.1	1 204.2 (M:204.2)	4	5.1	6.93	783	1.36	2
1401	true	ENSGALP00000022674	ubiquilin 4 - CGNC Symbol 52757	59.5	5.1	1 103.4 (M:103.4)	2	6.8	9.01	1187		
1402	true	ENSGALP00000011475	ubiquinol-cytochrome c reductase complex III subunit VII 9.5kDa - CGNC Symbol 5357	9.6	9.6	1 144.5 (M:144.5)	3	45.1	4.33	990 0.77!	2	31.8
1403	true	ENSGALP00000009286	ubiquinol-cytochrome c reductase core protein I - CGNC Symbol 4319	52.7	6.6	1 593.1 (M:593.1)	10	20.7	7.34	244 0.89!	6	47.57
1404	true	ENSGALP00000039194	ubiquinol-cytochrome c reductase core protein II - CGNC Symbol 1783	48.5	9	1 571.3 (M:571.3)	9	15.1	7.37	258 0.92!	4	22.07
1405	true	ENSGALP00000041886	ubiquinol-cytochrome c reductase Rieske iron-sulfur polypeptide 1 - CGNC Symbol 3283	29.4	8.7	1 92.7 (M:92.7)	3	8.5	2.59	1240 5.51!	1	
1406	true	ENSGALP00000039878	ubiquitin associated protein 2-like - CGNC Symbol 17025	116.3	6.6	1 392.7 (M:392.7)	7	5.8	11.6	397 0.86!	3	12.78
1407	true	ENSGALP00000023022	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) - CGNC Symbol 10625	25.1	5.7	1 201.5 (M:201.5)	2	12.9	7.51	795		
1408	true	ENSGALP00000027305	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) - CGNC Symbol 12703	26.3	4.9	1 219.1 (M:219.1)	4	17	6.13	737 0.58!	2	0.28
1409	true	ENSGALP00000012940	ubiquitin conjugating enzyme E2 H - CGNC Symbol 6039	20.6	4.6	1 204.5 (M:204.5)	2	8.2	3.06	781 1.56!	1	
1410	true	ENSGALP00000010363	ubiquitin conjugating enzyme E2 I - CGNC Symbol 4844	18	8.9	1 40.9 (M:40.9)	1	7.6	1.13	1446	0.79	1
1411	true	ENSGALP00000003058	ubiquitin conjugating enzyme E2 O - CGNC Symbol 1396	140.8	5.1	1 149.7 (M:149.7)	3	2.3	2.23	969	0.7	1
1412	true	ENSGALP00000009085	ubiquitin specific peptidase 10 - CGNC Symbol 4228	85.7	5	1 370.7 (M:370.7)	7	7.1	3.45	419	0.81	4
1413	true	ENSGALP00000041193	ubiquitin specific peptidase 39 - CGNC Symbol 64119	28.3	9.3	1 91.6 (M:91.6)	1	7.6	4.54	1244		
1414	true	ENSGALP00000023395	ubiquitin specific peptidase 5 (isopeptidase T) - CGNC Symbol 10793	95.7	5	1 703.8 (M:703.8)	14	11.9	4.63	184 0.67!	6	68.72

1415	true	ENSGALP00000039011	ubiquitin specific peptidase 7 (herpes virus-associated) - CGNC Symbol 5523	125.4	5.4	1 326.8 (M:326.8)	12	9.5	5.6	482	0.59!	6	68.63
1416	true	ENSGALP00000026130	ubiquitin specific peptidase 9 X-linked - CGNC Symbol 50795	290	5.6	1 468.8 (M:468.8)	13	4.2	11.08	319	0.76!	5	20.67
1417	true	ENSGALP00000023065	ubiquitin-conjugating enzyme E2 K - Refseq NP_001026711	19.8	5.1	1 38.1 (M:38.1)	1	10.1	6.63	1455			
1418	true	ENSGALP00000012992	ubiquitin-conjugating enzyme E2 variant 1 - CGNC Symbol 62089	16.3	7.7	2 142.9 (M:142.9)	4	17.9	7.86	998	0.57!	2	11.74
1419	true	ENSGALP00000014072	ubiquitin-conjugating enzyme E2A - CGNC Symbol 6564	17.3	5.1	1 64.7 (M:64.7)	2	11.2	9.65	1359	0.77	1	
