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**A comprehensive compilation and alignment of histones and histone genes**

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This collection of histones and histone genes is a revision and update of an earlier compilation (Wells, 1986). During the past three years close to 150 new histone sequences have been published. As was done in the previous compilation, we have attempted to gather and align all histone sequences available in the GenBank and MBL nucleic acid sequence databases, and in the PIR protein data base. In addition, a comprehensive attempt was made to include all recently published sequence data not currently available in these data bases to make this compilation as current as possible. In situations in which the same gene or protein has been sequenced twice, only one of these sequences was used. For each histone class, the sequences are arranged into phylogenetically related groups (*vertebrates at the beginning and fungi at the end*). Table 1 is a quick reference guide to the sequences shown in figures 1–14 and refers the reader to the full citations listed at the end of the compilation. The BIONET computer resource operated by IntelliGenetics (Mountain View, CA) was used to collect sequence data using the QUEST program. Using the original manuscripts, new sequences not currently available in the data bases, were entered in duplicate. To detect typing and other entry errors, these duplicate sequences were aligned using the IFIND program and errors were corrected. GENALIGN was used to produce the initial multiple alignments used in figures 1–9. This initial alignment was modified slightly based on previous analysis. QUEST, GENALIGN, and IFIND are products of IntelliGenetics. Any information regarding missing sequence data or erroneous presentation is encouraged.

**PROTEIN SEQUENCES**

Data from direct amino acid sequence analysis along with data from translated gene sequences are presented for each of the histone subtypes (Figures 1–5). Consensus sequences were generated for each histone subgroup and numbering is based on the consensus sequence. Figure 1 shows the alignments for the H1 proteins. In this figure, the alignments of H1 and H5/H1.0 variants are shown separately to emphasize the similarity of the vertebrate H5 group. The (●) symbols immediately above the H5 consensus indicate amino acids shared in the two variant groups. For the H1 histones, only the central conserved hydrophobic region could be aligned with any degree of certainty. A dash (–) in a sequence indicates an unsequenced region and a colon (:) in a sequence indicates an ambiguous sequence compared to the consensus. Blank spaces in the protein alignments indicate deletions with respect to the consensus. An asterisk (\*) in the consensus indicates the absence of a consensus amino acid for that position. A gap in the consensus sequence indicates an insertion was introduced into at least one of the aligned sequences to maximize sequence

similarity. A dot (.) below a consensus amino acid indicates identity with that amino acid.

### GENE SEQUENCES

Histone gene alignments are displayed for each of the five subtypes with the coding, upstream, and downstream regions displayed separately. No alignment was attempted for the histone H1 genes due to their extremely diverged nature. In an effort to draw some functional conclusions from these alignments, genes known or presumed to be nonfunctional have been excluded from this compilation.

#### *Coding regions*

In each coding region alignment, the consensus (cos) sequence is displayed on the top line followed by each individual histone gene sequence (Figures 6–9). The numbering begins at the first base of the consensus and only bases within the consensus are numbered. A dot (.) below a consensus base indicates identity with the consensus. A dash (–) in a sequence indicates an unsequenced region and a colon (:) in a sequence indicates an ambiguously sequenced base. Blank spaces within a sequence indicates a deletion with respect to the consensus was introduced to maximize the alignment. A gap in the consensus indicates an insertion was introduced into at least one of the sequences to maximize the alignment.

#### *Flanking regions*

Where available, up to 150 nucleotides of the sequences upstream and downstream of the coding region were compiled and are shown in figures 10–14. The upstream sequences include the 5' untranslated portion of the mRNA and the proximal promoter regions upstream of the ATG initiation codon. The sequences downstream of the termination codon includes the 3' untranslated portion of the mRNA as well as the more distal downstream sequences. No alignments were attempted for these flanking regions and no consensus sequences are shown. The upstream sequences are numbered backward away from the ATG initiation codon and the downstream sequences are numbered immediately after the termination codon. The initiation and termination codons are in bold type.

### CONSERVED FLANKING REGIONS

Due to space considerations and the large number of histone genes currently published, a compilation of conserved flanking regions could not be included in this compilation. However, this compilation of conserved flanking regions will be included in subsequent manuscripts currently in preparation on the evolution of the histone multigene family.

Table 1. Sequence List

#### HISTONE H1

1. Human H1.b (Ohe. *et al.*, 1986)
2. Human H1 (Carozzi *et al.*, 1984)
3. Pig H1t (Cole *et al.*, 1984)
4. Bovine H1–1 (Liao & Cole, 1981)
5. Rabbit H1–3 (Jones *et al.*, 1974)
6. Rabbit H1–4 (Rall & Cole, 1971)
7. Rat testis H1 (Cole *et al.*, 1986)
8. Chicken H1–1A1 (Sugarman *et al.*, 1983)
9. Chicken H1–11 (Coles & Wells, 1985)
10. Chicken H1 H1.10 (Coles *et al.*, 1987)
11. Chicken H1 Ch03 H1 (Coles *et al.*, 1987)
12. Chicken H1 pCH11.5E-I (Coles *et al.*, 1987)
13. Chicken H1 pCH11.5E-r (Coles *et al.*, 1987)
14. Duck H1 (Tonjes & Doenecke, 1987)
15. *Xenopus* H1-C8 (Turner *et al.*, 1983)
16. *Xenopus* H1-C2 (Turner *et al.*, 1983)
17. *Xenopus* H1B-XLH1 (Perry *et al.*, 1985)
18. *Xenopus* H1A-XLH3 (Perry *et al.*, 1985)
19. Newt H1 (Stephenson *et al.*, 1981)
20. Trout H1 (McLeod *et al.*, 1977)
21. Rainbow Trout H1 (Mezquita *et al.*, 1985)
22. Sea Urchin H1-Sp (Levy *et al.*, 1982)
23. Sea Urchin H1-h22 (Schaffner *et al.*, 1978)
24. Sea Urchin H1B-SP (Lai & Childs, 1988)
25. Sea Urchin late H1-Lp (Knowles & Childs, 1986)
26. Sea Urchin late H1-Sp-g (Knowles *et al.*, 1987)
27. *Parachinus* H1 (Strickland *et al.*, 1980)

