

Table S1. 49 histone variants were identified with high sequence coverage through LC-MS/MS analysis

Uniprot IDs	Protein Name	Sequence Coverage	Protein Description	Ratio E2+/E2-	RSD
P07305	H10_HUMAN	67.5%	Histone H1.0 OS=Homo sapiens GN=H1F0 PE=1 SV=3	4.85	23.3%
Q02539	H11_HUMAN	74.4%	Histone H1.1 OS=Homo sapiens GN=HIST1H1A PE=1 SV=3	0.35	92.6%
P16403	H12_HUMAN	67.1%	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	0.73	80.6%
P16402	H13_HUMAN	63.8%	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	0.75	77.7%
P10412	H14_HUMAN	69.0%	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	0.70	80.3%
P16401	H15_HUMAN	79.6%	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	0.29	98.3%
Q75WM6	H1FNT_HUMAN	7.8%	Testis-specific H1 histone OS=Homo sapiens GN=H1FNT PE=2 SV=3	\	\
Q8IZA3	H1FOO_HUMAN	5.2%	Histone H1oo OS=Homo sapiens GN=H1FOO PE=2 SV=1	\	\
P22492	H1T_HUMAN	31.4%	Histone H1t OS=Homo sapiens GN=HIST1H1T PE=2 SV=4	1.42	65.0%
Q92522	H1X_HUMAN	82.6%	Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	1.15	33.2%
P0C0S8	H2A1_HUMAN	99.2%	Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2	0.57	26.8%
Q96QV6	H2A1A_HUMAN	58.0%	Histone H2A type 1-A OS=Homo sapiens	0.90	11.2%

P04908	H2A1B_HUMAN	99.2%	GN=HIST1H2AA PE=1 SV=3 Histone H2A type 1-B/E OS=Homo sapiens	0.92	30.2%
Q93077	H2A1C_HUMAN	100.0%	GN=HIST1H2AB PE=1 SV=2 Histone H2A type 1-C OS=Homo sapiens	0.76	27.6%
P20671	H2A1D_HUMAN	99.2%	GN=HIST1H2AC PE=1 SV=3 Histone H2A type 1-D OS=Homo sapiens	1.06	32.6%
Q96KK5	H2A1H_HUMAN	99.2%	GN=HIST1H2AD PE=1 SV=2 Histone H2A type 1-H OS=Homo sapiens	1.02	30.5%
Q99878	H2A1J_HUMAN	99.2%	GN=HIST1H2AH PE=1 SV=3 Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ	1.27	21.5%
Q6FI13	H2A2A_HUMAN	100.0%	PE=1 SV=3 Histone H2A type 2-A OS=Homo sapiens	0.63	25.0%
Q8IUE6	H2A2B_HUMAN	100.0%	GN=HIST2H2AA3 PE=1 SV=3 Histone H2A type 2-B OS=Homo sapiens	0.96	37.8%
Q16777	H2A2C_HUMAN	100.0%	GN=HIST2H2AB PE=1 SV=3 Histone H2A type 2-C OS=Homo sapiens	0.72	39.7%
Q7L7L0	H2A3_HUMAN	100.0%	GN=HIST2H2AC PE=1 SV=4 Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A	0.92	32.0%
Q9BTM1	H2AJ_HUMAN	96.9%	PE=1 SV=3 Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1	1.06	25.0%
Q71UI9	H2AV_HUMAN	81.3%	SV=1 Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1	2.12	49.5%
Q9P0M6	H2AW_HUMAN	13.7%	SV=3 Core histone macro-H2A.2 OS=Homo sapiens	\	\
P16104	H2AX_HUMAN	97.2%	GN=H2AFY2 PE=1 SV=3 Histone H2AX OS=Homo sapiens GN=H2AFX PE=1	1.06	50.9%

Accession	Gene	Expression	Description	Score	Percentage
P0C0S5	H2AZ_HUMAN	81.3%	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2	1.21	30.7%
Q96A08	H2B1A_HUMAN	52.8%	Histone H2B type 1-A OS=Homo sapiens GN=HIST1H2BA PE=1 SV=3	0.99	10.4%
P33778	H2B1B_HUMAN	100.0%	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	0.89	18.0%
P62807	H2B1C_HUMAN	100.0%	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4	\	\
P58876	H2B1D_HUMAN	100.0%	Histone H2B type 1-D OS=Homo sapiens GN=HIST1H2BD PE=1 SV=2	0.89	17.7%
Q93079	H2B1H_HUMAN	100.0%	Histone H2B type 1-H OS=Homo sapiens GN=HIST1H2BH PE=1 SV=3	\	\
P06899	H2B1J_HUMAN	100.0%	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3	1.32	14.0%
O60814	H2B1K_HUMAN	100.0%	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3	1.04	20.4%
Q99880	H2B1L_HUMAN	100.0%	Histone H2B type 1-L OS=Homo sapiens GN=HIST1H2BL PE=1 SV=3	0.99	18.5%
Q99879	H2B1M_HUMAN	100.0%	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3	0.89	18.3%
Q99877	H2B1N_HUMAN	100.0%	Histone H2B type 1-N OS=Homo sapiens GN=HIST1H2BN PE=1 SV=3	0.90	19.1%
P23527	H2B1O_HUMAN	100.0%	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3	1.00	17.9%
Q6DN03	H2B2C_HUMAN	48.2%	Putative histone H2B type 2-C OS=Homo sapiens	1.26	14.2%

Q6DRA6	H2B2D_HUMAN	56.7%	GN=HIST2H2BC PE=5 SV=3 Putative histone H2B type 2-D OS=Homo sapiens GN=HIST2H2BD PE=5 SV=3	\	\
Q16778	H2B2E_HUMAN	100.0%	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3	\	\
Q5QNW6	H2B2F_HUMAN	100.0%	Histone H2B type 2-F OS=Homo sapiens GN=HIST2H2BF PE=1 SV=3	0.89	21.4%
Q8N257	H2B3B_HUMAN	100.0%	Histone H2B type 3-B OS=Homo sapiens GN=HIST3H2BB PE=1 SV=3	0.99	18.2%
P57053	H2BFS_HUMAN	100.0%	Histone H2B type F-S OS=Homo sapiens GN=H2BFS PE=1 SV=2	1.40	9.1%
P68431	H31_HUMAN	95.6%	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	1.10	23.2%
Q16695	H31T_HUMAN	72.1%	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3	1.01	15.2%
Q71DI3	H32_HUMAN	72.1%	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	1.09	18.3%
P84243	H33_HUMAN	72.1%	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	1.12	18.4%
Q6NXT2	H3C_HUMAN	77.8%	Histone H3.3C OS=Homo sapiens GN=H3F3C PE=1 SV=3	1.05	23.4%
P62805	H4_HUMAN	97.1%	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	1.21	15.6%

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