Cellular Component		A	B
GO:0000172	ribonuclease MRP complex	2	1
GO:0005655	nucleolar ribonuclease P complex	5	3
GO:0030530	heterogeneous nuclear ribonucleoprotei	10	7
GO:0000178	exosome (RNase complex)	6	8
GO:0005663	DNA replication factor C complex	5	17
GO:0000786	nucleosome	19	101
GO:0005732	small nucleolar ribonucleoprotein compl	6	37
GO:0005694	chromosome	18	118
GO:0005730	nucleolus	18	122
GO:0005842	cytosolic large ribosomal subunit (sensu	14	95
GO:0005840	ribosome	42	302
GO:0005654	nucleoplasm	10	74
GO:0005843	cytosolic small ribosomal subunit (sens	10	91
GO:0000785	chromatin	11	103
GO:0030529	ribonucleoprotein complex	10	113
GO:0005681	spliceosome complex	14	191

Molecular Function		A	B
GO:0004526	ribonuclease P activity	6	6
GO:0000175	3'-5'-exoribonuclease activity	9	17
GO:0008408	3'-5' exonuclease activity	8	19
GO:0004527	exonuclease activity	14	34
GO:0003690	double-stranded DNA binding	6	33
GO:0004004	ATP-dependent RNA helicase activity	10	58
GO:0008026	ATP-dependent helicase activity	24	142
GO:0004003	ATP-dependent DNA helicase activity	6	36
GO:0008094	DNA-dependent ATPase activity	6	39
GO:0003723	RNA binding	101	868
GO:0003725	double-stranded RNA binding	8	64
GO:0003697	single-stranded DNA binding	7	58
GO:0003735	structural constituent of ribosome	50	594
GO:0008248	pre-mRNA splicing factor activity	18	220

Biological Process		A	B
GO:0006337	nucleosome disassembly	2	1
GO:0006364	rRNA processing	22	34
GO:0008380	RNA splicing	21	51
GO:0007052	mitotic spindle assembly	5	19
GO:0008033	tRNA processing	7	33
GO:0006396	RNA processing	15	80
GO:0006334	nucleosome assembly	20	108
GO:0007001	chromosome organization and biogenes	21	140
GO:0006270	DNA replication initiation	6	40

GO:0006397	mRNA processing	13	142
GO:0006260	DNA replication	16	222
GO:0006412	protein biosynthesis	60	884

Note the values A, B, C and D are denoted from the following table

2x2 Contingency Table	**Nucleolar**	**Non-Nucleolar**
Presence of a specific GO annotatio	A	B
Absence of a specific GO annotation	C	D

Go to the following website to know more about the GO annotation
http://www.godatabase.org/cgi-bin/amigo/go.cgi?

Statistics:
If the frequency of any cell is less than 5, Fisher exact test was employed showing two P

C	D	Odd ratio	P value (Fisher tes	Chi square tes
659	18673	56.6707132	0.00342151	
656	18671	47.43648374	2.36E-06	
651	18667	40.96335308	3.19E-11	p<0.001 (chisq=
655	18666	21.37328244		p<0.001 (chisq=
656	18657	8.364867288		p<0.001 (chisq=
642	18573	5.442259647		p<0.001 (chisq=
655	18637	4.614070559		p<0.001 (chisq=
643	18556	4.402140391		p<0.001 (chisq=
643	18552	4.25689009		p<0.001 (chisq=
647	18579	4.23177418		p<0.001 (chisq=
619	18372	4.127700093		p<0.001 (chisq=
651	18600	3.861003861		p<0.001 (chisq=
651	18583	3.136847791		p<0.001 (chisq=
650	18571	3.051247199		p<0.001 (chisq=
651	18561	2.523143428		p<0.01 (chisq=
647	18483	2.093933337		p<0.025 (chisq=

C	D	Odd ratio	P value (Fisher tes	Chi square tes
655	18668	28.50076336		p<0.001 (chisq=
652	18657	15.14913389		p<0.001 (chisq=
653	18655	12.02869348		p<0.001 (chisq=
647	18640	11.86289663		p<0.001 (chisq=
655	18641	5.174462179		p<0.001 (chisq=
651	18616	4.930345887		p<0.001 (chisq=
637	18532	4.917062816		p<0.001 (chisq=
655	18638	4.742493639		p<0.001 (chisq=
655	18635	4.376981797		p<0.005 (chisq=
560	17806	3.699814845		p<0.001 (chisq=
653	18610	3.562404288		p<0.005 (chisq=
654	18616	3.435410735		p<0.005 (chisq=
611	18080	2.490811001		p<0.001 (chisq=
643	18454	2.348169094		p<0.001 (chisq=