28. *Echinolampus* H1 (Strickland *et al.*, 1982)  
 29. *Drosophila* H1 (Goldberg Ph.D. Thesis, 1979)  
 30. *Drosophila* H1 (Murphy & Blumenfeld, 1986)  
 31. *Platynereis* sperm H1a (Kmiecik *et al.*, 1985)  
 32. *Platynereis* sperm H1b (Kmiecik *et al.*, 1985)  
 33. Wheat H1.1 (Brandt & von Holt, 1986)  
 34. Wheat H1.3 (Brandt & von Holt, 1986)  
 35. *Tetrahymena* H1 (Wu *et al.*, 1986)
- HISTONE H5/H1.0**
36. Human H1-0 (Doenecke & Tonjes, 1986)  
 37. Chicken H5 (Ruiz-Carillo & Affolter, 1983)  
 39. Chicken H5 (Krieg *et al.*, 1983)  
 40. Goose H5 (Yaguchi *et al.*, 1979)  
 41. Duck H5 (Doenecke & Tonjes, 1984)
- HISTONE H2A**
42. Human H2A (Zhong *et al.*, 1983)  
 43. Human H2A.Z (Hatch & Bonner, 1988)  
 44. Human H2A.1-1 (Hayashi *et al.*, 1987)  
 45. Human H2A.1-2 (Hayashi *et al.*, 1987)  
 46. Human H2A.1-3 (Hayashi *et al.*, 1987)  
 47. Human H2A.1-4 (Hayashi *et al.*, 1987)  
 48. Bovine H2A (Sautiere *et al.*, 1974)  
 49. Bovine H2A.Z (Hatch & Bonner, 1988)  
 50. Rat H2A-1 (Laine *et al.*, 1976)  
 51. Rat H2A-2 (Laine *et al.*, 1976)  
 52. Rat H2A.Z (Hatch & Bonner, 1988)  
 53. Mouse H2A (Sittman *et al.*, 1981)  
 54. Chicken H2A (D'Andrea *et al.*, 1981)  
 55. Chicken I H2A (Wang *et al.*, 1985)  
 56. Chicken II H2A (Wang *et al.*, 1985)  
 57. Chicken H2A-F (Harvey *et al.*, 1983)  
 58. Chicken H2A (Laine *et al.*, 1978)  
 59. *Xenopus laevis* H2A-XLH1 (Perry *et al.*, 1985)  
 60. *Xenopus laevis* H2A-XLH3 (Perry *et al.*, 1985)  
 61. *Xenopus* H2A-L (Moorman *et al.*, 1982)  
 62. Newt H2A (Stephenson *et al.*, 1981)  
 63. Trout H2A (Connor *et al.*, 1984)  
 65. Sea Urchin H2A-E3 (Sures *et al.*, 1978)  
 66. Sea Urchin H2A-h22 (Schaffner *et al.*, 1978)  
 67. Sea Urchin H2A-h19 (Busslinger *et al.*, 1980)  
 68. Sea Urchin H2A-2.1-Pm (Kemler & Busslinger, 1986)  
 69. Sea Urchin H2A-2.2-Pm (Kemler & Busslinger, 1986)  
 70. Sea Urchin H2A-1 (Busslinger & Barberis, 1985)  
 71. Sea Urchin H2A-2 (Busslinger & Barberis, 1985)  
 72. Sea Urchin H2A-3 (Busslinger & Barberis, 1985)  
 73. Sea Urchin gonadal H2A-Pm (Wouters *et al.*, 1978)  
 74. Sea Urchin testis H2A-B-Sp (Lieber *et al.*, 1986)  
 75. Sea Urchin testis H2a-Lp (Lieber *et al.*, 1986)  
 76. Sea Urchin H2A.F/Z (Ernst *et al.*, 1987)  
 77. Starfish H2A (Martagine *et al.*, 1983)  
 78. *Drosophila* H2A (Goldberg Ph.D. Thesis, 1979)  
 79. *Drosophila* H2AvD (van Daal *et al.*, 1988)  
 80. *Sipunculus* H2A (Kmiecik *et al.*, 1983)  
 81. Cuttlefish H2A (Wouters-Tyrou *et al.*, 1982)  
 82. *Caenorhabditis* H2A (Vanfleteren *et al.*, 1987a)  
 83. *Tetrahymena* H2A-1 (Fusauchi *et al.*, 1983)  
 84. *Tetrahymena* H2A-2 (Fusauchi *et al.*, 1983)  
 85. *Tetrahymena* HV1 (White *et al.*, 1988)  
 86. Wheat germ H2A (Rodrigues *et al.*, 1979)  
 87. Wheat H2A1 (Rodrigues *et al.*, 1985)  
 88. *Aspergillus* H2A (May & Morris, 1987)  
 89. Yeast H2A-1 (Choe *et al.*, 1982)  
 90. Yeast H2A-2 (Choe *et al.*, 1982)
91. Yeast H2A-alpha (Choe *et al.*, 1985)  
 92. Yeast H2A-beta (Choe *et al.*, 1985)
- HISTONE H2B**
93. Human H2B-1 (Ohe *et al.*, 1979)  
 94. Human H2B-2 (Ohe *et al.*, 1979)  
 95. Human H2B (Zhong *et al.*, 1983)  
 96. Mouse H2B (Sittman *et al.*, 1981)  
 97. Rat testis TH2B (Kim *et al.*, 1987)  
 98. Rat somatic H2B (Kim *et al.*, 1987)  
 99. Bovine H2B (Iwai *et al.*, 1972)  
 100. Chicken H2B-A2B (Harvey *et al.*, 1982)  
 101. Chicken H2B-B (Harvey *et al.*, 1982)  
 102. Chicken H2B-2BA (Grandy *et al.*, 1982)  
 103. Chicken H2B PP2D-2.3 (Grandy & Dodgson, 1987)  
 104. Chicken H2B RR3C-3.5 (Grandy & Dodgson, 1987)  
 105. Chicken H2B BRA-5.4 (Grandy & Dodgson, 1987)  
 106. Chicken H2B PP2D-4.0 (Grandy & Dodgson, 1987)  
 107. Chicken H2B BBA-3.0 (Grandy & Dodgson, 1987)  
 108. Crocodile H2B (van Helden *et al.*, 1978)  
 109. *Xenopus* H2B-L (Moorman *et al.*, 1982)  
 110. *Xenopus laevis* H2B-XLH3 (Perry *et al.*, 1985)  
 111. *Xenopus laevis* H2B-XLH1 (Perry *et al.*, 1985)  
 112. Newt H2B (Stephenson *et al.*, 1981)  
 113. Trout H2B (Kootstra & Bailey, 1978)  
 114. Trout H2B (Winkfein *et al.*, 1985)  
 115. Sea Urchin H2B-E3 (Sures *et al.*, 1978)  
 116. Sea Urchin H2B-h22 (Schaffner *et al.*, 1978)  
 117. Sea Urchin sperm H2B-2 (Busslinger & Barberis, 1985)  
 118. Sea Urchin H2B-h19 (Busslinger *et al.*, 1980)  
 119. Sea Urchin testis H2B-2-Sp (Lieber *et al.*, 1986)  
 120. Sea Urchin sperm H2B-1-Sp (Lai *et al.*, 1986)  
 121. Sea Urchin testis H2B-Lp (Lieber *et al.*, 1986)  
 122. Sea Urchin testis H2B (Lai & Childs, 1986)  
 123. Sea Urchin sperm H2B-1 (Busslinger & Barberis, 1985)  
 124. Sea Urchin H2B-2.1-Pm (Kemler & Busslinger, 1986)  
 125. Sea Urchin H2B-2.2-Pm (Kemler & Busslinger, 1986)  
 126. Sea Urchin late H2B-1-Pm (Busslinger & Barberis, 1985)  
 127. Sea Urchin late H2B-2-Pm (Busslinger & Barberis, 1985)  
 128. Sea Urchin sperm H2B-Pa (Strickland *et al.*, 1977)  
 129. Starfish sperm H2B (Strickland *et al.*, 1977)  
 130. Starfish gonadal H2B (Martagine *et al.*, 1985)  
 131. *Drosophila* H2B (Goldberg Ph.D. Thesis, 1979)  
 132. Limpet H2B (van Helden *et al.*, 1979)  
 133. *Caenorhabditis* H2B (Vanfleteren *et al.*, 1986)  
 134. *Tetrahymena* H2B-1 (Nomoto, 1987)  
 135. *Tetrahymena* H2B-2 (Nomoto, 1987)  
 136. Yeast H2B-1 (Wallis *et al.*, 1980)  
 137. Yeast H2B-2 (Wallis *et al.*, 1983)  
 138. Yeast H2B (Choe *et al.*, 1985)  
 139. Yeast H2B.1-Pombe (Matsumoto & Yanagida, 1985)
- HISTONE H3**
140. Human H3-5B (Zhong *et al.*, 1983)  
 141. Human H3-26H (Clark *et al.*, 1981)  
 142. Human H3-B2 (Wells & Kedes, 1985)  
 143. Human H3 (Marashii *et al.*, 1986)  
 144. Bovine H3-1 (DeLange *et al.*, 1973)  
 145. Bovine H3-2 (Patty & Smith, 1975)  
 146. Mouse H3-1 (Sittman *et al.*, 1981)  
 147. Mouse H3-2 (Sittman *et al.*, 1981)  
 148. Mouse H3.2-614 (Taylor *et al.*, 1986)  
 149. Mouse H3.1-291 (Taylor *et al.*, 1986)  
 150. Chicken H3 (Wang *et al.*, 1985)  
 151. Chicken H3-3D (Engel *et al.*, 1982)

**Table 1.** Sequence List (cont.)

152. Chicken H3-4A (Brush *et al.*, 1985)  
 153. Chicken H3.3B (Dodge *et al.*, 1987)  
 155. *Xenopus* H3-LA (Ruberti *et al.*, 1982)  
 156. *Xenopus* H3-BOR (W. Bains Ph.D. Thesis, 1982)  
 157. *Xenopus* H3 (Old *et al.*, 1985)  
 158. *Xenopus laevis* H3-XLH3 (Perry *et al.*, 1985)  
 159. *Xenopus laevis* H3-XLH1 (Perry *et al.*, 1985)  
 160. *Xenopus laevis* H3-A-XLH1 (Perry *et al.*, 1985)  
 161. Newt H3 (Stephenson *et al.*, 1981)  
 162. Trout H3 (Connor *et al.*, 1984)  
 163. Buffalo Fish H3 (Hooper *et al.*, 1973)  
 164. Shark H3 (Brandt *et al.*, 1974)  
 165. Sea Urchin H3-E3 (Sures *et al.*, 1978)  
 166. Sea Urchin H3-h22 (Schaffner *et al.*, 1978)  
 168. Sea Urchin H3-h19 (Busslinger *et al.*, 1980)  
 169. Sea Urchin H3-LP19 (Childs *et al.*, 1982)  
 170. Sea Urchin H3-Lp21 (Roberts *et al.*, 1984)  
 171. Sea Urchin H3-LpE (Roberts *et al.*, 1984)  
 172. Sea Urchin H3 (Kaumeyer *et al.*, 1986)  
 173. Sea Star H3-PO (Cool *et al.*, 1988)  
 174. Sea Star H3-PB (Cool *et al.*, 1988)  
 175. Sea Star H3-DI (Cool *et al.*, 1988)  
 176. *Spisula* oocytes H3 (Swenson *et al.*, 1987)  
 177. *Drosophila* H3 (M. Goldberg Ph.D. Thesis, 1979)  
 178. *Caenorhabditis* H3 (Vanfleteren *et al.*, 1987b)  
 179. Wheat H3 (Tabata *et al.*, 1984)  
 180. Pea embryo H3 (Patty *et al.*, 1973)  
 181. Rice H3 (Peng & Wu, 1986)  
 182. Maize H3C2 (Chaubet *et al.*, 1986)  
 183. Maize H3C4 (Chaubet *et al.*, 1986)  
 184. Cycad H3 (Brandt & von Holt, 1986)  
 185. Barley H3 (Chojecki, 1986)  
 186. *Arabidopsis* H3-GB (Chaboute *et al.*, 1987)  
 187. *Arabidopsis* H3-GA (Chaboute *et al.*, 1987)  
 188. *Volvox* H3-I (Muller *et al.*, 1988)  
 189. *Volvox* H3-II (Muller *et al.*, 1988)  
 190. *Tetrahymena* H3-I (Horowitz & Gorovsky, 1985)  
 191. *Tetrahymena* H3-II (Horowitz & Gorovsky, 1985)  
 192. *Neurospora* H3 (Woudt *et al.*, 1983)  
 193. Yeast H3-1 (Smith & Andresson, 1983)  
 194. Yeast H3-2 (Smith & Andresson, 1983)  
 195. Yeast H3.1-Pombe (Matsumoto & Yanagida, 1985)  
 196. Yeast H3.2-Pombe (Matsumoto & Yanagida, 1985)  
 197. Yeast H3.3-Pombe (Matsumoto & Yanagida, 1985)
- HISTONE H4**
198. Human H4-A1 (Heintz *et al.*, 1981)  
 199. Human H4 (Sierra *et al.*, 1983)  
 200. Human fetal H4 (Pauli *et al.*, 1987)  
 201. Pig H4 (Sautiere *et al.*, 1971a)  
 202. Bovine H4 (Wilson *et al.*, 1970)  
 203. Mouse H4 (Seiler-Tuyns & Birnstiel, 1981)  
 204. Mouse H4 (Stauber *et al.*, 1986)  
 205. Rat H4 (Sautiere *et al.*, 1971b)  
 206. Chicken H4 (Sugarman *et al.*, 1983)  
 207. Chicken LH4 (Wang *et al.*, 1985)  
 208. Chicken RH4 (Wang *et al.*, 1985)  
 209. *Xenopus* H4-B (Turner & Woodland, 1982)  
 210. *Xenopus* H4-L (Turner & Woodland, 1982)  
 211. *Xenopus* H4-LB (Moorman *et al.*, 1981)
212. *Xenopus laevis* H4A-XLH1 (Perry *et al.*, 1985)  
 213. *Xenopus laevis* H4B-XLH1 (Perry *et al.*, 1985)  
 214. *Xenopus laevis* H4-XLH3 (Perry *et al.*, 1985)  
 215. *Xenopus* H4 (Clerc *et al.*, 1983)  
 216. *Xenopus* H4-Z (Zernik *et al.*, 1980)  
 217. Newt H4 (Stephenson *et al.*, 1981)  
 218. Trout H4 (Winkfein *et al.*, 1985)  
 219. Sea Urchin H4-h19 (Busslinger *et al.*, 1980)  
 220. Sea urchin H4-h22 (Schaffner *et al.*, 1978)  
 221. Sea urchin H4-Sp (Grunstein *et al.*, 1981)  
 222. Sea Urchin-Lp19 (Roberts *et al.*, 1984)  
 223. Sea Urchin-Lp21 (Roberts *et al.*, 1984)  
 224. Sea Urchin H4-Sp (Kaumeyer & Weinberg, 1986)  
 225. Sea Star H4-P.B. (Cool *et al.*, 1988)  
 226. Sea Star H4-D.I. (Cool *et al.*, 1988)  
 227. Sea Star H4-P.O. (Howell *et al.*, 1987)  
 228. *Drosophila* H4 (Goldberg Ph.D. Thesis, 1979)  
 229. Wheat H4 (Tabata *et al.*, 1983)  
 230. Wheat H4 (Tabata & Iwabuchi, 1984)  
 231. Pea seedling H4 (DeLange *et al.*, 1969)  
 232. Maize H4-C7 (Phillips *et al.*, 1986)  
 233. Maize H4-C14 (Phillips *et al.*, 1986)  
 234. *Arabidopsis* H4-GA (Chaboute *et al.*, 1987)  
 235. *Arabidopsis* H4-GB (Chaboute *et al.*, 1987)  
 236. *Volvox*-I H4 (Muller & Schmitt, 1988)  
 237. *Volvox*-II H4 (Muller & Schmitt, 1988)  
 238. *Tetrahymena* H4-I (Horowitz *et al.*, 1987)  
 239. *Tetrahymena* H4-II (Horowitz *et al.*, 1987)  
 240. *Tetrahymena* H4 (Bannon *et al.*, 1984)  
 241. *Physarum* H42 (Wilhelm & Wilhelm, 1987)  
 242. *Physarum* H41 (Wilhelm & Wilhelm, 1987)  
 243. *Neurospora* H4 (Woudt *et al.*, 1983)  
 244. Yeast H4-Sc (Woudt *et al.*, 1983)  
 245. Yeast (Smith & Andresson, 1983)  
 246. Yeast H4.1-Pombe (Matsumoto & Yanagida, 1985)  
 247. Yeast H4.2-Pombe (Matsumoto & Yanagida, 1985)  
 248. Yeast H4.3-Pombe (Matsumoto & Yanagida, 1985)

