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Nucleotide sequence of rat c-jun protooncogene

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We isolated a clone containing rat c-jun gene from a rat liver genomic DNA-λ charon 4A library by plaque hybridization with ^{32}P-labeled human c-jun cDNA (1) and determined the nucleotide sequence. The rat gene encodes a protein whose deduced amino acid sequence shares 96% and 99% identity with those of human (1) and mouse c-jun (2,3), respectively. The 3′-untranslated region contains three consensus signal sequences for poly(A) addition (shown by underlines). The 5′-promoter region contains putative AP1 (TGACATCA),CTF (GCCAAT) and SP1 (CCCGCCCC) binding sites (indicated as open boxes), and is highly conserved when compared with that of human c-jun gene (4). Nucleotide numbers are given with the initiation site of transcription as +1.

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-258  GGAGCAACGCGCGGGAGGGGGAGGGAGGTGGAGAAAGAAGGGCCCAACTGTAGGAGCGCAGCGGAGCATTACCTCATCCCGTGAGCCTTCGCGGGCCCAGAGAAGAATCTTCTAGGGTGA
-138  GGTCTCCATGGCGACGGGTGGGCCCCGCCCCCTTGAGAGCGACGCAAGCCAATGGGAAGGCCTTGGGGTGACATCATGGGCTATTTTTAGGGATTGACTGGTAGCAGATAAGTGTTGAGCT
-18   CAGGCTGGATAAGGACTCAGAGTTGCACTGAGTGTGCAGAGACTGCCTAGCTGGAGAGCGCTCAGGCAGACAGACAGACGGACGGACTCGGCTAACCTGGTCGTCCGCGGACTCCGGGCT
103   GTTCATCTGTTTGTCTTCATTTTCTGACCAACTGCCTGGATCCAGCGCCCGCAGCTCCTGCACCGGTGTTTTGGGGAGCACTTGGAGAGTCCCTTCTCCCGCTTTTCCCGGAGAAGAAGC
223   TCACAAGTCCCGGCACTGCTGACAGCATCGAGAACGGCTCCGGACCGCGCGAGGAAATAGGCGAGCGGCTACCGGCCAGCAACTTTCCTGACCCAGAGGACCGGGAACAAGTGGCCCGGA
343   GCGAACTTTTGCAAAACCTCTTCTGCGCCTAAGGCTGCCACCGAGACCGTAAAGAAAAGGGAGAAGAGGAACCTATACTCATACCAGCTCGCACAGGCGGCTGAAGTTGGGCGAGTGCTA
463   GCCGCGGCTGCCTAGCGTCCCCCTCCCCCTCACAGCGGAGGAGGGGACAGTTGTCGGAGGCCGGGCGCAGAGCCGATCGCGGGCTTCCACCAAGAATTCCGTGACGACTGGTCTGCGCCG
583   CCGGAGAACCTCTGTCGCTGGGGCTGGTCCGCGGGCTCCGAGGAACCGCTGCTTCCCGAGAGCGCTCCGTGAGTGACCGCGACTTTTCAAAGCTCCGGATCGCGCGGGAGCCAACCAACG
703   TGAGTGCAAGCGGTGTCTTAACCCTGCGCTCCCTGGAGCGAACTGGGGAGGAGGGCGCAGGGGGGAGCACTGCGGTCTGAGCGCACGCTCCTAAACAAACTTTGTTACTGAAGCGGGGAC
823   GCGCGGGTATCCCCCGCTTCCCGGCGCGCTGTTGCGGCCCCGAAACTTCTGCGCACAGCCCAGGCTAACCCCGCGTGAAGTGACCGACTGTTCTATGACTGCAAAGATGGAAACGACCTT