C	D	Odd ratio	P value (Fisher tes	Chi square tes
659	18673	56.6707132	0.00342151	
639	18640	18.87508055		p<0.001 (chisq=
640	18623	11.98170956		p<0.001 (chisq=
656	18655	7.483552632		p<0.001 (chisq=
654	18641	6.046103234		p<0.001 (chisq=
646	18594	5.396865325		p<0.001 (chisq=
641	18566	5.36372566		p<0.001 (chisq=
640	18534	4.34390625		p<0.001 (chisq=
655	18634	4.267328244		p<0.005 (chisq=

648	18532	2.618196835	p<0.005 (chisq
645	18452	2.061819959	p<0.01 (chisq=
601	17790	2.009094947	p<0.001 (chisq

proteome

-tail value; otherwise, chi-square test with Yates' correction value was employed to ca

t

=141.839767608565)
=54.5862561714679)
=19.3595619984588)
=52.6443767120455)
=11.4644168231828)
=37.0359535070412)
=35.2234971517161)
=26.6926529581422)
=79.2798319572109)
=15.9099060002094)
=11.023084424452)
=11.6508611351848)
6.94790195799473)
=6.29281685846839)

t

=65.4232989103424)
=67.5710462907459)
=48.5895542039732)
=88.9583501590083)
=13.5098372078082)
=23.0118375220793)
=58.4716786292768)
=11.9367440975216)
=10.5874119519454)
=149.35788692634)
=10.7188859449335)
=8.55564165880012)
=36.7474837019077)
=11.2962404701779)

t

=208.061860717325)
=137.385494530989)
=17.1064467979457)
=19.9872119615504)
=40.5643732993688)
=54.4832954769041)
=42.6581979026777)
=10.1797935386853)

=10.2142457808925)
6.98598551968528)
=25.0057456263428)

with Yates' correction value was

Cellular Component		**A**	**B**	**C**
GO:0005737	cytoplasm	28	1563	633
GO:0005667	transcription factor complex	4	428	657
GO:0005856	cytoskeleton	4	514	657
GO:0005624	membrane fraction	4	537	657
GO:0005739	mitochondrion	11	1578	650
GO:0005871	kinesin complex	1	174	660
GO:0005743	mitochondrial inner membrane	1	188	660
GO:0008372	cellular_component unknown	10	1875	651
GO:0005625	soluble fraction	1	205	660
GO:0005783	endoplasmic reticulum	3	682	658
GO:0005886	plasma membrane	2	1065	659
GO:0016020	membrane	6	3201	655
GO:0005829	cytosol	1	631	660
GO:0005887	integral to plasma membrane	2	1886	659
GO:0016021	integral to membrane	4	6392	657

Molecular Function		**A**	**B**	**C**
GO:0003677	DNA binding	77	2940	584
GO:0003676	nucleic acid binding	33	1601	628
GO:0005200	structural constituent of cytoskeleton	8	488	653
GO:0004871	signal transducer activity	7	542	654
GO:0005198	structural molecule activity	8	618	653
GO:0008270	zinc ion binding	18	1416	643
GO:0004674	protein serine/threonine kinase activit	13	1077	648
GO:0016740	transferase activity	27	2213	634
GO:0008565	protein transporter activity	5	525	656
GO:0003774	motor activity	2	218	659
GO:0004867	serine-type endopeptidase inhibitor ac	2	248	659
GO:0005554	molecular_function unknown	13	1728	648
GO:0005516	calmodulin binding	2	301	659
GO:0016874	ligase activity	2	344	659
GO:0003779	actin binding	3	518	658
GO:0016563	transcriptional activator activity	1	182	660
GO:0004842	ubiquitin-protein ligase activity	1	192	660
GO:0005488	binding	1	199	660
GO:0004725	protein tyrosine phosphatase activity	1	201	660
GO:0005515	protein binding	16	2838	645
GO:0016491	oxidoreductase activity	6	1212	655
GO:0003700	transcription factor activity	12	2388	649
GO:0005215	transporter activity	3	707	658
GO:0004888	transmembrane receptor activity	1	252	660
GO:0016829	lyase activity	1	256	660
GO:0030528	transcription regulator activity	1	301	660
GO:0000287	magnesium ion binding	1	335	660
GO:0008233	peptidase activity	1	413	660
GO:0005509	calcium ion binding	3	1331	658
GO:0016301	kinase activity	1	744	660