### Histone H5/H1.0 proteins

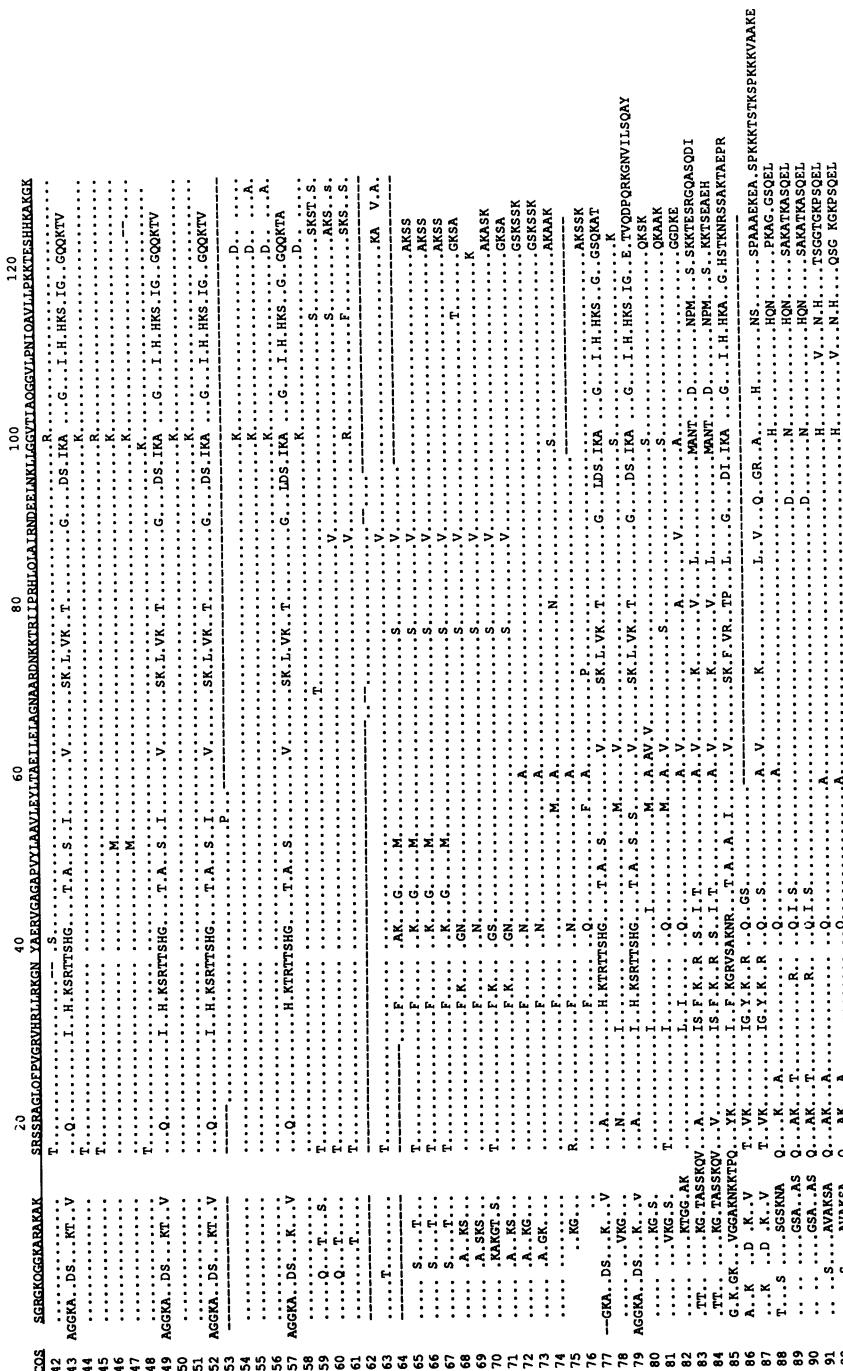
**Figure 1.** Histone H1 Protein Alignments

Figure 1. (cont.)

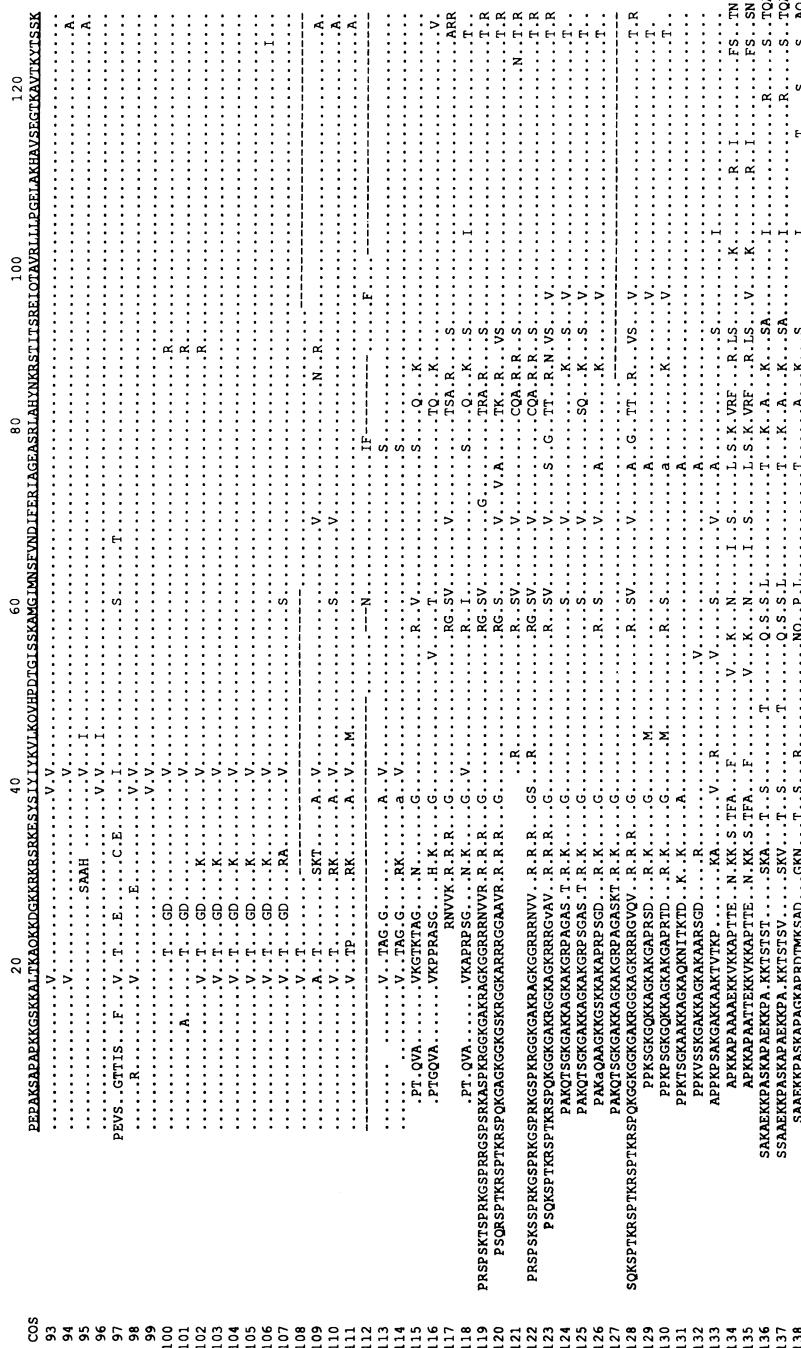
1 AASGEBAKPKAGAAKAKRPPAGAAKPKPATGATPKSKAKKTPKKAKPAAGAAKAKSPKAAPKKAAPKKAAPKPKAAKPKKAAPKPKAAKPKKAAPK  
 3 AAPPERIKGOKUKOPOAAAKTKUULI SIDSUSPKSAANTRAKKSRTAAQKKAARGRTKCAKUKDORKPKAARAKPKPAGNPKJIOKTKTRPKATNEK  
 5 AASGEAEKKEKKGAAKPKPAGATPKFCKAGAKVAKTKTPKPKPAAKPKPVAPKSPKAVTKSPKAVTKSPKAVTKSPKAVTKSPKAVTKSPKAVTKSPK  
 7 AASGNDIKGKGKSASAKTAKLGLISARSRSPKSITKVKCEPCKTGGTAKGLOOKSPKAKRPTGSERKTTGAKGLOOKSPKAKRPTGSERKTTGAKGLOOKSP  
 8 PGTETKATKKPKPAPKPKPAAKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPA  
 9 PGEVKEPKAPRKERKTAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 10 PGEVKEPKAPRKERKTAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 11 SEDYKEPKAPRKERKTAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 12 PGEVKEPKAPRKERKTAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 13 PGEGLERAKPKKKKSAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 14 PGETKERPKTICKPAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPK  
 15 QLETVKVAKVAKKLIVAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 16 QLETVKVAKVAKKLIVAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 17 QLETVKVAKVAKKLIVAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 18 QLEQSDRAAKKGEDZAAPKKTAAPKKTAGAKAKPKSLIKEPKKVUSAAKSPKVKVLPKAKKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPK  
 20 VEAKKPAPKAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPKPKPAAPK  
 22 AAKQASEPKAKKEKEKAKLIAKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAK  
 23 LDLTLSRKVTPK  
 24 KEGSDACKARDAAKCAKLAKKPKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAK  
 25 KAGTEAKPKARAIAKAKTAAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAK  
 26 KEGSDACKARDAAKCAKLAKKPKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAKKEKEKAK  
 27 AKPKKAKTTSAAAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKK  
 28 KRSAASANKLICATEKARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKAARAKKAKKA  
 29 AKKEKDPAKSKVLSAEKKVOSKSYTAKSKIGVSSKCTVATAEADKEPKAKKAVATTAAKNTKAKPKKAAPKPKPAAPKPKPAAPKPKPAAPKPKPA  
 30 AKKEKDPAKSKVLSAEKKVOSKSYTAKSKIGVSSKCTVATAEADKEPKAKKAVATTAAKNTKAKPKKAAPKPKPAAPKPKPAAPKPKPAAPKPKPA  
 31 KKAAPKPKAKKPKPSAACKCTNRAPKPKTKRN  
 32 KKAAPKPKAKKPKPSAACKCTNRAPKPKTKRN

