Table S1A Summary of human eAT-hook proteins

Nr.	Uniprot ID	peptide start position	peptide sequence	RNA binding
1	>sp|Q13219|PAPP1_HUMAN Pappalysin-1 OS=Homo sapiens GN=PAPPA PE=1 SV=3	POS: 34	AALGCGLAERPRRARRDPRAGRPPRPAAGPATCATRAARGRRA	
2	>tr|A6NCE0|A6NCE0_HUMAN Putative uncharacterized protein FOXO6 OS=Homo sapiens GN=FOXO6 PE=4 SV=1	POS: 434	AGALRCRRRRAAGRRARPLPGRPGPRHVQREPRVRRGVHHPQR	
3	>tr|Q96DR3|Q96DR3_HUMAN cDNA FLJ30206 fis, clone BRACE2001508, weakly similar to PROTEIN-LYSINE 6-OXIDASE OS=Homo sapiens PE=2 SV=1	POS: 118	AGTRQGESPLPRGRRPDLGQGRPSPRRLPRGPWTHRTRTRVRG	
4	>sp|Q8IV32|CCD71_HUMAN Coiled-coil domain-containing protein 71 OS=Homo sapiens GN=CCDC71 PE=2 SV=2	POS: 363	AKAKAVRAKAKVARTQPRGRGRPKGSAKARTTRKGQKNRPETV	
5	>sp|C9JRE6|YQ051_HUMAN Uncharacterized protein LOC283999, mitochondrial OS=Homo sapiens PE=4 SV=1	POS: 180	APRAPRRPRGPATPDPSPPAGRPHGPAGRAAPGRRPGCTAQLR	
6	>tr|Q6NUK7|Q6NUK7_HUMAN LYN protein (Fragment) OS=Homo sapiens GN=LYN PE=2 SV=1	POS: 32	APRPWRLRARRAAASSPRQAGRPRHPRPRASSPSPRVQRSRPA	
7	>tr|Q5RI17|Q5RI17_HUMAN Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) (Fragment) OS=Homo sapiens GN=HNRNPU PE=2 SV=1	POS: 120	ARQGQQQAGGKKKAEGGGGGGRPGAPAAGDGKTEQKGGDKKRG	Refs 40, 41, 42
8	>sp|Q5T5Y3|CAMP1_HUMAN Calmodulin-regulated spectrin-associated protein 1 OS=Homo sapiens GN=CAMSAP1 PE=1 SV=2	POS: 617	AVLKPAKEKQVITKEDERGEGRPRSIVSRRPSEGPQPLVRRKM	
9	>tr|Q6WG70|Q6WG70_HUMAN Antigen MLAA-35 OS=Homo sapiens PE=2 SV=1	POS: 59	AVLRPAKEKQITTKEDERGEGRPRTIMAKRPSEGSQPMVRKKV	
10	>tr|A8MZ83|A8MZ83_HUMAN Putative uncharacterized protein RBMS3 OS=Homo sapiens GN=RBMS3 PE=4 SV=2	POS: 239	CKFADGGQKKRQNQSKYTQNGRPWPREGEVLRGRTVPRQNREA	Ref 41 (candidate), Ref 42
11	>sp|Q15392|DHC24_HUMAN 24-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2	POS: 92	DIQKQVREWKEQGSKTFMCTGRPGWLTVSLRVGKYKKTHKNIM	Ref 41 (candidate)
12	>sp|Q6ZV29|PLPL7_HUMAN Patatin-like phospholipase domain-containing protein 7 OS=Homo sapiens GN=PNPLA7 PE=2 SV=3	POS: 340	EERLKKPPRLQESCDSDHGGGRPAAAGPLLKRSHSVPAPSIRK	
13	>sp|Q9NYQ6|CELR1_HUMAN Cadherin EGF LAG seven-pass G-type receptor 1 OS=Homo sapiens GN=CELSR1 PE=1 SV=1	POS: 82	ELLDVGRDGRLAGRRRVSGAGRPLPLQVRLVARSAPTALSRRL	
14	>sp|P51608|MECP2_HUMAN Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1	POS: 188	EQKPPKKPKSPKAPGTGRGRGRPKGSGTTRPKAATSEGVQVKR	Refs 41, 42
15	>sp|Q8N3Z0|PRS35_HUMAN Inactive serine protease 35 OS=Homo sapiens GN=PRSS35 PE=2 SV=2	POS: 244	ERAKGGRRRKKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGG	
16	>sp|Q96AQ6|PBIP1_HUMAN Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Homo sapiens GN=PBXIP1 PE=1 SV=1	POS: 519	ERKKNWGGQEDREPAGRWKEGRPRVEESGSKKEGKRQGPKEPP	
17	>tr|B4DMT7|B4DMT7_HUMAN cDNA FLJ55553 OS=Homo sapiens PE=2 SV=1	POS: 72	ERLKKPPRLQESCDSADHGGGRPAAAGPLLKRSHSVPAPSIRK	
18	>sp|Q2YD98|K1530_HUMAN Uncharacterized protein KIAA1530 OS=Homo sapiens GN=KIAA1530 PE=1 SV=2	POS: 597	ERQDRLKCPFHGKIVPRDDEGRPLDPEDRAREQRRQLQKQERP	
19	>sp|Q68DN1|CB016_HUMAN Uncharacterized protein C2orf16 OS=Homo sapiens GN=C2orf16 PE=1 SV=3	POS: 1917	ERSHRSSCERTRHSPSEMRPGRPSGRNHCSPSERSRRSPLKEG	
20	>sp|Q14781|CBX2_HUMAN Chromobox protein homolog 2 OS=Homo sapiens GN=CBX2 PE=1 SV=2	POS: 77	FQKKEHEKEVQNRKRGKRPRGRPRKLTAMSSCSRRSKLKEPDA	
21	>sp|Q8IZ69|TRM2A_HUMAN tRNA (uracil-5-)-methyltransferase homolog A OS=Homo sapiens GN=TRMT2A PE=1 SV=2	POS: 135	FRSAAERDKALRVLHGALWKGRPLSVRLARPKADPMARRRRQE	Refs 41, 42