GO:0001584	rhodopsin-like receptor activity	1	810	660
GO:0004672	protein kinase activity	1	814	660
GO:0004872	receptor activity	1	3268	660

Biological Process		**A**	**B**	**C**
GO:0008283	cell proliferation	9	569	652
GO:0006357	regulation of transcription from Pol II	11	702	650
GO:0006355	regulation of transcription, DNA-depen	45	3341	616
GO:0007283	spermatogenesis	3	301	658
GO:0008151	cell growth and/or maintenance	5	500	656
GO:0006366	transcription from Pol II promoter	4	404	657
GO:0006468	protein amino acid phosphorylation	14	1471	647
GO:0006605	protein targeting	2	261	659
GO:0006955	immune response	5	696	656
GO:0006915	apoptosis	4	574	657
GO:0007166	cell surface receptor linked signal tran	2	300	659
GO:0000004	biological_process unknown	12	1700	649
GO:0006520	amino acid metabolism	1	160	660
GO:0006950	response to stress	1	164	660
GO:0007165	signal transduction	11	1691	650
GO:0006512	ubiquitin cycle	1	171	660
GO:0007169	transmembrane receptor protein tyros	1	175	660
GO:0006886	intracellular protein transport	5	875	656
GO:0006810	transport	10	1708	651
GO:0030154	cell differentiation	1	187	660
GO:0007275	development	6	1101	655
GO:0006470	protein amino acid dephosphorylation	2	381	659
GO:0007264	small GTPase mediated signal transdu	2	384	659
GO:0007517	muscle development	1	215	660
GO:0006917	induction of apoptosis	1	228	660
GO:0006464	protein modification	1	254	660
GO:0006954	inflammatory response	1	265	660
GO:0007601	visual perception	1	293	660
GO:0006139	nucleobase, nucleoside, nucleotide an	1	303	660
GO:0006508	proteolysis and peptidolysis	5	1455	656
GO:0006118	electron transport	2	709	659
GO:0007242	intracellular signaling cascade	2	946	659
GO:0007186	G-protein coupled receptor protein sig	3	1561	658
GO:0007399	neurogenesis	1	600	660
GO:0008152	metabolism	1	761	660
GO:0006952	defense response	1	797	660
GO:0007155	cell adhesion	1	1010	660

Note the values A, B, C and D are denoted from the following table

2x2 Contingency Table	**Nucleolar**	**Non-Nucleolar proteome**
Presence of a specific GO annotati	A	B

Absence of a specific GO annotatio C D

Go to the following website to know more about the GO annotation
http://www.godatabase.org/cgi-bin/amigo/go.cgi?

Statistics:
If the frequency of any cell is less than 5, Fisher exact test was employed showing two P-tail v

D	Odd ratio	P value (Fisher test	Chi square test
17111	0.48425123	5.04E-05	p<0.001 (chisq=13.9050135805036)
18246	0.2595485	0.001777935	
18160	0.21510344	0.000182907	
18137	0.20562967	9.27E-05	
17096	0.18334406	2.03E-13	p<0.001 (chisq=38.0817597911428)
18500	0.1610937	0.033360252	
18486	0.14898453	0.023778027	
16799	0.13762622	2.34E-18	p<0.001 (chisq=51.8012366430226)
18469	0.13650407	0.011151904	
17992	0.12027917	1.54E-07	
17609	0.05017989	5.19E-14	
15473	0.0442791	1.49E-43	p<0.001 (chisq=120.431838323261)
18043	0.04332469	9.46E-09	
16788	0.02701481	4.95E-27	
12282	0.01169841	1.19E-109	