Histone\_H3/H1.0\_proteins

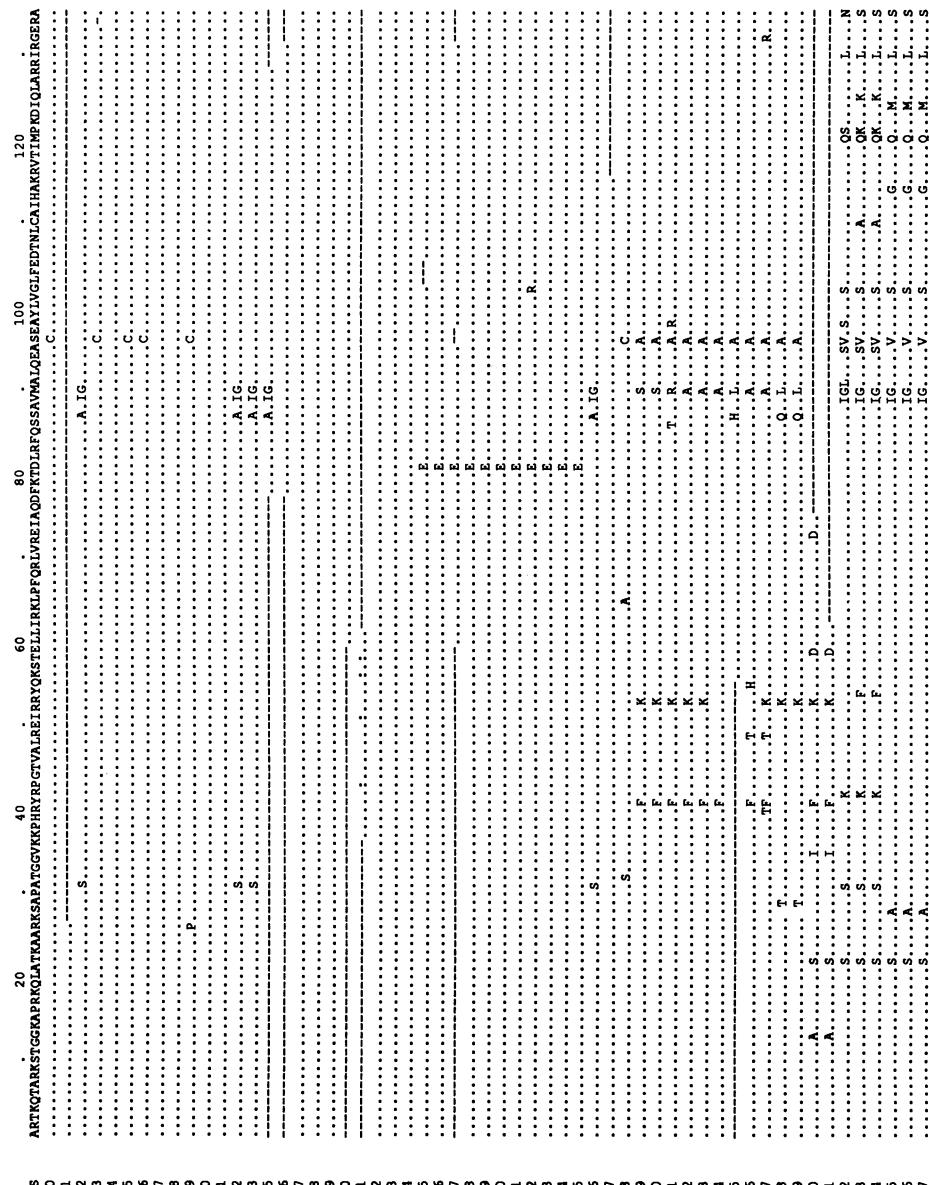
100	120	140	160	180
COS	DKAKRSPD--KKKKAVRRTSPKKAAPRMR--SPAKPKPAT-ARKARKRSASPKKKPKTVAKRSRKASK*KKAKRSRPAKSGARRSPPKK			
36	.EP..K..VA F..T..EIRKVAT....SK.K..ASKAPT....PV..K..LA.T.....P.V...P.V..K...S.K..AG..			
37	....G .....	....	....	A ..V .....
39	....G .....	....	....	A ..V .....
40	.GR.....A.K.....E.....A .....	....	....	L.T..P..R.....L.T..V .....
41	....	....	....	....



**Figure 2:** H2A Protein Sequence alignments



**Figure 3.** Histone H2B Protein Alignments



**Figure 4.** Histone H3 Protein Alignments

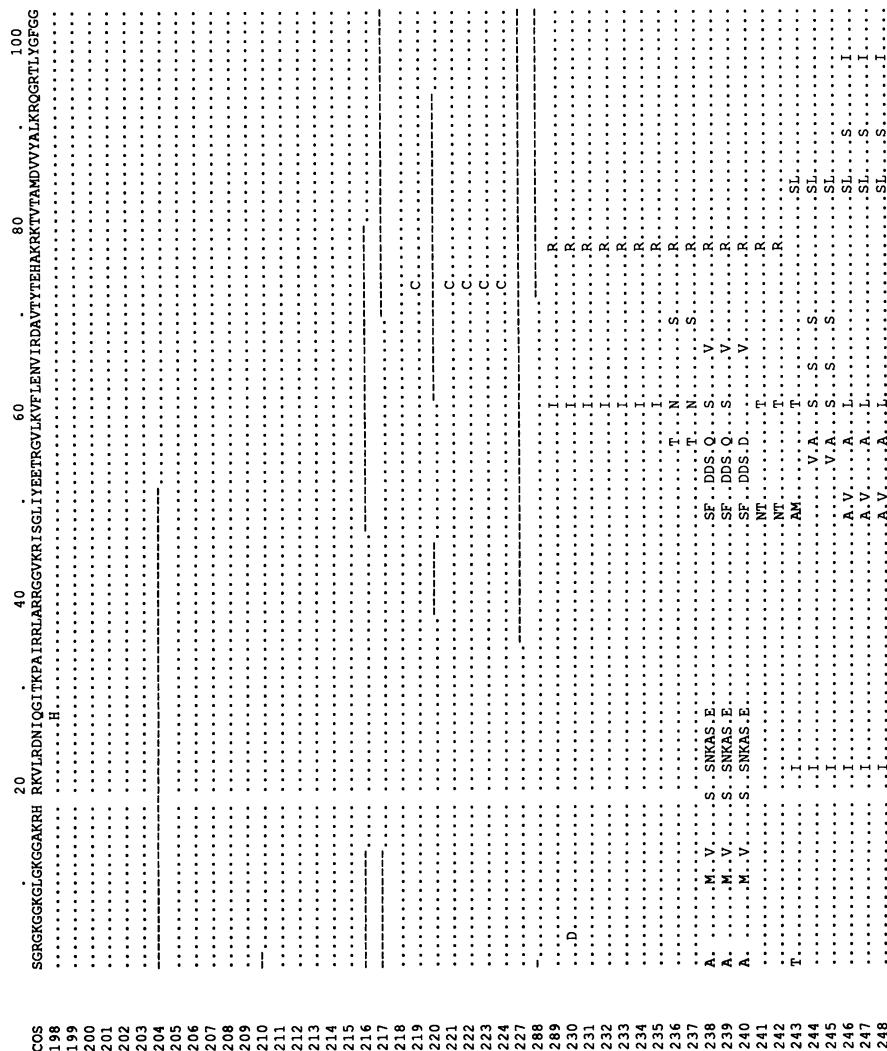


Figure 5. Histone H4 Protein Alignments

**Figure 6:** H2A Coding Sequence Alignments

Figure 6. (cont.)

