

TABLE 2 A statistically significantly enriched molecular functions and biological processes of proteins interacting with histone H1 subtypes identified using g:GOST algorithm of g:Profiler. Significant results were obtained with Fisher's test (one-tailed) using g:SCS algorithm to correct for multiple testing ($p < 0.05$ was set as the significance threshold)

Histone H1	GO Source:ID	GO Description	P value
H1.1	MF:0003723	RNA binding	1.915×10^{-22}
	MF:0003676	Nucleic acid binding	7.405×10^{-18}
	MF:0097159	Organic cyclic compound binding	8.400×10^{-15}
	MF:1901363	Heterocyclic compound binding	1.568×10^{-14}
	MF:0016538	Cyclin-dependent serine/threonine kinase regulator activity	1.818×10^{-9}
	BP:0051276	Chromosome organization	1.853×10^{-26}
	BP:0090304	Nucleic acid metabolic process	4.111×10^{-22}
	BP:0006325	Chromatin organization	1.789×10^{-20}
	BP:0016070	RNA metabolic process	2.234×10^{-20}
	BP:0006139	Nucleobase-containing compound metabolic process	8.063×10^{-19}
H1.2	MF:0031625	Ubiquitin protein ligase binding	6.083×10^{-10}
	MF:0044389	Ubiquitin-like protein ligase binding	1.253×10^{-9}
	MF:0019899	Enzyme binding	3.731×10^{-9}
	MF:0008134	Transcription factor binding	1.761×10^{-7}
	MF:0042393	Histone binding	1.876×10^{-5}
	BP:0051276	Chromosome organization	1.873×10^{-17}
	BP:0016567	Protein ubiquitination	2.338×10^{-15}
	BP:0090304	Nucleic acid metabolic process	2.488×10^{-15}
	BP:0006325	Chromatin organization	6.598×10^{-15}
	BP:0032446	Protein modification by small protein conjugation	2.448×10^{-14}
H1.3	MF:0004693	Cyclin-dependent serine/threonine kinase activity	4.943×10^{-6}
	MF:0030322	Cyclin binding	2.300×10^{-4}
	MF:0097472	Cyclin-dependent protein kinase activity	5.700×10^{-6}
	MF:0001618	Virus receptor activity	9.277×10^{-3}
	MF:0140272	Exogenous protein binding	9.653×10^{-3}
	BP:1901991	Negative regulation of mitotic cell cycle phase transition	4.493×10^{-6}

	BP:1901988	Negative regulation of cell cycle phase transition	5.700×10^{-6}
	BP:0071156	Regulation of cell cycle arrest	6.639×10^{-4}
	BP:0090068	Positive regulation of cell cycle process	9.365×10^{-4}
	BP:0061515	Myeloid cell development	9.810×10^{-4}
H1.4	MF:0003723	RNA binding	8.509×10^{-18}
	MF:0003676	Nucleic acid binding	1.748×10^{-14}
	MF:0097159	Organic cyclic compound binding	2.492×10^{-9}
	MF:1901363	Heterocyclic compound binding	3.164×10^{-9}
	MF:0003724	RNA helicase activity	3.574×10^{-7}
	BP:0022613	Ribonucleoprotein complex biogenesis	8.523×10^{-13}
	BP:0042254	Ribosome biogenesis	1.367×10^{-12}
	BP:0006396	RNA processing	1.648×10^{-12}
	BP:0006364	rRNA processing	5.008×10^{-10}
	BP:0016072	rRNA metabolic process	9.509×10^{-10}
H1.5	MF:0016538	Cyclin-dependent serine/threonine kinase regulator activity	1.390×10^{-6}
	MF:0094772	Cyclin-dependent protein kinase activity	3.421×10^{-5}
	MF:0016740	Transferase activity	3.530×10^{-5}
	MF:0004672	Protein kinase activity	1.878×10^{-4}
	MF:0016301	Kinase activity	2.127×10^{-4}
	BP:0051276	Chromosome organization	1.440×10^{-9}
	BP:0006325	Chromatin organization	3.264×10^{-8}
	BP:0006351	Transcription, DNA-templated	2.619×10^{-7}
	BP:0097659	Nucleic acid-templated transcription	3.550×10^{-7}
	BP:0032774	RNA biosynthetic process	3.891×10^{-7}