1420	true	ENSGALP00000020092	ubiquitin-conjugating enzyme E2D 3 - CGNC Symbol 51809	15.8	6.3	1 76.1 (M:76.1)	1	17.1	4.7	1308			
1421	true	ENSGALP00000027200	ubiquitin-conjugating enzyme E2L 6 - CGNC Symbol 64999	17.8	6.1	1 78.8 (M:78.8)	2	10.3	15.31	1300	2.77	1	
1422	true	ENSGALP00000030005	ubiquitin-conjugating enzyme E2N - CGNC Symbol 50617	16	5.2	1 170.8 (M:170.8)	6	33.8	3.37	894	0.75!	2	43.82
1423	true	ENSGALP00000023101	UDP-glucose 6-dehydrogenase - CGNC Symbol 51825	55	7	1 147.8 (M:147.8)	4	4.9	12.64	978	0.94!	2	8.05
1424	true	ENSGALP00000040466	UDP-glucose glycoprotein glucosyltransferase 1 - CGNC Symbol 1529	173.5	5.3	1 215.1 (M:215.1)	4	2.6	7.48	746	1.15!	1	
1425	true	ENSGALP0000002995	Uncharacterized protein - UniProtKB/TrEMBL A0A087WUJ7 - CGNC Symbol 49954	58.9	6.1	1 136.5 (M:136.5)	4	5.7	11.25	1027	1.13!	1	
1426	true	ENSGALP00000030471	Uncharacterized protein - UniProtKB/TrEMBL H3BT36 - CGNC Symbol 13915	25.9	7	1 410.2 (M:410.2)	7	20.9	9.26	375	1.17	3	11.87
1427	true	ENSGALP00000025745	Uncharacterized protein - UniProtKB/TrEMBL H7C0C1 - CGNC Symbol 11954	24.5	9.8	1 372.0 (M:372.0)	5	13.8	2.68	418	0.81!	2	1.93
1428	true	ENSGALP00000010662	Uncharacterized protein - UniProtKB/TrEMBL H7C469 - CGNC Symbol 4989	43.3	5.9	1 351.4 (M:351.4)	8	9.5	8.06	446	0.88!	5	95.43
1429	true	ENSGALP00000010241	Uncharacterized protein - UniProtKB/TrEMBL V9GY05 - CGNC Symbol 4773	44.8	6.9	1 160.7 (M:160.7)	3	6.8	3.36	926	0.66!	1	
1430	true	ENSGALP00000042201	up-regulated during skeletal muscle growth 5 homolog (mouse) - CGNC Symbol 52069	6.7	10.1	1 241.7 (M:241.7)	5	55.9	6.36	664	0.90!	1	
1431	true	ENSGALP00000005090	UPF1 RNA helicase and ATPase - CGNC Symbol 2340	123.1	6.9	1 382.5 (M:382.5)	7	4.8	3.02	407	1.07!	3	5.84
1432	true	ENSGALP00000010803	UPF2 regulator of nonsense transcripts homolog (yeast) - CGNC Symbol 5054	149.7	5.5	1 179.5 (M:179.5)	3	3.4	15.46	870			
1433	true	ENSGALP00000019192	uridine monophosphate synthetase - CGNC Symbol 8931	51.9	6.1	1 217.1 (M:217.1)	5	12.1	8.37	743	0.53!	1	
1434	true	ENSGALP00000005542	uridine-cytidine kinase 2 - CGNC Symbol 2561	29.4	5.7	1 77.5 (M:77.5)	1	5.4	6.45	1304			
1435	true	ENSGALP00000017661	USO1 vesicle transport factor - CGNC Symbol 8265	106.1	4.9	1 163.1 (M:163.1)	4	4.3	6.22	918	0.96!	1	
1436	true	ENSGALP00000020359	USP6 N-terminal like - CGNC Symbol 5064	55.3	7.3	1 83.5 (M:83.5)	2	2.5	4.13	1277	0.49!	1	
1437	true	ENSGALP00000039765	UTP14 U3 small nucleolar ribonucleoprotein homolog A (yeast) - CGNC Symbol 51631	84.5	6.1	1 122.6 (M:122.6)	4	4.1	6.18	1087	0.77	3	17.75
1438	true	ENSGALP00000036651	v-akt murine thymoma viral oncogene homolog 1 - CGNC Symbol 49557	55.8	5.8	2 104.8 (M:104.8)	3	3.8	14.95	1179	1.26!	2	0.25