	100	120	140	160	180
ccos	GCCGTTCACCGTTGCTGAGAAAGGCCAAC	TAGCCGAGGGTGTGGCCAGTGTGCCCATGCTGCGGCTGCCTGGAGTACCTGACCGTGATCCCTGA			
42	A...G...CC...CC...C	...T...C...G...G...G...T			C...A
43	....A...T...ACAC...A.A.TCTA.G.CGACCGATCAT.GA...G...GAC...G.T...ACC...A...A	....G...GAC...G.T...ACC...A...A			G.A.T
49	....A...T...ACAC...A.TCTA.G.CGACTAGCAT.GA...G...GAC...G.T...ACC...A...A	....G...GAC...G.T...ACC...A...A			G.A.T
52	....A...T...ACAC...A.TCTA.G.CAACAGCA.GA...G...GAC...G.T...ACC...A...A	....G...GAC...G.T...ACC...A...A			G.A.T
54	....C...G...C...C.C...C.C...C.C	....G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G			G.C...G
55	....C...G...C...C.C...C.C...C.C...C.C	....G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G			G.C...G
56	....C...G...C...C.C...C.C...C.C...C.C...C.C	....G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G			G.C...G
57	....CA.C...T...CAC...C...G.C...C...G.C...C...G.C...C	....G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G			G.C...G
59	T...T...T...TC...T...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	...T...T...A...G...G...A...C...A...T...G...C...T...T...A...G...G...C...T...T...T...G			G...G
60	....CT...T...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....T...G...G...A...C...A...T...C...C...G...G...A...C...T...C...A...G...C...T...T...T			T.G...G
61	....C...CT...G...A...C...C.T...A...T...T...T...T...T...T...T...T...T...T...T...T...T	....G...G...G...A...C...T...G...C...T...A...C...A...G...C...C...A...G...C...T...A...T			G...G
63	....T...T...T...CC...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....T...A...A...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G...G			C.T.C...A...T.G
65	....A...T...A...T...AC.C...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....T...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA			C.T.C...A...T.G
66	....A...T...T...T...CC...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....T...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA...AA			C.T.C...A...T.G
67	....G...T...CT...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....G...A...C...GT...T...A...A...CT...T...CG...AC...C...A...A...A...A...A...A...A			C.T.C...A...T.G
68	....G...T...CT...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....G...A...C...GT...T...A...A...CT...T...CG...AC...C...A...A...A...A...A...A...A			C.T.C...A...T.G
69	....G...T...CT...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....G...A...C...GT...T...A...A...CT...T...CG...AC...C...A...A...A...A...A...A...A			C.T.C...A...T.G
70	....T...G...T...CT...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....G...A...C...GT...T...A...A...CT...T...CG...AC...C...A...A...A...A...A...A...A			C.T.C...A...T.G
71	....T...C...T...CT...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....G...A...C...GT...T...A...A...CT...T...CG...AC...C...A...A...A...A...A...A...A			C.T.C...A...T.G
72	....T...C...T...CT...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....G...A...C...GT...T...A...A...CT...T...CG...AC...C...A...A...A...A...A...A...A			C.T.C...A...T.G
75	....T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C...C...C...C	....T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
76	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C...C	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
77	....T...A...A...ACATT...AG...CAAGAGAGCAT.GC...C...C...C...C...C...C...C...C...C...C	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
78	....T...A...A...T...CC...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
79	....T...CAC...T...TCAT...CAG...GCC...CTACT...CCAT...GA...C...A...CAC...AG...C...TCC	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
85	....TAA.AC...A.A...TT...AGGTAGTGCTPRAAG...CA...A...T...AC...TG...T...T...TGCT	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
89	....TA...A...G...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A...A	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
90	....TA...G...A	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
91	....T...C...T	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G
92	....T...C...T	....T...C...T...A...C...CC...C...C...C...C...C...C...C...C...C...C...C...C...C...C			C.T.C...A...T.G

Figure 6. (cont.)

200 GTTGGCGGCAACGGTGGCCGGACARAAAGACCCGTATCATCCCCCTACCTGCAGCTGGCCAAACGAGGAGCTGAACAAGCTCTGGGGGTGACC  
 42 .C.....G.....T.....G.....C.....G.....C.....G.....C.....C.....G.....C.....G.....C.....G.....C.....G.....C.....  
 43 AC....A.....T.....ATA.....TTA.....GTA.....AG.....T.....T.....A.....T.....T.....T.....T.....T.....T.....T.....  
 49 A.....A.....T.....AT.....GAA.....TTG.....GTA.....AG.....T.....T.....A.....T.....T.....T.....T.....T.....T.....  
 52 .....A.....A.....T.....AT.....AAA.....TTG.....GTA.....AG.....T.....T.....T.....A.....T.....T.....T.....T.....  
 53 .....A.....A.....T.....AT.....AAA.....TTG.....GTA.....AG.....T.....T.....T.....A.....T.....T.....T.....T.....  
 54 C.....A.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....  
 55 C.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....  
 56 C.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....G.....  
 57 .....A.....CT.....AAG.....CTG.....GT.....AG.....C.....CT.....A.....G.....A.....C.....TG.....G.....T.....A.....T.....  
 59 A.....G.....A.....A.....T.....A.....T.....A.....G.....A.....G.....C.....C.....G.....G.....C.....C.....A.....G.....C.....  
 60 .....C.....G.....T.....G.....T.....G.....T.....G.....A.....G.....A.....G.....C.....C.....G.....G.....C.....A.....G.....C.....  
 61 .....C.....T.....G.....T.....G.....T.....A.....C.....A.....G.....C.....T.....G.....G.....T.....C.....A.....G.....C.....  
 62 .....C.....G.....C.....G.....C.....A.....G.....C.....A.....G.....C.....C.....G.....C.....C.....A.....G.....C.....  
 63 .....C.....A.....T.....T.....T.....AT.....TA.....G.....A.....C.....T.....A.....C.....TG.....G.....T.....T.....A.....A.....C.....  
 65 AC.....C.....G.....T.....T.....AT.....TA.....G.....T.....A.....T.....G.....A.....C.....T.....G.....A.....C.....T.....A.....C.....  
 66 .....C.....C.....A.....C.....C.....A.....C.....A.....C.....G.....A.....C.....TG.....G.....T.....T.....A.....A.....C.....  
 67 AC.....C.....A.....C.....C.....C.....G.....A.....G.....A.....G.....A.....G.....A.....C.....T.....T.....A.....C.....  
 68 .....C.....C.....C.....C.....C.....G.....A.....G.....A.....G.....A.....G.....A.....C.....A.....C.....C.....A.....A.....C.....  
 69 .....C.....C.....C.....C.....C.....G.....A.....G.....A.....G.....A.....G.....A.....C.....C.....A.....B.....C.....  
 70 .....C.....C.....C.....C.....C.....G.....A.....G.....A.....G.....A.....G.....A.....C.....C.....A.....A.....C.....  
 71 .....C.....C.....C.....C.....C.....G.....A.....G.....A.....G.....A.....G.....A.....C.....C.....A.....A.....C.....  
 72 .....A.....C.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....A.....T.....  
 75 .....T.....C.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....A.....T.....  
 76 .....G.....G.....C.....G.....G.....C.....A.....G.....G.....C.....A.....G.....G.....C.....A.....G.....T.....T.....A.....B.....C.....  
 77 .....A.....T.....ACTAA.....TCTG.....GTA.....AG.....CA.....T.....A.....GSGA.....A.....AT.....G.....CTCG.....TAT.....AA.....CA.....  
 78 .....T.....T.....T.....AT.....GAAG.....TTG.....AGT.....AA.....CT.....T.....C.....T.....G.....T.....A.....T.....A.....G.....CTC.....C.....C.....A.....  
 79 .....A.....T.....T.....T.....TAAG.....TTT.....AGTC.....GAA.....A.....CT.....T.....T.....T.....T.....G.....GAGC.....AT.....AA.....CA.....  
 85 A.....A.....T.....T.....TAAG.....TTT.....AGTC.....GAA.....A.....CT.....T.....T.....T.....A.....AT.....A.....G.....TA.....T.....AT.....AA.....CT.....  
 89 A.....A.....T.....T.....TA.....G.....T.....A.....A.....T.....T.....AA.....A.....TT.....A.....AT.....T.....A.....AT.....T.....A.....T.....A.....  
 90 A.....A.....T.....T.....TA.....A.....A.....A.....A.....T.....T.....AA.....A.....TT.....A.....AT.....A.....A.....T.....T.....A.....AT.....A.....A.....  
 91 A.....A.....T.....T.....T.....T.....T.....T.....T.....A.....C.....T.....T.....A.....T.....T.....A.....T.....A.....AT.....A.....A.....T.....TCAT.....T.....  
 92 A.....A.....C.....T.....T.....T.....T.....T.....T.....T.....T.....A.....A.....T.....TCAT.....T.....A.....A.....T.....TCAT.....T.....T.....

Figure 6. (cont.)

		320
cos	ATCGCTAGGTGGTGTGCTGCCAACATCCAGGGCGTGTGCCAAGAGACCGACAAGCACCAGGGCAAG	
42	.....G.....C.....T.....T.....T.....G.....T.....A.....T.....G.....GCCATCAT.....	
43	.....T.....GGT.....CA.T.AC.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
49	.....T.....GGT.....CA.T.AC.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
50	.....T.....GGT.....CA.C.AC.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
53	.....G.....C.C.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
54	.....G.....C.G.....G.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
55	.....G.....C.G.....G.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
56	.....G.....C.G.....G.....CAAATCT.....A.....TGGG.....AGGAC.AC.....AG.....TGTC	
57	.....A.....GGG.....A.C.....CA.C.....C.....CAAATCT.....A.....CGGG.....GG..C..GC.....AA.....GC	
59	.....A.....C.....C.....CAAATCT.....A.....T.....T.....A.....GTT.....ATCCA.A.....A.....	
60	.....C.....C.....C.....CAAATCT.....A.....T.....T.....C.....A.....GCG.....AATCT.....A.....	
61	.....C.....G.....G.....CAAATCT.....A.....T.....T.....C.....A.....GCT.....AGTC.....A.....	
63	.....A.....A.....A.....CAAATCT.....A.....C.....A.....T.....G.....GT.....A.....	
65	.....A.....C.....A.....CAAATCT.....A.....C.....A.....TT.....AT.....A.....G	
66	.....C.A.....C.....CAAATCT.....A.....T.....T.....GGT.....TA.....AT.....G.....G	
67	.....A.....A.....A.....CAAATCT.....A.....T.....T.....A.....T.....CT.....AT.....A.....G	
68	.....C.....C.....C.....CAAATCT.....A.....T.....C.....C.....C.....G.....T.....TG.....A	
69	.....C.....C.....C.....CAAATCT.....A.....T.....C.....C.....C.....G.....T.....TG.....A	
70	.....C.....C.....C.....CAAATCT.....A.....T.....C.....C.....C.....C.....G.....T.....TG.....A	
71	.....C.....C.....C.....CAAATCT.....A.....T.....C.....T.....C.....C.....G.....T.....TG.....A	
72	.....C.....C.....C.....CAAATCT.....A.....C.....T.....C.....C.....T.....G.....T.....TG.....A	
76	.....C.....A.....C.....CAAATCT.....A.....C.....T.....T.....T.....T.....A.....CT.....AT.....A.....	
77	.....GGT.....CA.C.TC.....CAAAGTGT.....A.....CGGA.....GGATCAC.....GG.A.CA	
78	.....T.....A.....A.....C.....GT.....T.....T.....A.....T.....T.....T.....G	
79	.....GGT.....C.....CA.T.GC.....A.....CAAAGTC.....A.....GG.....A.GG.....A.C.GTGCAGG.TC.GC.....C.G.....GGCAACAGTCATTGTGCGAGGCTAC	
85	.....T.....GGT.....CA.T.TC.....TAAA.CT.....CT.....GGT.....C.C.T.TACT.....A.....A.....GATCPAGTGTAAAG.CTCCTGAACTCTAC	
89	.....T.....C.....A.....T.....A.....T.....TCAAAACT.....T.....A.....T.....T.....A.....T.....TG.....A.....TTCTCAGG.ATA	
90	.....T.....C.A.....T.....T.....TCAAAACT.....T.....A.....T.....T.....C.....C.....TG.....A.....TTCTCAGG.ATA	
91	.....T.....A.....G.T.....C.....CAT.....TT.....A.....CT.....T.....GTGCG.....TGG.....C.....T.....GTGCG.....CTG	
92	.....T.....C.....A.....G.A.....T.....T.....A.C.....TCAT.....CT.....AC.....AT.....T.....GT.....GC.....AGCCTAG.....C.A.....AGCTT	

