

The mouse histone H2a.2 gene from chromosome 3

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We report the sequence of the mouse H2a-614 gene (1), which encodes an H2a.2 protein (2), consistent with its assignment as a "partially replication-dependent" histone gene (3). The sequence extends to the previously reported H3.2-614 gene (4). Both of these genes are highly expressed accounting for 30-40% of the total histone mRNA (1). The four underlined amino acids distinguish the H2a.2 protein from the H2a.1 protein (2). The start and end of the mRNAs are indicated by italics. The TATAA, CCAAT, and Spl binding sites in the promoters and the stem-loop and purine-rich sequences necessary for proper 3' end formation are underlined.

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-857                                     GAATTCATGCTGTACGGT
-840 AAATCCCTCTTAATCTTGTGACCTGAAACAGGAAATTTAGTCACCGTATGTAAACTGAAAACCTGCCATA
-770 AAAAAAACAAGATCCAAGTTAAGCAATTTCTGACCCAAAAGACAAGTTACTTCACAGACCGCTCCGATG
-700 CTGATACTTTAATAAATGGACTGCCTAATGCTTCTACATTTCTGACAATATATTAACAATAAATTTATG
-630 TAATCCCTTACACTTACTCTCTGATTCAGAGGCACATGTAACCTTGAGTAGAAATGATTTCTAATGTC
-560 AATGGGAGGGAGGTAGAAAGAAAAAACAACAAAAAACCAGAAAGCAGACAGACCGCTGGGTGG
-490 TTTTCATACAGGAAACAGGGTAAGGCTGCTGGCTCTGCGGGACGACTCGCCAGTTTGGGCACAAAAGATGG
-420 ACGCTAGGAAAGAACTCACAGCCGCTGCTCCAGTCACTACCTGATACCTGCTGACACCATGCCTGTGGCCAAATTT
-350 ACGCGTGTCTACCGGCTCTATCTGTAGCTTCTCAGCAGGAGAAAACAGCGAGCAGGCCCGCGCGCGGG
-280 CGACCCGCGGAGTGTGCAACGACGCGCGCAGCAATGAAGCCAGCAGCAGCGCGCTCGTATTGGCG
-210 CTTTCCAGGGCGGGCGGGCGGGAGCGCGCTTATGTAATGACAGGCTTCTGTCCGCGCGCTCTC
-140 ATGGCCACCGCTTCAGGACCGCTGACGCCAATGAGAGCCTCGGCCGCAATCGGCTCGCGCTATC
-70 AAAGGGTGAGCGCTCGGGCGCGGAGTACCGTTTCTGCTTGTGGCCGTTTCGTCGTTTGGCGTTTCGTGC
ATG TCC GGT CGT GGC AAG CAA GGA GGC AAG GCC CGC GCC AAG GCC AAG TCG CGG TCT
Met Ser Gly Arg Gly Lys Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys Ser Arg Ser 18
TCC CGG GCC GGG CTA CAG TTC CCG GTG GGG CGT GTC CAC CGG CTG CTG CGG AAG GGC
Ser Arg Ala Gly Leu Gln Phe Pro Val Gly Arg Val His Arg Leu Leu Arg Lys Gly 37
AAC TAC CGG GAG CGC GTG GGC GCC GGC GCG CCG GTA TAC ATG GCG GCG GTC CTG GAG
Asn Tyr Ala Glu Arg Val Gly Ala Gly Ala Pro Val Tyr Met Ala Ala Val Leu Glu 56
TAC CTA ACC GCC GAC ATC CTG GAG CTG GCG GGC AAC GCG GCC CGC GAC AAC AAG AAG
Tyr Leu Thr Ala Glu Ile Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys 75
ACG CGC ATC ATC CCG CGC CAC CTG CAG CTG GCC ATC CGC AAC GAG GAG GAG CTG AAC
Thr Arg Ile Ile Pro Arg His Leu Gln Leu Ala Ile Arg Asn Asp Glu Glu Leu Asn 94
AAG CTG GGC AAA GTG ACG ATC GCG CAG GGC GGC GTC CCG AAC ATC CAG GCG
Lys Leu Leu Gly Lys Val Thr Ile Ala Gln Gly Gly Val Leu Pro Asn Ile Gln Ala113
GTG CTG CTG CCC AAG AAG ACG GAG AGC CAC CAT AAG GCG AAG GGC AAG TGA
Val Leu Leu Pro Lys Lys Thr Glu Ser His His Lys Ala Lys Gly Lys END
+1 GGCCACTGCTCGCTCGGCCGGGCTCTCTGTGATATAACCCCGGAGCTCCCAAAAAGCCTCTTTTCAG
+71 AGCCACCCACTGAATCAGATAAAGAGTTGTGTCACGGTAGCCGGTCTTGGTGGCCCTTCTGGCCCTTCC
+141 CCAAAAAGTAAGAGTGTTCGGTTCCTTCCTGCTTCCGATATGCGGATAGCCGCTGCTTACCCCTGGTTAGTTT
+211 TCTGTTGCTGCTTCTTTGGTTTCATGCCCTGCTCGCGAGCGGATAACCGGTTCTCGGTGACCCGTCCA
+281 AGCATTAGCCCTATCTGCCACACCCTTGTCTACACAACTGTCCCTCACTCAGCGTCCACCGCCG
+351 TGACCCTTCCCAGACTAAGACTCAACTAGGACCTTAGGCCAATCTAGACATAAGTCGCAGTCAGCGCG
+421 GCTCTCGTCCGGTCTTGGGGAATGCTAGGAGGAGGAGTGTCCCGGCGAGGACTGAACTACTCCGGC
+491 TTAGGGATCATGGGGGACTGGGGCTGGGACTGTGGCTGTGGCTGGGGGTTGCTGCACAAAACACTAGATT
+561 AGTTCTGCCCTGGGAATTTGGGGCGGGCGGGCGGGCGGAGCTCTCTTGGGCAGACCGGGCGCGCC
+631 CCGTCTACGGGACTGCGACACCTGGTCCACCTCGCAGAACTTGGCAATCGCCGCGAGTGGCGCGG
+701 TGACCTGGGGGGCGGTGGGGCGGGTCAAGTGGCGTGGCGGGCCCGAGCAATGGCCGAGTGGCGGG
+771 CGGTGACCCACCGCAATGCGCGGCGAGCGCGGAGTTCAAGTCTGCTTCTCGCCCGCGCGCGGGGA
+841 ACAGTCTGCGCTATAAAGCGCGCGCTCGGGCGGTACAGGTCGCCGAGTGTCTCTGTTGGCGGCTCT
+911 TCCTCTTCCGCC ATG GCC CGT
H3.2-614 gene Met Ala Arg
    
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