

TABLE 1 CELLO2GO output of top GO enrichment terms predicted for histone H1 subtypes partner proteins. The query sequences compared by BLAST were returned as homologous with the same or smaller value than a threshold 0.001. The values indicate a ratio of an amount of partner proteins with given GO to the total number of proteins interacting with histone H1 subtype

GO	GO ID	GO Description	H1.1	H1.2	H1.3	H1.4	H1.5
Molecular function	GO:0043167	Ion binding	0.3	0.25	0.36	0.23	0.38
	GO:0003677	DNA binding	0.08	0.15	0.09	0.08	0.1
	GO:0003723	RNA binding	0.15	0.04	0.06	0.2	0.04
	GO:0016787	Hydrolase activity	0.04		0.1	0.08	0.11
	GO:0016301	Kinase activity	0.09	0.04	0.1	0.14	0.16
	GO:0005515	Protein binding		0.04			
	GO:0008168	Methyltransferase activity		0.02			
	GO:0016740	Transferase activity			0.06		0.04
	GO:0003735	Structural constituent of ribosome	0.04	0.02		0.07	
	GO:0030234	Enzyme regulator activity					0.04
Biological process	GO:0009058	Biosynthetic process	0.17	0.11	0.1	0.19	0.13
	GO:0009056	Catabolic process		0.09	0.04		
	GO:0007049	Cell cycle	0.04		0.09		0.09
	GO:0007155	Cell adhesion			0.09		
	GO:0051301	Cell division					0.06
	GO:0036211	Cellular protein modification process		0.09	0.09	0.04	0.07
	GO:0034641	Cellular nitrogen compound metabolic process	0.33	0.28	0.23	0.39	0.3
	GO:0006950	Response to stress			0.04		
	GO:0042254	Ribosome biogenesis	0.06			0.09	
	GO:0007165	Signal transduction	0.04		0.04	0.03	0.06
Cellular component	GO:0006412	Translation	0.07	0.03		0.09	
	GO:0005623	Cell	0.66	0.70	0.64	0.79	0.66
	GO:0005737	Cytoplasm	0.04	0.08	0.04		
	GO:0005622	Intracellular	0.62	0.55	0.53	0.68	0.56
	GO:0005634	Nucleus	0.26	0.23	0.3	0.31	
	GO:0043226	Organelle	0.09	0.11	0.1	0.11	0.38

GO:0005737

Ribosome

0.08