

Nucleotide sequences of mouse histone genes H2A and H3.1

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A mouse testicular cDNA library in λ gt10 was screened with a human H3 gene probe. A recombinant phage with a 5 kb insert was isolated. It contains *two* histone coding sequences (H2A and H3.1, 1.75 kb apart, same orientation) and begins immediately upstream of the H2A coding sequence. Since both sequences show consensus 3' elements and since the H3 gene is preceded by CCAAT and TATA motifs (consensus elements underlined), we conclude that the insert DNA represents a genomic fragment copurified with mRNA and inserted into the vector. The deduced H3 sequence shows the H3.1 subtype (⁹⁶cys*). Another mouse H3.1 with identical amino acid sequence has been described 1 kb downstream of a (partially sequenced) H2A gene (1), which differs at positions 99^x (arg replaces lys) and 126^x (pro/ala) from the H2A described here. Thus, the newly described genes belong to a different histone gene cluster.

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AAAAATG TCC GGA CGC GGC AAG CAA GGC GGA AAG GCC CGA GCT AAG GCT AAG ACC CGC TCT TCG CGG GCC GGA CTC CAG TTC CCT
      S G R G K Q G G K A R A K A K T R S S R A G L Q F P .
H2A  GTG GGC CGC GTA CAC CGC TTG CTC CGC AAG GGC AAC TAC TCC GAG CGA GTC GGG GCC GGC GCG CCA GTG TAT CTG GCG
      V G R V H R L L R K G N Y S E R V G A G A P V Y L A
      GCG GTG TTG GAG TAC CTG ACC GCC GAG ATC CTG GAG CTG GCG GGC AAC GCC GCC CGC GAC AAC AAG AAG ACC CGC ATC
      A V L E Y L T A E I L E L A G N A A R D N K K T R I
      ATC CCC CGA CAC CTG CAG CTG GCC ATC CGC AAC GAC GAG GAG CTA AAC AAG TTG CTG GGT AAA GTC ACA ATT GCT CAG
      I P R H L Q L A I R N D E E L N K L L G Rx V T I A Q
      GGC GGT GIT CTG CCC AAC ATC CAG GCT GTA CTG CTC CCC AAG AAG ACT GAG AGT CAC CAC AAG GCC AAG GGC AAG TAA
      G G V L P N I Q A V L L P K K T E S H H K Ax K G K129
AACGAGAACTCTTATATTGGCTTTTAAAGGAAGCAGTCTTAAACAAGGCTCTTTTCAGAGCCACCCATGTATTC.....1750 ntd.....
.....AAAGGCTGCTCTGTCCAATCAGAAACAGGGTGTCTTTATATATACGGGTACGAAAGGCTAGACTTTGCTTTTTTCGTCAITTAGCAGGGTTTAGAAGTTCGCA
      ATG GCT CGT ACC AAG CAG ACT GCT CGC AAG TCC ACG GGT GGG AAA GCG CCA CGC AAG CAG CTG GCC ACC AAG GCT GCT CGA
      A R T K Q T A R K S T G G K A P R K Q L A T K A A R
H3.1  AAA AGC GCT CCA GCC ACC GGC GGC GTG AAG AAG CCC CAC CGT TAC CGG CCC GGC ACG GTG GCT CTG CGC GAG ATC CGC
      K S A P A T G G V K K P H R Y R P G T V A L R G I R
      CGC TAC CAG AAG TCG ACC GAG CTG GTG GCT CTG CGC GAG ATC CGC CGC TAC CAG AAG TCG ACC GAG CTG CTG ATT CGC
      R Y Q K S T E L V A L R G I R R Y Q K S T E L L I R
      AAA CTG CCA TTC CAG CGT CTA GTC CGT GAG ATC GCG CAG GAC TTC AAG ACC GAT CTG CGT TTT CAG AGC TCG GCG GTG
      K L P F Q R L V R E I A Q D F K T D L R F Q S S A V
      ATG GCG CTG CAG GAG GCC TGC GAG GCC TAC CTG GTG GGG CTG TTT GAG GAC ACC AAC CTA TGC GCC ATT CAC GCC AAG
      H A L Q E A C E A Y L V G L F E D Y N L C* A I H A K
      CGA GTG ACT ATC ATG CCC AAG GAC ATC CAG CIT GCT CGC CGC ATT CGT GGG GAG AGG GCG TAA ATTGCTTTGTGAATGTGTG
      R V T I H P K D I Q L A R R I R G E R A135
CTAACAAAACCCAAAGGCTCTTTTCAGAGCAACCCACCTTTTCTATAAAAAGTTGCGT

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Reference: (1) Sittman, D.B., Graves, R.A. and Marzluff, W.F.:
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