22	>sp|Q9Y520|BA2L2_HUMAN Protein BAT2-like 2 OS=Homo sapiens GN=BAT2L2 PE=1 SV=2	POS: 1356	GEPTRRGRGGTFRRGGRDPGGRPSRPSTLRRPAYRDNQWNPRQ	Ref 40 (candidate)
23	>tr|A4D2M3|A4D2M3_HUMAN LOC401367 OS=Homo sapiens GN=LOC401367 PE=4 SV=1	POS: 75	GEVRNGRTGVRASRLSATGAGRPGVSGRGRRGGRSVPSARLGQ	
24	>sp|Q14005|IL16_HUMAN Pro-interleukin-16 OS=Homo sapiens GN=IL16 PE=1 SV=4	POS: 483	GKERHQWSLEGVKRLESSWHGRPTLEKEREKNSAPPHRRAQKV	
25	>sp|Q7RTU7|SCX_HUMAN Basic helix-loop-helix transcription factor scleraxis OS=Homo sapiens GN=SCXA PE=2 SV=1	POS: 67	GLQGARRRAGGRRAGGGGPGGRPGREPRQRHTANARERDRTNS	
26	>sp|Q5JV73|FRPD3_HUMAN FERM and PDZ domain-containing protein 3 OS=Homo sapiens GN=FRMPD3 PE=2 SV=2	POS: 1340	GPGMSREQRRSCDCKRICRGGRPQATQTPVPSLRGRERDRVLP	
27	>sp|Q92794|MYST3_HUMAN Histone acetyltransferase MYST3 OS=Homo sapiens GN=MYST3 PE=1 SV=2	POS: 335	GRKLLQKKAAQIKRRYTNPIGRPKNRLKKQNTVSKGPFSKVRT	
28	>tr|B8ZZP9|B8ZZP9_HUMAN Putative uncharacterized protein HES6 OS=Homo sapiens GN=HES6 PE=4 SV=1	POS: 38	GWETRGDRKVRAGAMGEQAGGRPCGAGIQCPAPRRPGSPWWRR	
29	>sp|Q8NAT2|TDRD5_HUMAN Tudor domain-containing protein 5 OS=Homo sapiens GN=TDRD5 PE=1 SV=3	POS: 106	IASLVAKQRSSHKLRNSMHKGRPSIYSGPRSHRRVPYRGRVAP	Ref 42
30	>sp|Q5JTH9|RRP12_HUMAN RRP12-like protein OS=Homo sapiens GN=RRP12 PE=1 SV=2	POS: 1245	KAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNRRKKMK	Ref 40 (candidate), Refs 41, 42

31	>sp|Q86US8|EST1A_HUMAN Telomerase-binding protein EST1A OS=Homo sapiens GN=SMG6 PE=1 SV=2	POS: 235	KGKRMGKGEGVRETHDDPARGRPGSAKRYSRSDKRRNRYRTRS	
32	>tr|Q59F71|Q59F71_HUMAN Bone morphogenetic protein 1 isoform 1, variant (Fragment) OS=Homo sapiens PE=2 SV=1	POS: 785	KKGFKAHFFSEKRPALQPPRGRPHQLKFRVQKRNRTPQ	
33	>tr|Q5JR95|Q5JR95_HUMAN 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=3 SV=1	POS: 29	KRRKTGGKRKPYHKKRKYELGRPAANTKIGPRRIHTVRVRGGC	Refs 40, 41, 42
34	>tr|Q1M182|Q1M182_HUMAN HMGA2f OS=Homo sapiens GN=HMGA2 PE=2 SV=1	POS: 77	KSPSKAAQKKAEATGEKRPRGRPRKWDNLLPRTSSKKKTSLGN	
35	>sp|Q02040|SF17A_HUMAN Splicing factor, arginine/serine-rich 17A OS=Homo sapiens GN=SFRS17A PE=1 SV=2	POS: 614	LADRHKRERSRARRASSREDGRPRKERRPHKKHAYKDDSPRRR	Refs 40, 42
36	>sp|Q6PH81|CP087_HUMAN UPF0547 protein C16orf87 OS=Homo sapiens GN=C16orf87 PE=2 SV=1	POS: 100	LENRKRSRSNSHSDHIRRGRGRPKSASAKKHEEEREKQEKEID	
37	>sp|A6NJI1|CK086_HUMAN Uncharacterized protein C11orf86 OS=Homo sapiens GN=C11orf86 PE=2 SV=2	POS: 24	LRSQSLREPRPSYGKLQEPWGRPQEGQLRRALSLRQGQEKSRS	
38	>sp|Q8WZ42|TITIN_HUMAN Titin OS=Homo sapiens GN=TTN PE=1 SV=2	POS: 19558	MRKLVIVRAGCPIRLFAIVRGRPAPKVTWRKVGIDNVVRKGQV	
39	>sp|Q86YD1|PTOV1_HUMAN Prostate tumor-overexpressed gene 1 protein OS=Homo sapiens GN=PTOV1 PE=1 SV=1	POS: 20	MVRPRRAPYRSGAGGPLGGRGRPPRPLVVRAVRSRSWPASPRG	
40	>sp|O15235|RT12_HUMAN 28S ribosomal protein S12, mitochondrial OS=Homo sapiens GN=MRPS12 PE=1 SV=1	POS: 53	NQMHRLGPPKRPPRKLGPTEGRPQLKGVVLCTFTRKPKKPNSA	Ref 40 (predicted), Ref 42
41	>tr|D4PHA4|D4PHA4_HUMAN GC-rich promoter binding protein 1, isoform CRA_c OS=Homo sapiens GN=GPBP1 PE=4 SV=1	POS: 57	NRYDVNRRRHNSSDGFDSAIGRPNGGNFGRKEKNGWRTHGRNG	
42	>sp|Q6ZRS2|SRCAP_HUMAN Helicase SRCAP OS=Homo sapiens GN=SRCAP PE=1 SV=3	POS: 2735	PARPPRRRTSADVEIRGQGTGRPGQPPGPKVLRKLPGRLVTVV	
43	>sp|Q9P281|BAHC1_HUMAN BAH and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=BAHCC1 PE=1 SV=3	POS: 2237	PKNKTCKALLMGDKDFSPKLGRPLPSPSYVHPALVGKDKKGRA	