D	Odd ratio	P value (Fisher test	Chi square test
15734	0.70561807	0.003797866	p<0.01 (chisq=7.82044550169752)
17073	0.56036733	0.00078188	p<0.005 (chisq=10.1234711207644)
18186	0.45655612	0.023219349	p<0.05 (chisq=4.48173845760007)
18132	0.35806899	0.002665081	p<0.01 (chisq=7.20973795547642)
18056	0.35793971	0.00110779	p<0.005 (chisq=8.32161131014681)
17258	0.34118407	2.10E-07	p<0.001 (chisq=21.2541011739509)
17597	0.32778666	4.24E-06	p<0.001 (chisq=16.6281751953267)
16461	0.31677384	8.70E-12	p<0.001 (chisq=36.8344597458628)
18149	0.26348722	0.000384946	p<0.005 (chisq=9.35602361347948)
18456	0.25693642	0.037434811	
18426	0.22548828	0.013591381	
16946	0.19673961	4.95E-14	p<0.001 (chisq=40.4860883763202)
18373	0.18524998	0.003536166	
18330	0.16171437	0.000862377	
18156	0.15980331	2.42E-05	
18492	0.15394605	0.022932551	
18482	0.14584912	0.01596362	
18475	0.14066545	0.016517286	
18473	0.13925072	0.016847765	
15836	0.13841826	2.44E-27	p<0.001 (chisq=81.8209221717114)
17462	0.13197793	2.58E-12	p<0.001 (chisq=32.7679357208821)
16286	0.12610046	4.84E-24	p<0.001 (chisq=69.6895730212998)
17967	0.1158648	7.39E-08	
18422	0.11076239	0.002602275	
18418	0.10900805	0.002667106	
18373	0.09248465	0.000605351	
18339	0.08294437	0.000197652	
18261	0.06699318	1.40E-05	
17343	0.05940753	5.20E-17	
17930	0.03651434	1.84E-10	

17864	0.03341564	1.67E-11
17860	0.03324399	1.73E-11
15406	0.00714272	1.90E-52

D

	Odd ratio	P value (Fisher test	Chi square test
18105	0.43921906	0.009974976	p<0.025 (chisq=5.68578213253599)
17972	0.43325005	0.003070525	p<0.01 (chisq=7.31106466688527)
15333	0.33526056	4.66E-16	p<0.001 (chisq=53.5232571391568)
18373	0.27829727	0.01542559	
18174	0.27704268	0.000729065	p<0.005 (chisq=8.52281929660586)
18270	0.2753289	0.003363742	
17203	0.2530552	3.91E-10	p<0.001 (chisq=29.0575214633627)
18413	0.2141059	0.009703094	
17978	0.1968785	3.66E-06	p<0.001 (chisq=15.2849032929198)
18100	0.19198235	2.25E-05	
18374	0.18587759	0.003516086	
16974	0.18461706	2.83E-14	p<0.001 (chisq=41.1194794100949)
18514	0.17532197	0.047025449	
18510	0.17100887	0.048181982	
16983	0.16996133	7.32E-15	p<0.001 (chisq=42.5282131700934)
18503	0.16394648	0.032860586	
18499	0.1601645	0.033597898	
17799	0.15504355	1.87E-08	p<0.001 (chisq=21.7927881066519)
16966	0.15258457	5.46E-16	p<0.001 (chisq=45.0114402113164)
18487	0.14978934	0.023571651	
17573	0.14620713	1.14E-10	p<0.001 (chisq=28.5124749150181)
18293	0.14571509	0.000300045	
18290	0.14455298	0.000306101	
18459	0.13008457	0.007744324	
18446	0.12258107	0.005392887	
18420	0.10987831	0.002627452	
18409	0.10525443	0.001814322	
18381	0.09505119	0.000908548	
18371	0.09186419	0.00061686	
17219	0.09020095	9.22E-17	p<0.001 (chisq=44.259559104058)
17965	0.07689986	9.85E-09	
17728	0.05687392	2.66E-12	
17113	0.04998257	1.33E-20	
18074	0.04564141	3.16E-08	
17913	0.0356648	8.17E-11	
17877	0.0339854	2.47E-11	
17664	0.02649865	1.89E-14	

value; otherwise, chi-square test with Yates' correction value was employed to calculate the

p-value.