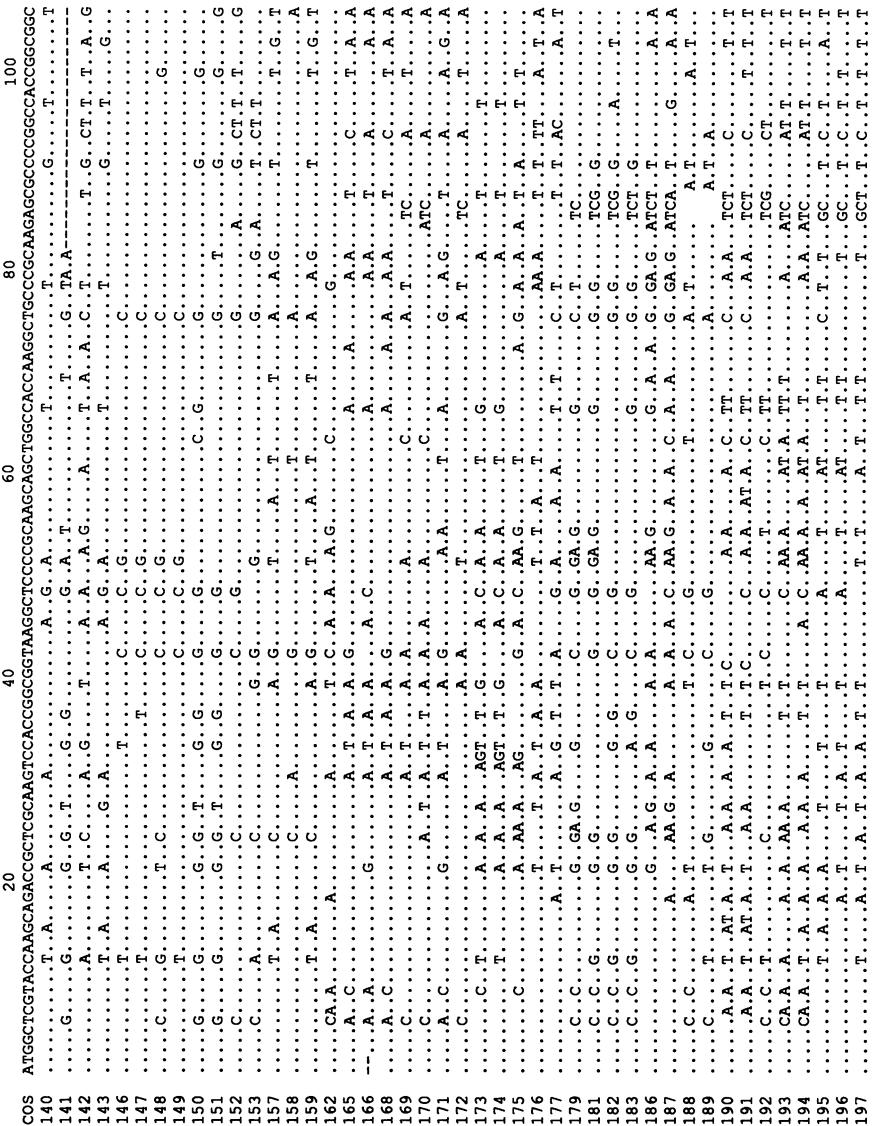
**Figure 7.** Histone H2B Coding Sequence alignments

**Figure 7** (cont.)

**Figure 7** (cont.)

cos	180	200	220	240	260
95	CCTCAAGGCCATCTGGCATCATGACCTCGTCAAGACATCTGGGAGGCATCAGCCCTGGCAACTACACAGCTCCCATCACCTCCGG	G..	T.G.	A.T.	T.
96	.....	.....	.....	.....	G..
97	T..	G..	G..	G..	G..
98	.....	.....	.....	.....	G..
99	G..	G..	G..	G..	G..
100	G..	G..	G..	G..	G..
101	G..	G..	G..	G..	G..
102	G..	G..	G..	G..	G..
103	A..	A..	A..	A..	G..
104	G..	G..	G..	G..	G..
105	G..	G..	G..	G..	G..
106	G..	G..	G..	G..	G..
107	A..	T.A..	A..	T..	G..
109	G..	A..	T..	T.G..	G..
110	T..	A..	T..	T..	A..
111	.....	.....	.....	.....	.....
112	.....	.....	.....	.....	.....
114	.....	.....	.....	.....	.....
115	AGTCG..	T..	AG..	AT..	A..
116	AG.CG..	ACA..	AG..	T..	G..
117	TAG.CGT..	TC.G..	AG..	.....	.....
118	AGTCG..	AT..	AG..	AT..	AT..
119	AG.CGT..A..	TC.G.G..	AG..	T..	G..
120	TAG.CCG..	TC..	AGT..	T..	T..
121	TAG.CGT..A..	TC(G..	AG..	TG..	G..
122	TAG.CGT..	TC(G..	AG..	TG..	T..
123	AG.CGT..	TC.G..	AG..	T..	AG..
124	AG..A..	TC..	AG..	TG..	T..
125	AG..A..	TC..	AG..	TG..	T..
126	AG.CCT..	TC..	AGT..	AG..	AG..
127	AG..A..	TC..	AG..	TG..	T..
128	AG..A..	TC..	AG..	TG..	T..
134	AG..T..	AA..A..	T..	A..T..	T..
135	AG..T..	TCT..	T..	T..	T..
136	CAA..	T..	T..	T..	T..
137	CAA..T..	T..	T..	T..	T..
138	AA.CA..	CCT..	T..	T..	T..

**Figure 7** (cont.)



**Figure 8.** Histone H3 Coding Sequence Alignments.

Figure 8. (cont.)

COS

120 GTGAAAGCCTACCGTTACGGCCGGACCTCGCTCGTGAGATCCAGAAGTCCAGCTACAGAAGTCGCTGATCCGCAAAGTCAGCTGCAGGCC  
 140 .....A.....C.T.G.T.T.G.....C.....A.....G.....T.....T.G.....G.....  
 142 .....A.....T.....T.T.G.....G.C.....A.....T.A.....T.....A.....T.....T.....  
 143 .....C.C.G.....T.G.....C.....C.....A.....T.....T.....T.....T.....  
 146 .....C.....C.T.....T.G.....A.....C.....G.....G.....G.....  
 147 .....A.....C.T.....G.G.....C.....G.....G.....G.....  
 148 .....G.....C.....C.....G.G.....G.....G.....G.....  
 149 .....C.....C.T.....G.G.....C.....G.....G.....G.....  
 150 .....G.....C.....C.....G.G.....C.....G.....G.....  
 151 .....A.....TC.....T.G.....G.....C.....A.....G.....G.....A.....  
 152 .....G.....C.....C.....T.T.G.....C.....A.....A.G.....T.....A.....TTA.....T.....  
 153 .....C.....C.....C.....G.....G.....C.....G.....G.....  
 157 .....C.....C.....C.....A.....T.....T.....C.....A.....A.....T.....A.....T.....  
 158 .....C.....A.C.T.C.....TC.C.....A.....G.....C.G.....A.....T.C.....T.....A.....T.....  
 159 .....C.....A.....T.....C.C.....P.....T.....C.....A.....A.....A.....T.....  
 160 .....C.....C.....C.....T.....G.....C.....C.....T.....C.....  
 161 .....C.....C.....T.....G.....C.....C.....T.....C.....  
 162 .....C.....T.....A.....C.....A.....T.....C.....AG.....T.....T.....C.....A.....A.....  
 165 .....A.....T.C.....A.....T.....A.....AT.....A.A.....T.....A.....A.....  
 166 .....A.....T.....T.....A.....A.....A.....A.....T.....A.....A.....  
 167 .....C.....T.....A.....C.....A.....A.....A.....T.....  
 168 .....C.....T.....A.....C.....A.....A.....A.....A.....  
 169 .....C.....T.....T.....A.....A.....C.....A.....A.....  
 170 .....C.....T.....A.....A.....A.....C.....A.....A.....  
 171 .....T.....A.....A.....T.A.....C.....A.....A.....T.....C.....A.....A.....  
 172 .....C.....T.....A.....T.....A.....C.....A.....T.....C.....A.....A.....  
 173 .....A.....C.....A.....A.....T.G.....G.....T.C.....T.....AGT.....A.....C.....C.....  
 174 .....A.....C.....A.....A.....T.G.....A.....G.....T.C.....T.....AAGT.....A.....T.....A.....C.....  
 175 .....C.....A.C.....G.....C.A.....G.....A.....A.....C.....A.....A.....A.....  
 176 .....C.....T.....A.....A.....A.....T.....A.....A.....A.....AA.....A.....  
 177 .....C.....TC.....C.....T.....A.....C.....G.....CT.....A.....T.....A.....A.....  
 179 .....C.....C.....C.....G.....G.....C.....C.....CAAG.....A.G.....C.....C.....  
 181 .....G.....C.....T.....G.....G.....C.....C.....C.....C.....  
 182 .....C.....T.....C.....G.....G.....C.....G.....G.....C.....  
 183 .....C.....C.....T.....C.....G.....C.....G.....G.....C.....  
 186 .....A.....AA.....T.....A.....A.....T.....T.....T.....AA.....A.....G.....A.....  
 187 .....A.....ACA.....T.....C.....T.....A.....T.....T.....C.....ACA.....A.....A.....GAG.....T.....AG.....T.....T.....G.....  
 188 .....G.....C.....C.....T.....T.G.....C.....C.....T.....AG.....T.....T.....T.....G.....  
 189 .....C.....T.....C.....TC.....C.....G.....A.....A.....GAG.....T.....AG.....G.....C.....C.....  
 190 .....A.....T.....C.....A.....T.....T.....CT.....A.....A.....AA.....A.....T.....A.....T.....T.....A.....  
 191 .....A.C.....C.....AA.....T.....A.....T.....T.....CA.....A.....A.....AA.....A.....  
 192 .....C.....C.....A.....A.....T.....C.....T.....C.....C.....  
 193 .....T.....AA.....T.A.....A.....T.....T.....A.....T.....A.....T.....T.....AA.....  
 194 .....T.....AA.....T.A.....A.....T.....T.....CT.....A.....A.....AA.....A.....T.....A.....T.....AA.....  
 195 .....T.....T.....TC.....T.....T.....T.....T.....T.....A.....T.....T.....A.....T.....  
 196 .....T.....T.....TC.....T.....T.....T.....T.....A.....T.....T.....A.....T.....  
 197 .....T.....T.....TC.....T.....T.....T.....A.....T.....T.....A.....T.....A.....