44	>sp|Q02779|M3K10_HUMAN Mitogen-activated protein kinase kinase kinase 10 OS=Homo sapiens GN=MAP3K10 PE=1 SV=3	POS: 875	PRLPDPQALFPARRRPPEFPGRPTTLTFAPRPRPAASRPRLDP	
45	>tr|Q8WYU8|Q8WYU8_HUMAN Putative uncharacterized protein pp6170 OS=Homo sapiens GN=pp6170 PE=4 SV=1	POS: 70	PSPTSRARRPPRPWEVAPRCGRPKLNGATRSGCACRVRSHRHP	
46	>sp|O14578|CTRO_HUMAN Citron Rho-interacting kinase OS=Homo sapiens GN=CIT PE=1 SV=2	POS: 1972	PSTPHRYREGRTELRRDKSPGRPLEREKSPGRMLSTRRERSPG	
47	>sp|P51532|SMCA4_HUMAN Transcription activator BRG1 OS=Homo sapiens GN=SMARCA4 PE=1 SV=2	POS: 1443	PTTSTRSRDKDDESKKQKKRGRPPAEKLSPNPPNLTKKMKKIV	
48	>tr|Q8TC09|Q8TC09_HUMAN TTLL7 protein (Fragment) OS=Homo sapiens GN=TTLL7 PE=2 SV=2	POS: 42	RAVGGRRRAPDHQCRLPSRGGRPRGSCEAREHLGDRLQRGRED	
49	>sp|P05997|CO5A2_HUMAN Collagen alpha-2(V) chain OS=Homo sapiens GN=COL5A2 PE=1 SV=3	POS: 128	RGRKGQKGEPGLVPVVTGIRGRPGPAGPPGSQGPRGERGPKGR	Ref 41 (candidate)
50	>sp|Q9H5J8|TAF1D_HUMAN TATA box-binding protein-associated factor RNA polymerase I subunit D OS=Homo sapiens GN=TAF1D PE=1 SV=1	POS: 106	RKKRYKKKKKRRYQPTGRPRGRPEGRRNPIYSLIDKKKQFRSR	
51	>tr|C9J2A8|C9J2A8_HUMAN Putative uncharacterized protein C20orf12 OS=Homo sapiens GN=C20orf12 PE=4 SV=1	POS: 560	RKLRLREVKQPASSKGTKLAGRPLIKNFKTKTFQEKKEQLIPE	
52	>sp|Q96NR7|CD038_HUMAN Uncharacterized protein C4orf38 OS=Homo sapiens GN=C4orf38 PE=2 SV=1	POS: 89	RPAARPRMSPHRSPAVARRCGRPRRRDPRRRRTPALPRPWPGR	
53	>tr|Q6IPL9|Q6IPL9_HUMAN HMGA1 protein OS=Homo sapiens GN=HMGA1 PE=4 SV=1	POS: 47	RPRKQPPKEPSEVPTPKRPRGRPKGSKNKGAAKTRKTTTLHST	
54	>tr|Q5T6U8|Q5T6U8_HUMAN High mobility group AT-hook 1 OS=Homo sapiens GN=HMGA1 PE=2 SV=1	POS: 47	RPRKQPPKEPSEVPTPKRPRGRPKGSKNKGAAKTRKTTTTPGR	
55	>sp|Q9UIF9|BAZ2A_HUMAN Bromodomain adjacent to zinc finger domain protein 2A OS=Homo sapiens GN=BAZ2A PE=1 SV=4	POS: 673	RPRNTEKAKTKEVPKVKRGRGRPPKVKITELLNKTDNRPLKKL	Ref 42
56	>tr|Q8N9G5|Q8N9G5_HUMAN cDNA FLJ37429 fis, clone BRAWH2001666 OS=Homo sapiens PE=2 SV=1	POS: 166	RRAAEFTQARPTRKRRTPGGGRPEAGCWLENRRQRRRKAGAER	
57	>sp|O15417|TNC18_HUMAN Trinucleotide repeat-containing gene 18 protein OS=Homo sapiens GN=TNRC18 PE=1 SV=3	POS: 1526	RRDSEDRREEPHRSLARRGPGRPRKRTHAPSALSPPRKRGKSG	
58	>sp|Q6UX72|B3GN9_HUMAN UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9 OS=Homo sapiens GN=B3GNT9 PE=2 SV=1	POS: 113	RRFPLLINQPHKCRGDGAPGGRPDLLIAVKSVAEDFERRQAVR	
59	>sp|Q96PV0|SYGP1_HUMAN Ras GTPase-activating protein SynGAP OS=Homo sapiens GN=SYNGAP1 PE=1 SV=4	POS: 91	RRSESSRNKLLRRTVSVPVEGRPHGEHEYHLGRSRRKSVPGGK	
60	>tr|B4DM08|B4DM08_HUMAN cDNA FLJ60021, moderately similar to Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens PE=2 SV=1	POS: 32	RRVSCFLRLGRSTLLELEPAGRPCSGRTRHRALHRRLVACVTV	
61	>sp|O95996|APC2_HUMAN Adenomatous polyposis coli protein 2 OS=Homo sapiens GN=APC2 PE=1 SV=1	POS: 1469	RSAEQSRGAGKNRAGLELPLGRPPSAPADKDGSKPGRTRGDGA	
62	>sp|Q9UDY2|ZO2_HUMAN Tight junction protein ZO-2 OS=Homo sapiens GN=TJP2 PE=1 SV=1	POS: 177	RSRLNSHGGRSRSWEDSPERGRPHERARSRERDLSRDRSRGRS	

63	>tr|Q5JRI1|Q5JRI1_HUMAN FUS interacting protein (Serine/arginine-rich) 1 OS=Homo sapiens GN=FUSIP1 PE=2 SV=1	POS: 149	RSRSFDYNYRRSYSPRNRPTGRPRRSRSHSDNDSQVSKKKNER	
64	>sp|Q8IY82|CC135_HUMAN Coiled-coil domain-containing protein 135 OS=Homo sapiens GN=CCDC135 PE=2 SV=2	POS: 553	RVDGLMKREETPRTMTEYYQGRPDFLSYRHASFGPRVKKLTLS	
65	>sp|P20929|NEBU_HUMAN Nebulin OS=Homo sapiens GN=NEB PE=1 SV=3	POS: 5775	SEVEYRAKHRKEGSHGLSMLGRPDIEMAKKAAKLSSQVKYREN	