1439	true	ENSGALP00000010305	v-crk avian sarcoma virus CT10 oncogene homolog-like - CGNC Symbol 4810	33.7	6.2	1 154.5 (M:154.5)	2	5	10.65	954	0.75!	1	
1440	true	ENSGALP00000020091	v-ral simian leukemia viral oncogene homolog A (ras related) - CGNC Symbol 9353	23.5	6.7	2 84.2 (M:84.2)	2	3.4	1.58	1271	1.11	1	
1441	true	ENSGALP00000039504	v-rel avian reticuloendotheliosis viral oncogene homolog - CGNC Symbol 5934	66.9	6	1 182.9 (M:182.9)	4	6.5	6.69	854	0.82!	1	
1442	true	ENSGALP00000013480	V-set and immunoglobulin domain containing 1 - CGNC Symbol 6282	36.5	5.3	1 169.8 (M:169.8)	3	13.1	12.22	901			
1443	true	ENSGALP0000003869	Vac14 homolog (S. cereviciae) - CGNC Symbol 1758	87.8	5.9	1 151.4 (M:151.4)	2	1.4	8.54	963	0.56	1	
1444	true	ENSGALP00000018087	vaccinia related kinase 1 - CGNC Symbol 8440	47	9.5	1 586.6 (M:586.6)	10	24	6.13	249	0.42!	5	28.63
1445	true	ENSGALP0000006624	vacuolar protein sorting 26 homolog A (S. pombe) - CGNC Symbol 3064	38	6.1	1 51.2 (M:51.2)	1	4	1.77	1417			
1446	true	ENSGALP0000003089	valosin containing protein - CGNC Symbol 53073	89.3	5.1	2 1613.0 (M:1613.0)	37	34.7	6.59	42	0.95!	16	40.75
1447	true	ENSGALP00000028374	VAMP (vesicle-associated membrane protein)-associated protein A 33kDa - CGNC Symbol 54859	16.9	9.2	1 139.1 (M:139.1)	2	9.3	3.35	1017	0.92!	1	
1448	true	ENSGALP00000038259	vascular endothelial zinc finger 1 - CGNC Symbol 4119	59.8	9.5	1 122.3 (M:122.3)	4	7.2	8.61	1091			
1449	true	ENSGALP0000002942	vav 3 guanine nucleotide exchange factor - CGNC Symbol 1353	89.8	6.4	2 53.0 (M:53.0)	1	1.3	0.76	1409			
1450	true	ENSGALP00000014107	vimentin - CGNC Symbol 51275	53.2	5.1	5 1617.4 (M:1617.4)	34	48.5	6.06	41	1.22!	16	95.72
1451	true	ENSGALP00000008131	vinculin - CGNC Symbol 3778	114.3	5.4	1 279.4 (M:279.4)	4	5.5	6.19	581			
1452	true	ENSGALP00000043363	visual system homeobox 1 - Refseq NP_990100	24.6	8.9	1 199.3 (M:199.3)	4	6	5.17	802	0.75!	3	38.27
1453	true	ENSGALP0000007997	voltage-dependent anion channel 2 - CGNC Symbol 49348	30.2	8.6	1 329.3 (M:329.3)	8	25.1	9.09	476	1.02!	4	9.54
1454	true	ENSGALP00000069695	VPS35 retromer complex component - CGNC Symbol 3222	91.7	5.4	1 539.3 (M:539.3)	10	9.7	8.61	277	0.84!	6	63.95
1455	true	ENSGALP00000015447	VPS50 EARP/GARPII complex subunit - CGNC Symbol 7228	109.5	5.5	2 78.8 (M:78.8)	1	0.7	11.11	1299	0.82!	1	
1456	true	ENSGALP00000002944	WAPL cohesin release factor - CGNC Symbol 1347	133.4	5.1	1 156.4 (M:156.4)	4	3.8	9.74	943	0.99!	3	44.27
1457	true	ENSGALP00000037871	WAS/WASL interacting protein family member 1 - CGNC Symbol 7084	49.9	11.5	1 314.7 (M:314.7)	6	15.8	11.56	508	0.38!	1	
1458	true	ENSGALP00000024078	WD repeat domain 1 - CGNC Symbol 1108	66.5	6.2	1 229.9 (M:229.9)	7	9	10.04	698	0.82!	4	28.02