Figure 8. (cont.)

**Figure 8.** (cont.)

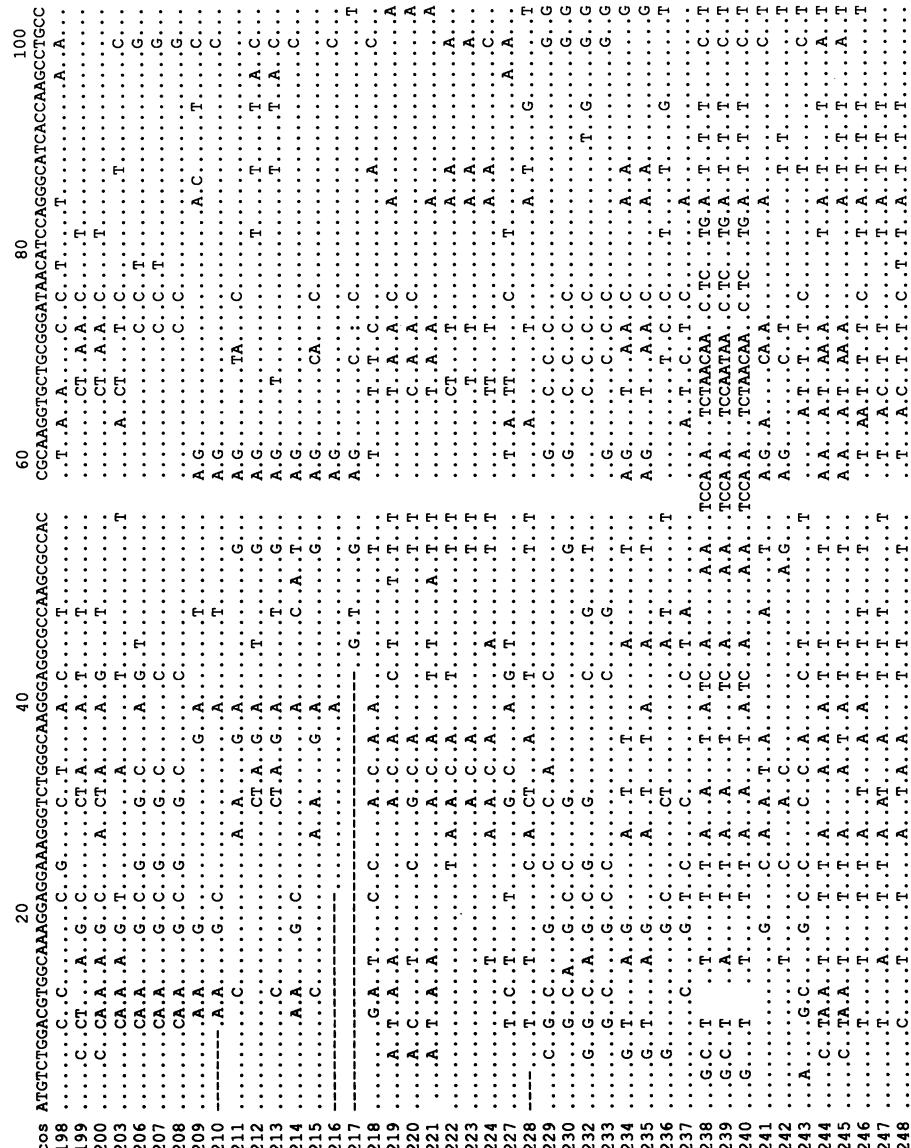


Figure 9: H4 Coding Sequence Alignments

Figure 9. (cont.)

Figure 9. (cont.)

cos	CGCGTACCTAACCGGACCCAAAGAGGAAGACGTCAACGCCATGGAGCTGTCAGGCTCAAGGCCAGGGCGACCCCTACGGTTTCGGAGGTTAA
198	.....A....T.A.....C.C.....G.....T.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G
199	.....A.....C.C.....A.....G.....A.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G
200	.....A.....C.C.....A.....G.....A.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G
203	.....A.....C.C.....T.....T.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G
204	.....A.....C.C.....G.....T.....T.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G.....T.....G
206	.....G.....G.....G.....G.....G.....G.....G.....A.....A.....A.....C.....C.....C.....C.....C.....C.....C.....C
207	.....G.....G.....G.....G.....G.....G.....G.....G.....A.....A.....A.....C.....C.....C.....C.....C.....C.....C
208	.....G.....G.....G.....G.....G.....G.....G.....G.....A.....A.....A.....C.....C.....C.....C.....C.....C.....C
209	.....G.....G.....T.....T.....T.....G.....T.....G.....T.....G.....A.....T.....T.....T.....G.....A.....T.....T.....T
210	.....G.....G.....T.....T.....T.....G.....T.....G.....T.....G.....A.....T.....T.....T.....G.....A.....T.....T.....T
211	.....T.....T.....A.....A.....A.....T.....T.....G.....T.....G.....A.....A.....T.....G.....A.....T.....G.....A.....A
212	.....A.....A.....A.....T.....T.....T.....G.....T.....G.....G.....T.....G.....A.....T.....G.....A.....T.....G.....A
213	.....A.....A.....A.....T.....T.....T.....T.....G.....T.....G.....A.....T.....T.....G.....A.....T.....G.....A.....A
214	.....T.....T.....T.....T.....T.....G.....T.....G.....T.....G.....A.....A.....T.....G.....A.....T.....G.....A.....A
215	.....T.....T.....T.....T.....T.....G.....T.....G.....T.....G.....A.....A.....T.....G.....A.....T.....G.....A.....A
206	.....T.....T.....T.....T.....T.....G.....T.....G.....T.....G.....A.....A.....A.....T.....G.....A.....A.....T.....G.....A
218	.....T.....T.G.....C.A.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T
219	.....T.A.....TG.....C.A.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T
220	.....G.....T.....A.....G.....A.....G.....T.....A.....G.....A.....G.....T.....A.....G.....A.....G.....T.....A.....G.....A.....G
221	.....T.....A.....TG.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....A.....G
222	.....T.....T.G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G.....T.....A.....G
223	.....T.....TG.....C.A.....A.....T.....G.....A.....T.....G.....A.....T.....G.....A.....T.....G.....A.....T.....G.....A.....A
224	.....T.....T.G.....A.....A.....T.....G.....A.....T.....G.....A.....T.....G.....A.....T.....G.....A.....T.....G.....A.....A
228	.....G.....T.....T.....A.....T.....G.....T.....G.....T.....G.....T.....G.....A.....A.....AA.....T.....T.....A.....T.....A.....C
229	.....T.....GGCC.C.....T.....G.....T.....G.....T.....G.....T.....G.....A.....AA.....T.....T.....A.....T.....A.....C.....C
230	.....G.....GGCC.C.....A.....C.....C.....G.....G.....G.....G.....A.....AA.....T.....T.....A.....G.....A.....AA.....T.....A.....C.....C
232	.....T.....G.....GGCC.C.....C.....C.....G.....G.....G.....A.....AA.....T.....A.....T.....G.....A.....T.....C.....C.....G.....G
233	.....T.....T.....GGCC.C.....G.....C.....C.....G.....G.....A.....AA.....T.....T.....A.....A.....AA.....T.....T.....G.....G
234	.....T.....T.....T.....T.....G.....T.....G.....T.....G.....T.....G.....A.....AA.....T.....T.....A.....A.....AA.....T.....T.....A.....C
235	.....T.....T.....A.....T.....G.....T.....G.....T.....G.....T.....G.....A.....AA.....T.....T.....A.....A.....AA.....T.....A.....C.....C
236	.....T.G.....G.....T.....A.....T.....G.....T.....G.....T.....G.....A.....AA.....T.....T.....A.....A.....AA.....T.....T.....A.....C.....C
237	.....TT.A.....T.....T.....T.....T.....G.....A.....A.....T.....A.....A.....T.....G.....T.....T.....G.....A.....T.....T.....G.....C.....G
238	.....T.....T.....T.....T.....T.....G.....A.....A.....T.....T.....T.....C.....T.....A.....A.....A.....A.....T.....T.....G.....G
239	.....T.....T.....T.....T.....A.....T.....G.....A.....A.....T.....T.....T.....C.....A.....A.....A.....A.....T.....T.....T.....G.....G
240	.....T.....T.....T.....T.....A.....T.....G.....A.....A.....T.....T.....T.....C.....A.....A.....A.....A.....A.....T.....T.....T.....G.....G
241	.....T.....T.....G.....G.....A.....T.....T.....G.....A.....A.....T.....T.....C.....A.....A.....A.....T.....A.....A.....T.....A.....C.....C
242	.....T.....G.....T.....C.G.....C.....A.....G.....T.....T.....C.....A.....A.....T.....G.....A.....A.....T.....G.....A.....C.....C
243	.....T.....T.....G.....T.....C.G.....C.....A.....G.....T.....T.....C.....A.....A.....T.....G.....A.....A.....T.....G.....A.....C.....C
244	.....T.....T.....T.....T.....A.....A.....T.....T.....T.....T.....T.....T.....G.....A.....A.....TA.....A.....T.....T.....T.....G.....G
245	.....T.....T.....T.....T.....A.....A.....T.....T.....T.....T.....T.....T.....G.....A.....A.....TA.....A.....T.....T.....T.....T.....G.....G
246	.....T.....T.....T.....T.....C.T.....T.....T.....T.....T.....T.....T.....T.....T.....G.....T.....A.....T.....A.....T.....T.....T.....T.....T.....G.....G
247	.....T.....A.....T.....T.....A.....C.T.....T.....T.....T.....T.....T.....T.....T.....G.....T.....A.....T.....A.....T.....T.....T.....T.....T.....T.....T.....T.....G.....G
248	.....T.....T.....T.....T.....A.....T.....T.....T.....T.....T.....T.....T.....T.....G.....T.....A.....T.....A.....T.....T.....T.....T.....T.....T.....T.....T.....T.....G.....G