66	>sp|O95785|WIZ_HUMAN Protein Wiz OS=Homo sapiens GN=WIZ PE=1 SV=2	POS: 1458	SEWIKHRPQKVGAYRSYIQGGRPFTKKFRSAGHGRDSDKRPSL	
67	>sp|Q8TEK3|DOT1L_HUMAN Histone-lysine N-methyltransferase, H3 lysine-79 specific OS=Homo sapiens GN=DOT1L PE=1 SV=2	POS: 411	SKARKKKLNKKGRKMAGRKRGRPKKMNTANPERKPKKNQTALD	
68	>sp|Q0P651|CD029_HUMAN Uncharacterized protein C4orf29 OS=Homo sapiens GN=C4orf29 PE=1 SV=1	POS: 23	SKLDILYRRLLLTKLFIRGWGRPEDLKRLFEFRKMIGNRERCQ	Ref 41 (candidate)
69	>sp|Q9H611|PIF1_HUMAN ATP-dependent DNA helicase PIF1 OS=Homo sapiens GN=PIF1 PE=1 SV=2	POS: 63	SLGRNERRELMLRLQAPGPAGRPRCFPLRAARLFTRFAEAGRS	
70	>sp|Q9UKV3|ACINU_HUMAN Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2	POS: 624	SPLRSKQRDVAQARTHANPRGRPKMGSRSTSESRSRSRSRSRS	Refs 40, 41
71	>sp|Q5VWQ0|RSBN1_HUMAN Round spermatid basic protein 1 OS=Homo sapiens GN=RSBN1 PE=2 SV=2	POS: 100	SPRGVKRQRRSSSGGSQEKRGRPSQEPPLAPPHRRRRSRQHPG	
72	>sp|O75494|SRS10_HUMAN Serine/arginine-rich splicing factor 10 OS=Homo sapiens GN=SRSF10 PE=1 SV=1	POS: 150	SRSFDYNYRRSYSPRNSRPTGRPRRSRSHSDNDRFKHRNRSFS	Refs 40, 42
73	>sp|Q9UKY1|ZHX1_HUMAN Zinc fingers and homeoboxes protein 1 OS=Homo sapiens GN=ZHX1 PE=1 SV=1	POS: 757	SSLRKRGRGRPKGRGRGRPRGRPRGSKRINNWDRGPSLIKFKT	
74	>sp|Q9UHJ3|SMBT1_HUMAN Scm-like with four MBT domains protein 1 OS=Homo sapiens GN=SFMBT1 PE=1 SV=2	POS: 647	SVLTKTKYTHYYGKKKNKRIGRPPGGHSNLACALKKASKRRKR	
75	>tr|A8KA56|A8KA56_HUMAN cDNA FLJ77678, highly similar to Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 23, mRNA OS=Homo sapiens PE=2 SV=1	POS: 632	VERLARSYLRRPAVVYIGSAGRPHERVEQKVFLMSESEKRKKL	Ref 40
76	>sp|Q9NSD7|RL3R1_HUMAN Relaxin-3 receptor 1 OS=Homo sapiens GN=RXFP3 PE=1 SV=1	POS: 310	VRFIADRRAAGTKGGAAVAGGRPTGASARRLSKVTKSVTIVVL	
77	>tr|A1E4F0|A1E4F0_HUMAN G protein-coupled receptor 144 splice variant (Fragment) OS=Homo sapiens GN=GPR144 PE=2 SV=1	POS: 229	VRSLRLREASTRGCLFTMPGGRPEGPGHIHIPASEVRRLLRKG	
78	>sp|Q96MU7|YTDC1_HUMAN YTH domain-containing protein 1 OS=Homo sapiens GN=YTHDC1 PE=1 SV=3	POS: 520	YQVIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIH	Refs 40, 41, 42
79	>sp|Q9UBI9|HDC_HUMAN Headcase protein homolog OS=Homo sapiens GN=HECA PE=1 SV=1	POS: 211	YQVKRMQDEKKKKSGSEKNTGRPPGEAAEEAKKCRPPNKPQKG	
80	>sp|Q15027|ACAP1_HUMAN Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ACAP1 PE=1 SV=1	POS: 533	YVEKKFLTKLPEIRGRRGGRGRPRGQPPVPPKPSIRPRPGSLR	

Table S1B Summary of mouse eAT-hook proteins

Nr.	Uniprot ID	peptide start position	peptide sequence
1	>tr|Q5DTK3|Q5DTK3_MOUSE MKIAA4165 protein (Fragment) OS=Mus musculus GN=Prkci PE=2 SV=1	POS: 44	AAKRPLARSAPRARRVGRRGGRPRLPDRLGRPRPSRRPALPRP
2	>tr|Q8BHN4|Q8BHN4_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Dlst PE=4 SV=1	POS: 52	AEHGCGRTGRPKGRDAVCWPGRPPRAPGRGGCRRPRSRPAACT
3	>tr|Q3TU60|Q3TU60_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Jmjd1c PE=2 SV=1	POS: 148	AGQRRSRGAEQRLPRSRGAEGRPRRSRAEPAARRGAAPRSRAH
4	>sp|Q9D3E6|STAG1_MOUSE Cohesin subunit SA-1 OS=Mus musculus GN=Stag1 PE=1 SV=2	POS: 37	AHSDHGRQLEETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRI
5	>tr|B2RWZ0|B2RWZ0_MOUSE Abi3bp protein OS=Mus musculus GN=Abi3bp PE=2 SV=1	POS: 445	AKTTQAPHRLHTAPVRPRIPGRPHGRPALNKTTTRPDKTKPRG
6	>tr|Q3UZI6|Q3UZI6_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Noc2l PE=2 SV=1	POS: 64	ARGAAWNRERRGARTSPGPAGRPRKGRASEHKDQLSRLKDRDP
