

Table 6. Top hub histone H1 subtypes interacting proteins ranked by MCC method of Cytoscape cytoHubba app.

Histone H1 subtype	Protein name	Degree	Betweenness centrality	Closeness centrality	Clustering coefficient	Neighborhood connectivity
H1.1	Nucleolar GTP-binding protein 1	27	0.0059	0.4432	0.80626	25.11
	Ribosome production factor 2 homolog	25	0.0038	0.4352	0.9	26.4
	Protein KRI1 homolog	26	0.0046	0.4368	0.84923	25.84
	Probable rRNA-processing protein EBP2	29	0.0405	0.4840	0.68719	24.34
	Pumilio homolog 3	29	0.0256	0.4297	0.68472	22.89
	RRP12-like protein	25	0.0021	0.4019	0.88	25.08
	KRR1 small subunit procesome component homolog	25	0.0010	0.4060	0.88666	25.44
	Nucleolar protein 14	24	2.4085	0.4006	0.94565	26.0
	Ribosome biogenesis regulatory protein homolog	24	2.4085	0.4006	0.94565	26.0
	H/ACA ribonucleoprotein complex subunit DKC1	35	0.0753	0.5105	0.48739	20.91
H1.2	E3 ubiquitin-protein ligase RBX1	22	0.0282	0.5064	0.57575	16.81
	NEDD8	22	0.0342	0.4875	0.51515	15.72
	Cullin-5	18	0.0091	0.4216	0.66666	15.88
	Cullin-1	17	0.0104	0.4406	0.73529	17.05
	Cullin-3	18	0.0247	0.4765	0.62091	16.5
	Cullin-2	15	0.0294	0.40625	0.8	16.46
	Kelch-like ECH-associated protein 1	17	0.0125	0.44067	0.69852	16.58
	von Hippel-Lindau disease tumor suppressor	14	0.0047	0.42162	0.85714	17.35
	Ankyrin repeat and SOCS box protein 9	13	1.6158	0.38613	0.96153	17.0
	Ankyrin repeat and SOCS box protein 16	13	1.7615	0.38613	0.96153	17.0
H1.3	Cyclin-dependent kinase 1	7	0.0597	0.5428	0.6666	6.142
	Histone acetyltransferase p300	9	0.3312	0.5757	0.3055	5.555
	Cyclin-dependent kinase 2	7	0.2942	0.5937	0.5238	6.285
	Cyclin-dependent kinase 4	6	0.0476	0.5277	0.7333	6.666
	Nucleophosmin	6	0.2050	0.5	0.5333	5.833
	Histone H1.3	6	0.2046	0.4871	0.4	5.166
	DNA replication licensing factor MCM5	5	0.1115	0.4318	0.4	5.0

H1.4	Double-strand-break repair protein rad21 homolog	4	0.0198	0.4412	0.6666	6.75
	Fibronectin	5	0.2352	0.4523	0.2	3.2
	Intercellular adhesion molecule 1	3	0.0097	0.3518	0.6666	3.333
	Pumilio homolog 3	29	0.0300	0.4340	0.7389	23.689
	Probable rRNA-processing protein EBP2	28	0.0463	0.4270	0.7830	24.25
	Protein MAK16 homolog	27	0.0030	0.4051	0.8376	24.888
	RNA-binding protein 28	27	0.0040	0.4072	0.8319	24.814
	RRP12-like protein	27	0.0040	0.4030	0.8319	24.629
	ATP-dependent RNA helicase DDX55	29	0.0181	0.4202	0.7216	23.413
	Suppressor of SWI4 1 homolog	25	7.6829	0.3989	0.9133	25.88
H1.5	Nucleolar GTP-binding protein 2	28	0.0285	0.4157	0.7566	24.035
	Nucleolar protein 14	25	9.0862	0.3989	0.91	25.8
	Protein KRI1 homolog	25	0.0060	0.3989	0.8833	25.72
	Cyclin-dependent kinase 1	14	0.0573	0.5588	0.4835	9.714
	G2/mitotic-specific cyclin-B1	14	0.0654	0.5588	0.4725	9.5
	Cyclin-dependent kinase 2	13	0.0794	0.5757	0.4871	10.692
	Cyclin-A2	12	0.0343	0.5277	0.5303	10.416
	G1/S-specific cyclin-E1	11	0.0350	0.5205	0.5818	10.272
	Cyclin-A1	9	0.0171	0.4810	0.6944	10.555
	Histone H1.5	17	0.2542	0.6031	0.25	0.835
	Maternal embryonic leucine zipper kinase	6	0.0	0.4086	1.0	12.166
	Nucleophosmin	11	0.0954	0.5352	0.4181	9.636
	Cyclin-dependent-like kinase 5	7	0.0403	0.4418	0.4761	10.428