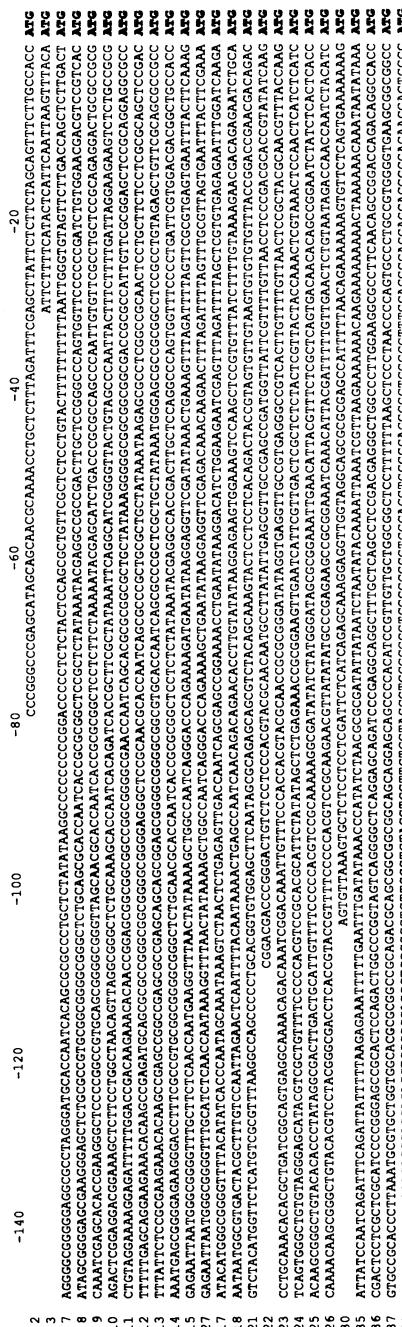


Figure 10A. Histon H1 5' Upstream Alignments

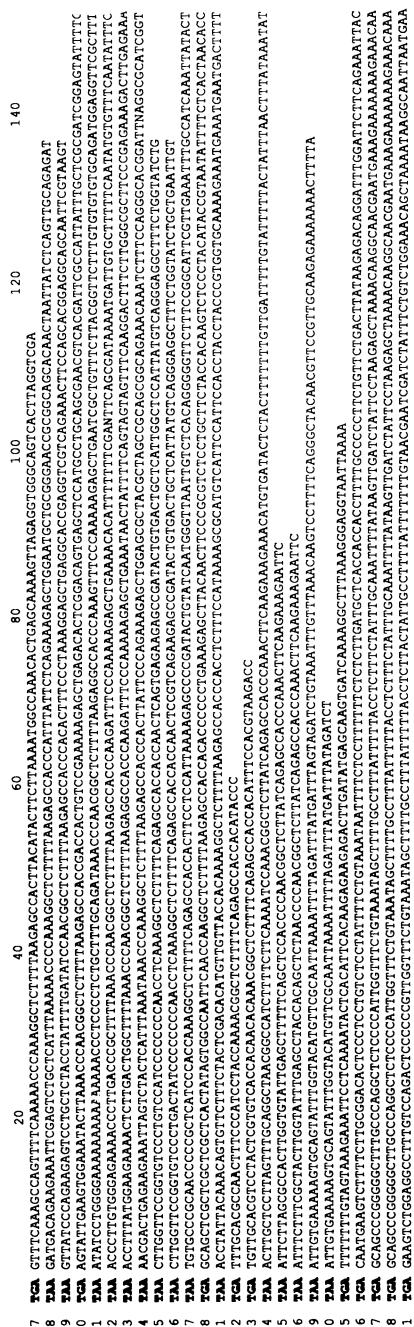


Figure 10B. Histon H1 3' Downstream Alignments

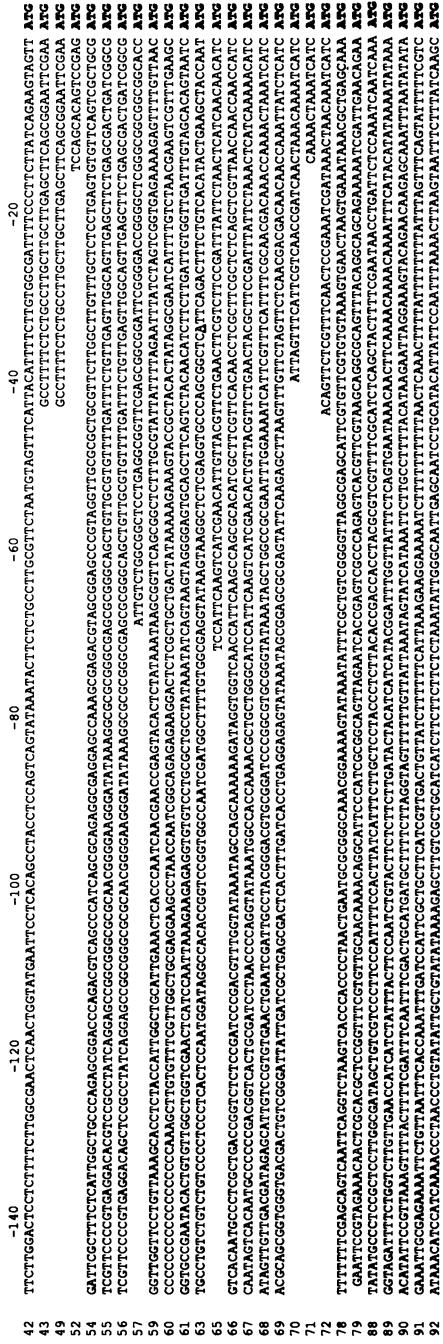


Figure 11A. HPA\_5 Upstream Sequences

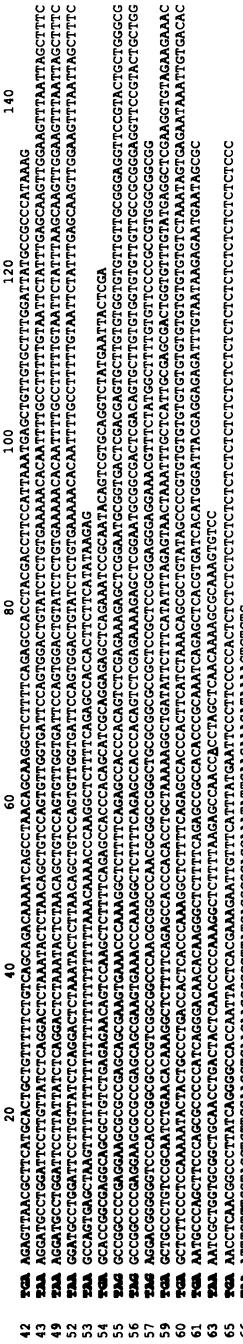


Figure 11B. HPA\_5 Downstream Sequences

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**Figure 12A Histone H2B 5' Upstream Sequences**

**Figure 12B. Histone H2B 3' Downstream Sequences**

**Figure 13A: Histone H3 5' Upstream Sequences**

Figure 13B. Histone H3 3' Downstream Sequences



Figure 14A. Histone H4 5' Upstream Sequences.

20	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	100	120
21	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	140	160
22	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	180	200
23	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	220	240
24	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	260	280
25	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	300	320
26	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	340	360
27	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	400	420
28	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	460	480
29	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	520	540
30	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	580	600
31	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	640	660
32	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	720	740
33	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	780	800
34	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	840	860
35	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	920	940
36	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	980	1000
37	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1040	1060
38	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1100	1120
39	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1160	1180
40	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1220	1240
41	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1280	1300
42	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1340	1360
43	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1400	1420
44	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1480	1500
45	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1540	1560
46	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1600	1620
47	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1660	1680
48	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1720	1740
49	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1780	1800
50	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1840	1860
51	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1920	1940
52	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	1980	2000
53	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2040	2060
54	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2100	2120
55	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2160	2180
56	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2220	2240
57	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2280	2300
58	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2340	2360
59	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2400	2420
60	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2480	2500
61	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2560	2580
62	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2640	2660
63	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2720	2740
64	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2800	2820
65	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2880	2900
66	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	2960	2980
67	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3040	3060
68	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3120	3140
69	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3200	3220
70	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3280	3300
71	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3360	3380
72	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3440	3460
73	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3520	3540
74	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3600	3620
75	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3680	3700
76	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3760	3780
77	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3840	3860
78	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	3920	3940
79	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4000	4020
80	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4080	4100
81	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4160	4180
82	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4240	4260
83	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4320	4340
84	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4400	4420
85	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4480	4500
86	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4560	4580
87	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4640	4660
88	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4720	4740
89	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4800	4820
90	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4880	4900
91	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	4960	5000
92	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5080	5120
93	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5200	5240
94	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5320	5360
95	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5440	5480
96	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5560	5600
97	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5720	5760
98	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	5920	5960
99	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	6120	6160
100	TAA	GGCGCCTTCCTCAACAGGCCCCCTTTAGGCCCCAATACCTAAAGGTGTAAT	6320	6360

Figure 14B. Histone H4 3' Downstream sequences.

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