7	>sp|A2AHC3|CAMP1_MOUSE Calmodulin-regulated spectrin-associated protein 1 OS=Mus musculus GN=Camsap1 PE=1 SV=1	POS: 614	AVLRPAKEKQITTKEDERGEGRPRTIMAKRPSEGSQPMVRKKV
8	>sp|Q8VCH6|DHC24_MOUSE 24-dehydrocholesterol reductase OS=Mus musculus GN=Dhcr24 PE=2 SV=1	POS: 92	DIQKQVREWKEQGSKTFMCTGRPGWLTVSLRVGKYKKTHKNIM
9	>sp|Q9Z2D6|MECP2_MOUSE Methyl-CpG-binding protein 2 OS=Mus musculus GN=Mecp2 PE=1 SV=1	POS: 188	EQKPPKKPKSPKAPGTGRGRGRPKGSGTGRPKAAASEGVQVKR
10	>tr|Q3TZG6|Q3TZG6_MOUSE Putative uncharacterized protein OS=Mus musculus GN=Cbx2 PE=2 SV=1	POS: 77	FQKKEHEKEVQNRKRDKRPRGRPRKHTVTSSCSRRSKLKEPDA
11	>sp|P30658|CBX2_MOUSE Chromobox protein homolog 2 OS=Mus musculus GN=Cbx2 PE=1 SV=1	POS: 77	FQKKEHEKEVQNRKRGKRPRGRPRKHTATSSCSRRSKLKEPDA
12	>tr|A2ABG2|A2ABG2_MOUSE Chromobox homolog 2 (Drosophila Pc class) OS=Mus musculus GN=Cbx2 PE=4 SV=1	POS: 77	FQKKEHEKEVQNRKRGKRPRGRPRKHTVTSSCSRRSKLKEPDA
13	>sp|Q3TLH4|BA2L2_MOUSE Protein BAT2-like 2 OS=Mus musculus GN=Bat2l2 PE=1 SV=2	POS: 1327	GEPTRRGRGGTFRRGGRDPGGRPSRPATLRRPAYRDNQWNTRQ
14	>sp|O54824|IL16_MOUSE Pro-interleukin-16 OS=Mus musculus GN=Il16 PE=1 SV=3	POS: 480	GKDRHQWSLEGVKRLESSWHGRPTLEKEREKHSAPPHRRAQKI
15	>sp|Q8BZ21|MYST3_MOUSE Histone acetyltransferase MYST3 OS=Mus musculus GN=Myst3 PE=1 SV=2	POS: 335	GRKLLQKKAAQIKRRYANPIGRPKNRLKKQNTVSKGPFSKVRT
16	>tr|Q3TNM4|Q3TNM4_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus PE=2 SV=1	POS: 52	GRRVGRGEACTRRPALAPAGGRPERRRGSLRRGSPRSSRVGVS
17	>tr|D3Z4R5|D3Z4R5_MOUSE Putative uncharacterized protein E130309D14Rik OS=Mus musculus GN=E130309D14Rik PE=4 SV=1	POS: 241	GVHNGPAALRRRLPRVRAGTGRPGKTPIPCRTPRSFSTHGGRR
18	>sp|Q9D4V4|TAF1D_MOUSE TATA box-binding protein-associated factor RNA polymerase I subunit D OS=Mus musculus GN=Taf1d PE=2 SV=2	POS: 102	KKKKRKKRKKRKYEPKLRPRGRPRGKPSGTRITRRSQIDAKQI
19	>sp|Q9Z1N6|SFRP4_MOUSE Secreted frizzled-related sequence protein 4 OS=Mus musculus GN=Sfrp4 PE=2 SV=1	POS: 320	KKQIASRTSRTSRSNPPKSKGRPPAPKPASPKKNIKARSAPKK
20	>sp|Q3UMU9|HDGR2_MOUSE Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1	POS: 429	KKSQLPGSESARKPGQKEKRGRPDEKPRARPVKVERTRKRSEG
21	>tr|D3Z6G6|D3Z6G6_MOUSE 40S ribosomal protein S8 OS=Mus musculus GN=Rps8-ps1 PE=3 SV=1	POS: 29	KRRKTGGKRKPYHKKGKYELGRPAANTKIGPRRIHTVRVRGGN
22	>sp|P62242|RS8_MOUSE 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	POS: 29	KRRKTGGKRKPYHKKRKYELGRPAANTKIGPRRIHTVRVRGGN
23	>tr|B2KFS0|B2KFS0_MOUSE Novel protein (1700023A16Rik) (Fragment) OS=Mus musculus GN=1700023A16Rik PE=4 SV=1	POS: 43	KTHLRHRRPEEDPPPSQEARGRPTSVTGSQRKTHLHHRRAPAR
24	>sp|Q9CR55|CP087_MOUSE UPF0547 protein C16orf87 homolog OS=Mus musculus PE=2 SV=1	POS: 100	LENRKRSRSNSHSDHIRRGRGRPKSSSAKKHEEEREKQEKEID

25	>sp|A2ASS6|TITIN_MOUSE Titin OS=Mus musculus GN=Ttn PE=1 SV=1	POS: 20420	MRKLVVVRAGCPIRLFAIVRGRPAPKVTWRKVGIDNVVRKGQV
26	>sp|Q91VU8|PTOV1_MOUSE Prostate tumor-overexpressed gene 1 protein homolog OS=Mus musculus GN=Ptov1 PE=2 SV=1	POS: 20	MVRPRRAPHRSGAGGPLGGRGRPPRPLVVRAVRSRSWPGGPRG
27	>sp|Q91YE5|BAZ2A_MOUSE Bromodomain adjacent to zinc finger domain protein 2A OS=Mus musculus GN=Baz2a PE=1 SV=2	POS: 1015	NKWIVEGRLRRLKTALAKRTGRPEVMMEGAEDGLGRRRSSRIM
28	>sp|O35680|RT12_MOUSE 28S ribosomal protein S12, mitochondrial OS=Mus musculus GN=Mrps12 PE=2 SV=1	POS: 53	NQMHRLGPRKEPPKRLGPTEGRPQLKGVVLRTFIRKPKKPNSA
29	>sp|Q6NXH3|GPBP1_MOUSE Vasculin OS=Mus musculus GN=Gpbp1 PE=1 SV=1	POS: 57	NRYDVSRRRHNSSDGFDSGIGRPNGGNFGRKEKNGWRTHGRNG