1459	true	ENSGALP0000004180	WD repeat domain 5 - CGNC Symbol 50449	36.6	8.5	1 140.0 (M:140.0)	3	8.1	7.27	1013	1.31!	2	111.36
1460	true	ENSGALP00000033991	WD repeat domain 61 - CGNC Symbol 2341	33.3	5.2	1 232.2 (M:232.2)	4	7.2	4.51	691	0.89!	2	13.48
1461	true	ENSGALP00000003872	WD repeat domain 75 - CGNC Symbol 1760	93.6	5.6	1 126.1 (M:126.1)	2	3.3	11.76	1075			
1462	true	ENSGALP00000002186	WD repeat domain 77 - CGNC Symbol 991	30.8	5	1 114.2 (M:114.2)	3	9.5	9.27	1134	0.16	1	
1463	true	ENSGALP00000019038	Wilms tumor 1 associated protein - CGNC Symbol 8862	44.5	5.2	1 284.5 (M:284.5)	6	12.8	8.4	571	0.58!	2	29.51
1464	true	ENSGALP00000019161	WW domain binding protein 11 - CGNC Symbol 53212	66.4	5.4	1 141.8 (M:141.8)	3	5.7	9.67	1003			
1465	true	ENSGALP00000013870	X-prolyl aminopeptidase (aminopeptidase P) 1 soluble - CGNC Symbol 6466	70	5.8	1 215.4 (M:215.4)	5	4.5	13.91	745	0.71!	3	56.86
1466	true	ENSGALP00000038408	Y box binding protein 1 - CGNC Symbol 3598	31.5	10	3 1011.5 (M:1011.5)	16	48.4	6.02	98	1.94!	6	72.59
1467	true	ENSGALP00000009213	YTH domain family member 1 - CGNC Symbol 4283	61.2	9	2 96.7 (M:96.7)	1	2.5	5.02	1219			
1468	true	ENSGALP00000028022	YY1 transcription factor - CGNC Symbol 51971	21.3	9.1	1 110.9 (M:110.9)	3	20.1	14.69	1153	0.49!	1	
1469	true	ENSGALP00000002252	zeta-chain (TCR) associated protein kinase 70kDa - CGNC Symbol 1027	69.5	7.2	1 511.9 (M:511.9)	10	17.1	9.01	297	0.51!	6	208.02
1470	true	ENSGALP00000002112	zinc finger and BTB domain containing 2 - CGNC Symbol 51512	56.9	5.6	1 88.0 (M:88.0)	2	5.9	6.88	1262			
1471	true	ENSGALP00000000747	zinc finger CCCH-type containing 11A - CGNC Symbol 51431	79	8.4	1 278.9 (M:278.9)	3	5.3	6.85	583	0.33!	1	
1472	true	ENSGALP00000004959	zinc finger CCCH-type containing 7A - CGNC Symbol 2278	109.7	6.7	1 51.9 (M:51.9)	1	2.4	0.39	1413			
1473	true	ENSGALP00000007220	zinc finger MYND-type containing 8 - CGNC Symbol 3357	126.6	6.2	1 207.5 (M:207.5)	4	3.5	14.07	770	0.65!	2	62.07

1474	true	ENSGALP00000009853	zinc finger protein 326 - CGNC Symbol 4587	63.5	5.5	1 762.1 (M:762.1)	12	21	6.49	162	0.70!	6	65.61	
1475	true	ENSGALP00000042800	Zinc finger protein 706 - UP O5ZMM5	8.6	9.9	1 101.1 (M:101.1)	3	27.6	2.38	1202	0.40!	1		
1476	true	ENSGALP00000042962	zinc finger protein 740 - CGNC Symbol 63794	21.3	9.5	1 134.2 (M:134.2)	4	23.1	9.03	1045	0.31!	1		
1477	true	ENSGALP00000002348	zinc finger ZZ-type and EF-hand domain containing 1 - CGNC Symbol 1069	330	5.7	1 328.8 (M:328.8)	9	3	9.08	478	0.67!	4	27.35	
1478	true	ENSGALP00000023166	ZPR1 zinc finger - CGNC Symbol 5362	25.8	4.4	1 62.6 (M:62.6)	2	13	14.74	1370				
1479	true	ENSGALP0000023626	zyxin - CGNC Symbol 10889	58.5	6.8	1 275.1 (M:275.1)	5	8.9	14.67	588		0.75	3	42.3