                                                                                                                M  T  A  K  M  E  T  T  F
943   CTACGACGATGCCCTCAACGCCTCGTTCCTCCAGTCCGAGAGTGGCGCCTACGGCTACAGTAACCCTAAGATTCTGAAGCAGAGCATGACCTTGAACCTGGCCGACCCGGTGGGCAATCT
       Y  D  D  A  L  N  A  S  F  L  Q  S  E  S  G  A  Y  G  Y  S  N  P  K  I  L  K  Q  S  M  T  L  N  L  A  D  P  V  G  N  L
1063  GAAGCCGCACCTCCGAGCCAAGAACTCGGACCTTCTCACGTCGCCCGACGTCGGGCTGCTCAAGCTGGCGTCGCCGGAGCTGGAGCGCCTGATCATCCAGTCCAGCAATGGGCACATCAC
       K  P  H  L  R  A  K  N  S  D  L  L  T  S  P  D  V  G  L  L  K  L  A  S  P  E  L  E  R  L  I  I  Q  S  S  N  G  H  I  T
1183  CACTACACCGACCCCCACTCAGTTCTTGTGCCCCAAGAACGTGACCGACGAGCAGGAGGGCTTCGCCGAAGGCTTCGTGCGCGCCCTAGCTGAACTGCATAGCCAGAATACGCTGCCCAG
       T  T  P  T  P  T  Q  F  L  C  P  K  N  V  T  D  E  Q  E  G  F  A  E  G  F  V  R  A  L  A  E  L  H  S  Q  N  T  L  P  S
1303  TGTCACCTCCGCGGCACAACCTGTCAGTGGGGCGGGCATGGTCGCTCCCGCTGTGGCCTCAGTAGCTGGCGCTGGCGGCGGCGGCGGCTACAGCGCCAGCCTGCACAGTGAGCCTCCGGT
       V  T  S  A  A  Q  P  V  S  G  A  G  M  V  A  P  A  V  A  S  V  A  G  A  G  G  G  G  G  Y  S  A  S  L  H  S  E  P  P  V
1423  CTACGCCAACCTCAGCAACTTCAACCCGGGTGCGCTGAGCAGCGGCGGTGGGGCGCCCTCCTATGGCGCGACCGGGCTGGCCTTTCCATCGCAGCCCCAGCAGCAGCAGCAGCCGCCTCA
       Y  A  N  L  S  N  F  N  P  G  A  L  S  S  G  G  G  A  P  S  Y  G  A  T  G  L  A  F  P  S  Q  P  Q  Q  Q  Q  Q  P  P  Q
1543  GCCGCCGCACCACTTGCCCCAACAGATCCCGGTGCAGCACCCGCGGCTGCAGGCGCTGAAGGAAGAGCCGCAGACGGTACCGGAGATGCCGGGAGAGACGCCGCCCTTGTCCCCCATCGA
       P  P  H  H  L  P  Q  Q  I  P  V  Q  H  P  R  L  Q  A  L  K  E  E  P  Q  T  V  P  E  M  P  G  E  T  P  P  L  S  P  I  D
1663  CATGGAGTCTCAGGAGCGGATCAAGGCGGAGAGGAAGCGCATGAGGAACCGCATCGCTGCCTCCAAGTGCCGGAAAAGGAAGCTGGAGCGGATCGCCCGGCTAGAGGAAAAAGTGAAAAC
       M  E  S  Q  E  R  I  K  A  E  R  K  R  M  R  N  R  I  A  A  S  K  C  R  K  R  K  L  E  R  I  A  R  L  E  E  K  V  K  T
1783  CTTGAAAGCGCAAAACTCCGAGCTGGCGTCCACCGCCAACATGCTCAGGGAACAGGTGGCACAGCTTAAACAGAAAGTCATGAACCACGTTAACAGTGGGTGCCAACTCATGCTAACGCA
       L  K  A  Q  N  S  E  L  A  S  T  A  N  M  L  R  E  Q  V  A  Q  L  K  Q  K  V  M  N  H  V  N  S  G  C  Q  L  M  L  T  Q
1903  GCAGTTGCAAACGTTTTGAGGACAGACTGTCAGGGCTGAGGGGCAGTGGAAGAAAAAAATAACAGAGATAAACTTGAGAACTTGACTGGTTGCGACAGAGAAAAAAAAGTGTCCGAGTAC
       Q  L  Q  T  F  *