30	>sp|Q810K9|GXLT2_MOUSE Glucoside xylosyltransferase 2 OS=Mus musculus GN=Gxylt2 PE=2 SV=1	POS: 81	PGAAGRRSPRRQPPRLRPRAGRPRAASREKLARRPGETRSLHS
31	>sp|Q3UHR0|BAHC1_MOUSE BAH and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Bahcc1 PE=2 SV=2	POS: 2277	PKNKNCKALLMSDKDFGPKLGRPLSNPSYAHPALIGKDKKGRA
32	>tr|Q3ULV3|Q3ULV3_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=1700022K14Rik PE=2 SV=1	POS: 130	PLSVRPGKSSRAGARRERAGGRPRGEGSRGRRNGCHVARWISA
33	>sp|Q66L42|M3K10_MOUSE Mitogen-activated protein kinase kinase kinase 10 OS=Mus musculus GN=Map3k10 PE=2 SV=2	POS: 861	PRLPDPQALFPTRRRPLEFPGRPTTLTFAPRPRPAASRPRLDP
34	>tr|Q3V0L6|Q3V0L6_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Gm10638 PE=2 SV=1	POS: 35	PRLREGTRRPSPGRGQLLPPGRPLTCGRRARRGPRPRLTRPVA
35	>sp|Q3TKT4|SMCA4_MOUSE Transcription activator BRG1 OS=Mus musculus GN=Smarca4 PE=1 SV=1	POS: 1410	PTTSTRSRDKDEESKKQKKRGRPPAEKLSPNPPNLTKKMKKIV
36	>sp|Q64124|SCX_MOUSE Basic helix-loop-helix transcription factor scleraxis OS=Mus musculus GN=Scx PE=1 SV=1	POS: 70	QGARRRAGGRRAAGSGPGPGGRPGREPRQRHTANARERDRTNS
37	>tr|B2RQC2|B2RQC2_MOUSE Ubiquitin carboxyl-terminal hydrolase OS=Mus musculus GN=Usp42 PE=2 SV=1	POS: 1097	RDAREWRPLHGREHDRLVQSGRPYKDSYWGRKGWELQSRGKER
38	>tr|Q8BY93|Q8BY93_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=Usp42 PE=2 SV=1	POS: 248	RDSREWRPLHGREHDRLVQSGRPYKDSYWGRKGWELQSRGKER
39	>sp|Q8C0F9|PRS35_MOUSE Inactive serine protease 35 OS=Mus musculus GN=Prss35 PE=2 SV=1	POS: 240	RESTTQRPGKKSRRGPRVTQGRPSFQWTRVKSTHIPKGWVRGE
40	>sp|Q3U962|CO5A2_MOUSE Collagen alpha-2(V) chain OS=Mus musculus GN=Col5a2 PE=1 SV=1	POS: 126	RGRKGQKGEPGLVPVVTGIRGRPGPAGPPGSQGPRGDRGPKGR
41	>sp|Q8K4R9|DLGP5_MOUSE Disks large-associated protein 5 OS=Mus musculus GN=Dlgap5 PE=1 SV=2	POS: 244	RKPVTRATNEKGSERMRPSGGRPAKKPEGKPDKVIPSKVERDE
42	>sp|Q9Z277|BAZ1B_MOUSE Tyrosine-protein kinase BAZ1B OS=Mus musculus GN=Baz1b PE=1 SV=2	POS: 1301	RLRPRKTIRGKQSVIPAARPGRPPGKKSHPARRSRPKDDPEVD
43	>tr|Q3TVP0|Q3TVP0_MOUSE MCG120563, isoform CRA_a OS=Mus musculus GN=Hmga1 PE=2 SV=1	POS: 47	RPRKQPPKEPSEVPTPKRPRGRPKGSKNKGAAKTRKVTTAPGR
44	>sp|Q91YE5|BAZ2A_MOUSE Bromodomain adjacent to zinc finger domain protein 2A OS=Mus musculus GN=Baz2a PE=1 SV=2	POS: 665	RPRNNEKAKNKEVPKVKRGRGRPPKIKMPELLNKTDNRLPKKL
45	>tr|Q8CCB8|Q8CCB8_MOUSE Putative uncharacterized protein (Fragment) OS=Mus musculus GN=6030445D17Rik PE=2 SV=1	POS: 40	RRGFLAAFRRRSFAPQVPSPGRPAQETQRKPGTRPARPRGPPP
46	>tr|Q80TU0|Q80TU0_MOUSE MKIAA0705 protein (Fragment) OS=Mus musculus GN=Magi2 PE=4 SV=3	POS: 1165	RSASPQRSARPRLEEVPGGQGRPEAGRPASEAADGKEALRGRR
47	>tr|Q9JL90|Q9JL90_MOUSE Nebulin (Fragment) OS=Mus musculus GN=Neb PE=2 SV=1	POS: 99	SEVEYRAKHRKEGSHGLSVLGRPDIEMAKKAAKLSSQVKYREN
48	>sp|O88286|WIZ_MOUSE Protein Wiz OS=Mus musculus GN=Wiz PE=1 SV=2	POS: 1491	SEWIKHRPQKVGAYRSYIQGGRPFTKKFRSAGHGRDSDKRPPL
49	>tr|Q679P5|Q679P5_MOUSE Histone H3 methyltransferase DOT1 variant b OS=Mus musculus GN=Dot1l PE=2 SV=1	POS: 301	SKARKKKLNKKGRKMAGRKRGRPKKMSAASAERKSKKSQSTLD

50	>sp|Q8C1A9|CD029_MOUSE Uncharacterized protein C4orf29 homolog OS=Mus musculus PE=2 SV=1	POS: 23	SKLDILYRRLLLTKLFIRGWGRPEDLKRLFEFRKMIGNRERCQ
51	>sp|Q80SX8|PIF1_MOUSE ATP-dependent DNA helicase PIF1 OS=Mus musculus GN=Pif1 PE=1 SV=2	POS: 76	SLGRNERRELMLRLQAPGPTGRPRCFPLRAVRLFTRFAATGRS
52	>sp|Q9CR13|CG055_MOUSE UPF0562 protein C7orf55 homolog OS=Mus musculus PE=2 SV=1	POS: 25	SPARTLRGLLRELRYLNAATGRPYRDTAAYRYLVKAFRAHRVT
53	>sp|Q80T69|RSBN1_MOUSE Round spermatid basic protein 1 OS=Mus musculus GN=Rsbn1 PE=1 SV=3	POS: 99	SPRGVKRQRRASSGGSQEKRGRPSQDPPLAPPHRRRRSRQHPG
54	>sp|Q9R0U0|SRS10_MOUSE Serine/arginine-rich splicing factor 10 OS=Mus musculus GN=Srsf10 PE=1 SV=2	POS: 150	SRSFDYNYRRSYSPRNSRPTGRPRRSRSHSDNDRFKHRNRSFS
55	>sp|P70121|ZHX1_MOUSE Zinc fingers and homeoboxes protein 1 OS=Mus musculus GN=Zhx1 PE=1 SV=2	POS: 757	SSLRRRGRGRPKGRGRGRPRGRPRGGKRMNTWDRVPSLIKFKT
56	>tr|Q61710|Q61710_MOUSE IB3/5-polypeptide OS=Mus musculus GN=Cep110 PE=2 SV=1	POS: 242	SSMKKWLSSKRNWRMVKRSSGRPAKEHLKPELKFDKRQHNARI
57	>sp|Q9JMD1|SMBT1_MOUSE Scm-like with four MBT domains protein 1 OS=Mus musculus GN=Sfmbt1 PE=2 SV=1	POS: 644	SVLTKTKYTHYYGKKKNKRIGRPPGGHSNLSCALKKSSKRRKR
58	>sp|P49025|CTRO_MOUSE Citron Rho-interacting kinase OS=Mus musculus GN=Cit PE=1 SV=3	POS: 2000	TPHRYRDREGRTELRRDKSPGRPLEREKSPGRMLSTRRERSPG
59	>sp|P56931|E2F2_MOUSE Transcription factor E2F2 OS=Mus musculus GN=E2f2 PE=1 SV=2	POS: 96	VRCAPAGRLPAKRKLDLEGIGRPTVPEFRTPKGKCIRVDGLPS
60	>tr|Q69Z54|Q69Z54_MOUSE MKIAA1966 protein (Fragment) OS=Mus musculus GN=Ythdc1 PE=2 SV=1	POS: 300	YQLIHKMRHKRRMHSQPRSRGRPSRREPVRDVGRRRPEDYDIH

Table S1C Summary of human AT-hook proteins

Nr.	Uniprot ID	peptide start position	peptide sequence
1	sp|Q9UMN6|MLL4_HUMAN	POS: 2	AAAAGGGSCPGPGSARGRFPGRPRGAGGGGGRGGRGNGAERVR
2	sp|Q6ZRS2|SRCAP_HUMAN	POS: 2266	AELAEFNENDGFPAGEGEEAGRPGAEDEEMSRAEQEIAALVEQ
3	sp|O43167|ZBT24_HUMAN	POS: 143	AGAPVVVISNKKNDPPKRKRGRPKKVNTLQEEKSELAAEEEIQ
4	sp|Q9UIF9|BAZ2A_HUMAN	POS: 1388	AGDPGEMPQSPTGLGQPKRRGRPPSKFFKQMEQRYLTQLTAQP
5	sp|Q9UMN6|MLL4_HUMAN	POS: 205	APRSRACEPSTPRRSRGRPPGRPAGPCRRKQQAVVVAEAAVTI
6	sp|Q8NFC6|BD1L1_HUMAN	POS: 2856	DDDTIKSQEEDQPIIIKRKRGRPRKYPVETTLKMKDDSKTDTG
7	sp|Q96CK0|ZN653_HUMAN	POS: 15	EAGAGGEAAAEEGAAGRKARGRPRLTESDRARRRLESRKKYDV
8	sp|Q9NR48|ASH1L_HUMAN	POS: 871	EIEIPSFKQGLSVSPFPKKRGRPKRQMRSPVKMKPPVLSVAPF
9	sp|P51608|MECP2_HUMAN	POS: 169	EQKPPKKPKSPKAPGTGRGRGRPKGSGTTRPKAATSEGVQVKR
10	sp|Q03164|MLL1_HUMAN	POS: 203	ETKSGDKIKKKDSKSIEKKRGRPPTFPGVKIKITHGKDISELP
11	sp|Q14781|CBX2_HUMAN	POS: 58	FQKKEHEKEVQNRKRGKRPRGRPRKLTAMSSCSRRSKLKEPDA
12	sp|Q6ZRS2|SRCAP_HUMAN	POS: 2920	GPQPVHRPNPLLSPVEKRRRGRPPKARDLPIPGTISSAGDGNS
13	sp|P52926|HMGA2_HUMAN	POS: 30	GRPRKQQQEPTGEPSPKRPRGRPKGSKNKSPSKAAQKKAEATG
14	sp|Q9NR48|ASH1L_HUMAN	POS: 2750	IPLEAVVGTCCVLDLYTYCKGRPKGVKEQDVYICDYRLDKSAH
15	sp|Q9NR48|ASH1L_HUMAN	POS: 1831	KAKKLQRQARTGNNFVKRRPGRPRKCPLQAVVSMQAFQAAQFV
16	sp|Q9Y6X0|SETBP_HUMAN	POS: 1435	KAKRLQRQSKTGNNFVKKRRGRPRKQPTQFDEDSRDQMPVLEK
17	sp|Q03164|MLL1_HUMAN	POS: 284	KFKTGKLQIGRKGVQIVRRRGRPPSTERIKTPSGLLINSELEK
18	sp|P17096|HMGA1_HUMAN	POS: 65	KNKGAAKTRKTTTTPGRKPRGRPKKLEKEEEEGISQESSEEEQ
19	sp|P52926|HMGA2_HUMAN	POS: 58	KSPSKAAQKKAEATGEKRPRGRPRKWPQQVVQKKPAQEETEET
20	sp|Q9NR48|ASH1L_HUMAN	POS: 809	LSSSMCVSSDLLSDIYKPKRGRPKSKEMPQLEGPPKRTLKIPA
21	sp|Q6ZRS2|SRCAP_HUMAN	POS: 2716	PARPPRRRTSADVEIRGQGTGRPGQPPGPKVLRKLPGRLVTVV
22	sp|Q9BVI0|PHF20_HUMAN	POS: 241	PENDIVKSPQENLREPKRKRGRPPSIAPTAVDSNSQTLQPITL
23	sp|Q6ZRS2|SRCAP_HUMAN	POS: 2841	PENGDGALLAITPPAVKRRRGRPPKKNRSPADAGRGVDEAPSS
24	sp|Q6P995|F171B_HUMAN	POS: 780	PGRKSTVEDFEANTSPTKRRGRPPLAKRDSKTNIWKKREERPL
25	sp|Q8NEZ4|MLL3_HUMAN	POS: 18	PPEEPGAPAPSPAAADKRPRGRPRKDGASPFQRARKKPRSRGK
26	sp|P78545|ELF3_HUMAN	POS: 228	PSDGFRDCKKGDPKHGKRKRGRPRKLSKEYWDCLEGKKSKHAP