2023  TGAAGCCAAGGGTACACAAGATGGACTGGGTTGCGACCTGACGGCGCCCCCAATGTGCTGGAGTGGGAAGGACGTGGCGCGCCTGGCTTTGGCGAGGAGCCAGAGAGCAGCGCCTGTTGC
2143  GCACGCTTTGCGAACGGGCTGTGCCGCGACCAGAACGATGGACTTTTCGTTAACATTGACCAAGAACTGCATGGACCTTAACATTCGATCTCATTCAGTATTAAGGGGGGTGGGTGGGGG
2263  CTTACAAACTGCAATAGAGACTGTAGATTGCTTCTGTAGTGCTCCGTAAGAACACAAAGCAGGGAGGGCTGGGAAGGGGAGGGAGGCTTGTGAGTACCAGGCTAGATTGCGGATGAACTC
2383  CCCTGGCCTGCCTCTCTCAACTGTGTATGTACATATATTTTTTTTTAATTTGATGAAAGCTGATTACTGTCTATAATAAACAGCTTCCTGCCTTTGTAAGTTATTTCATGTTTGTTTGTT
2503  TGGGTGTCCTACCCAGTGTTTGTAAATAAGAGATTTGAAGCATTCTGAGTTTACCATTTGTAATAAAGTATATAATTTTTTTATGTTTTGTTTCTGAAAATTTCCAGAAAGGATATTTAA
2623  GAAAACACAATAAACCATTGAGAAGTAGCCCCCAACCTCTCTGCTGCATTATCGATAGATAATGAGAGCTAGGTGAAATGACAGCTGAGTGTCTGTATGCTGGGGTGAGAGCCTGTAGTC
2743  CCTCCCGTCTGGTTGTAGGAATAGACACCCTGCATGCTATCATTGACTCATACTCTCTCCCCAGCAACCCACAAGTCCAGACTGTTGACCAGAAGATGGTGCAGTGTTTCTTAAGGCTGG
2863  AAGAAGAGGGTGTTGCAAGGGGAGAGGGACAGCCCACTGGAAAGCAGACGCTTGAGTTGAGAGCCATATCAAGTAGCATGCGCTGTGATCGTTTATAATAATAATAAAGACTTCAGCAAT
2983  TAGATGTTTATCTCAAAGCAGGGACCCATGGAAGGTTTTACAAAAGGTGTCTCCTTCCAACTTGGATTCTGACGACTCCTAGAAAAAGATGACCTTTGCTTGTGCATATTTATAATAGTT
3103  CGTATCACAATAAATGTATTCAAATAATGGTTTTAAAAATCTTGAATTCCTTTTCCGTTGCTAATCTTTGTTTCCTAAGCCGCACACTGAAGATTTTCCAAGTTTCTGGGGGAATTAGTG
3223  CATTCTACACTTTGCAATTTAGAAGCCAAGCATTTAGGAAGAGTCAAAGGAGGATCTGGAACCTGGGTGACTCTTCTCCCAACCCTCTCCCAATTCCCACTTGGACCCTCCCCATCCCCC
3343  CACCTCTCGCTCCTACCAAGGAAGTGACCAGTGTAGTGAGTCCTTATTTATTTTTTAATTTGTTTCAAAATAATCAATCTGGCTTAATTATTGAGGTAGTCTGGGAAGTTCCTAGTATAT
3463  ATACTATGGAGCGGAGTCACAAGAGAAATGACTATATAGCACATCTGTGATCCAAACCTCAGCTCCGGGGAGACGGAAAACCTGAATCGTGTCTCAGATACAGCTGAGGTTATCAACAGG
3583  TTTGTATTCAACGAGGGAATCATTTTTGCCTGCTCCCTTCTCATCCCCATGAGCTGCTGTGATTATCAAGCAGCAACAGCAATTGATATCCAGAAACACTTTCAGAAACCACTAATTGAA
3703  GCCTGGCTGTTAACTCATTAGCACTGCTCCAATGTTCAACGGGTCTGGGAGTGCCTGTGGTAGTAAATCCAAACACACAATTCCTCAGGAGTACACCTAGGTCTGCAGGGCCTCTCAGAG
3823  GCCTTTCAGACATCCCATAGAAGGCAGTCACTTGGCCTGGCCTCTTTAAGGCCCACTCTGGCTACAGGAAGGCAAATGTTGATAGGTCATCATCTTACTCTCAAGGAACTCACTCTGGAG
3943  AGAGGGCACAGGAAAGGAAAGAGAGACTATTCTATGAGGCGCATGGTATAAGCAAGTGATGCCAAGTGGAGAGGAGAAGCCATTATAAAGATTTCACCGAAGTGACATTTGAACCAACCC
4063  AGGCACAGACATGTAGATTTGAAGCAGGAAAGCACCATGTGATGGGGGTAGGGGTTGGGATCTTTTTGAAGAGGCCGAATTC  4144
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