27	sp|Q9NR48|ASH1L_HUMAN	POS: 1331	PSFPLDPLHYIRKPDLKKKRGRPPKMREAMAEMPFMHSLSFPL
28	sp|Q9UMN6|MLL4_HUMAN	POS: 201	QAPQAPRSRACEPSTPRRSRGRPPGRPAGPCRRKQQAVVVAEA
29	sp|Q9UMN6|MLL4_HUMAN	POS: 450	QEEQEESPPPVVPATCSRKRGRPPLTPSQRAEREAARAGPEGT
30	sp|P52926|HMGA2_HUMAN	POS: 10	QPSTSAQGQPAAPAPQKRGRGRPRKQQQEPTGEPSPKRPRGRP
31	sp|Q9Y6X0|SETBP_HUMAN	POS: 1000	QYDPLLYLRRTSDLKSKKKRGRPAKTNDTMTKVPFLQGFSYPI
32	sp|Q96BD5|PF21A_HUMAN	POS: 409	RKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQSS
33	sp|Q5TGY3|AHDC1_HUMAN	POS: 528	RNVVVVFPPGEMPIILKRKRGRPPKNLLLGPGKPKEPAVVAAE
34	sp|Q96C55|ZN524_HUMAN	POS: 35	RPGGATSSNRTLKASLPRKRGRPPKSGQEPPLVQVQGVTAPVG
35	sp|Q9UIF9|BAZ2A_HUMAN	POS: 654	RPRNTEKAKTKEVPKVKRGRGRPPKVKITELLNKTDNRPLKKL
36	sp|Q9UIF9|BAZ2A_HUMAN	POS: 1170	SMKMELAGSNTTASSPARARGRPRKTKPGSMQPRHLKSPVRGQ
37	sp|Q9Y6X0|SETBP_HUMAN	POS: 568	SPLYTNTDSLTVITPVKKKRGRPKKQPLLTVETIHEGTSTSPV
38	sp|Q8NEZ4|MLL3_HUMAN	POS: 818	SVTPKIGMGKPAITKRKFSPGRPRSKQGAWSTHNTVSPPSWSP
39	sp|P17096|HMGA1_HUMAN	POS: 39	TALVGSQKEPSEVPTPKRPRGRPKGSKNKGAAKTRKTTTTPGR
40	sp|Q9HBE1|PATZ1_HUMAN	POS: 248	TSPFPSVASSAPPLTGKRGRGRPRKANLLDSMFGSPGGLREAG
41	sp|Q6ZRS2|SRCAP_HUMAN	POS: 2988	TVANTVTTVTISTSPPKRKRGRPPKNPPSPRPSQLPVLDRDST
42	sp|Q03164|MLL1_HUMAN	POS: 157	VRVRSPTRSPSVKTSPRKPRGRPRSGSDRNSAILSDPSVFSPL
43	sp|Q8NEZ4|MLL3_HUMAN	POS: 4587	WSTRYANRRCRYLCSIEEKDGRPVFVIRIVEQGHEDLVLSDIS
44	sp|Q9UIF9|BAZ2A_HUMAN	POS: 633	WVQLSAEEIPSRIQAITGKRGRPRNTEKAKTKEVPKVKRGRGR

Table S1D Summary of mouse AT-hook proteins

Nr.	Uniprot ID	peptide start position	peptide sequence
1	sp|Q4VA53|PDS5B_MOUSE	POS: 1354	AESPETSAVESTQSTPQKGRGRPSKAPSPSQPPKKIRVGRSKQ
2	sp|Q91YE5|BAZ2A_MOUSE	POS: 1160	ASVKRELTGSNASTSPARSRGRPRKPKPGSLQPQHLQSTIREC
3	sp|Q8CJF7|ELYS_MOUSE	POS: 1939	DSSQLPLQTGLDVPATPRKRGRPRKVVPLEADGGTTGKEQTSP
4	sp|Q6YND2|ZN653_MOUSE	POS: 13	EAGAGGEAAAEEGAAGRKARGRPRLTESDRARRRLESRKKYDV
5	sp|P97445|CAC1A_MOUSE	POS: 2037	EGQTRAASMPRLPAENQRRRGRPRGNDLSTISDTSPMKRSASV
6	sp|Q9Z2D6|MECP2_MOUSE	POS: 169	EQKPPKKPKSPKAPGTGRGRGRPKGSGTGRPKAAASEGVQVKR
7	sp|P52927|HMGA2_MOUSE	POS: 30	GRPRKQQQEPTCEPSPKRPRGRPKGSKNKSPSKAAQKKAETIG
8	sp|Q9Z180|SETBP_MOUSE	POS: 1424	KAKRLQRQSKTGNNFVKKRRGRPRKQPSQFDEDSRDQMPVLEK
9	sp|Q4VA53|PDS5B_MOUSE	POS: 1269	KEELLENEDEQNSPPKKGKRGRPPKPLGGGTSKEEPTMKTSKK
10	sp|P52927|HMGA2_MOUSE	POS: 58	KSPSKAAQKKAETIGEKRPRGRPRKWPQQVVQKKPAQETEETS
11	sp|Q9D0B1|ZN524_MOUSE	POS: 13	LSGEEEKPLALLPPVPRGRRGRPPGGATTSNRTLKSSLPRKRG
12	sp|Q8BRH4|MLL3_MOUSE	POS: 18	PPEEPGAPAPSPAAADKRPRGRPRKDGASPFQRARKKPRSRGK
13	sp|Q9D0B1|ZN524_MOUSE	POS: 35	PPGGATTSNRTLKSSLPRKRGRPPRSEQETPLTAPVDSGGSSD
14	sp|Q3UPW2|ELF3_MOUSE	POS: 248	PRDGFPDYKKGEPKHGKRKRGRPRKLSKEYWDCLEGKKSKHAP
15	sp|P52927|HMGA2_MOUSE	POS: 10	QPSTSAQGQPAAPVPQKRGRGRPRKQQQEPTCEPSPKRPRGRP
16	sp|Q9Z180|SETBP_MOUSE	POS: 991	QYDPLLYLRRTSDLKSKKKRGRPAKTNDTMTKVPFLQGFSYPI
17	sp|Q6ZPK0|PF21A_MOUSE	POS: 389	RKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPPSS
18	sp|Q6PAL7|AHDC1_MOUSE	POS: 525	RNVVVVFPPGEMPIILKRKRGRPPKNLLLGPGKPKEPTVVAAE
19	sp|Q91YE5|BAZ2A_MOUSE	POS: 646	RPRNNEKAKNKEVPKVKRGRGRPPKIKMPELLNKTDNRLPKKL
20	sp|Q91YE5|BAZ2A_MOUSE	POS: 1374	SGDSEEMSQSPTGLGQPKRRGRPPSKFFKQVEQHYLTQLTAQP
21	sp|Q9Z180|SETBP_MOUSE	POS: 559	SPLYTNTDSLTVITPVKKKRGRPKKQPLLTVETIHEGTSTSPV
22	sp|Q8BRH4|MLL3_MOUSE	POS: 811	SVTPKIGMGKPAITKRKFSPGRPRSKQGAWSNHNTVSPPSWAP
23	sp|Q80X44|ZBT24_MOUSE	POS: 143	TGTPVVVISNKKNDPLKRKRGRPRKANGLQEGRSELAAEGELQ
24	sp|Q91YE5|BAZ2A_MOUSE	POS: 625	WVQLSAEEIPSRIQAITGKRGRPRNNEKAKNKEVPKVKRGRGR