Promoter structure of the human intestinal alkaline phosphatase gene

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Human alkaline phosphatases (ALPs) are oncodevelopmentally regulated enzymes that display different degrees of tissue-specificity. In order to understand the regulation, tissue-specific expression and tumor re-expression of ALP isozymes the cloning of these genes was undertaken. A full length placental alkaline phosphatase (PLAP) cDNA (1) was used to identify and clone the PLAP-like (Millán, J.L. *et al.*, to be published) and intestinal ALP genes from a human genomic library constructed in λ Charon 28 (2). In this report, the nucleotide sequence of the 5' end of the intestinal ALP gene is presented. The deduced amino acid sequence of the first three exons corresponds exactly to the sequence derived from two independently cloned intestinal ALP cDNAs (3, 4). The promoter region contains a TATA and a CAAT Box as well as a consensus sequence for the binding of Sp1 transcription factor. Arrows indicate unique direct repeats. Transfection experiments aimed at defining the exact sequences responsible for the tissue-specific expression of this gene are in progress.

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CAGCTGATCTCCGAACCAATTCTCATCTGCAACCTTGAAGCTGTGCTCCCTCTTAACTCCAACCTAACCCCTAACCCCAACCCATTGCTCTCTCCCTCAAGTCTCAGGAACC 120
TCCATTCATTCTGTCTCTATGATTGATCTCCCTCGGACCTCAGAGAAGTGTGTTGCTGCGATGTTGTGCTTTTGCACTGGTATATTTCACTGAGCATTGGTATATTTCACTGAGC 240
ATTAATGTCTTAAGGTTTCATCATGTTGTAGCAGGTGTGAGGTCGCTTTGTTTTCAAGGCTGCGTGATACCTCATGTTATGTGTGACCCCTGTTGGTTTCTCCATTCTCTTTGCT 360
GGACACTTGGTAGCTTCATCTCTTGCTGCTGTGATAATGCTGCTGGGAACAGTGGGTGTGAGTTATCTGTTGCACTCCCTAGTTCGCATTCTTTGGCTACACACTCAGAAGTGG 480
GATGCTGGAAGTGAAGCAATATTTGAAGTCAAGCTGAGGTTACCAAACTCTCTGAACCTCTTATCAGAGGCTACACTTCTGGGTGTTCCCGGGGGCCCATGGAAACAGACTCACCCCA 600
TGGCTCCATCTACCTGTGCAAGGGAACAGGGGTCAACCTCAAGTGCACAGGCTGCTCTGGAAGACCCAGCCAGGCTGTTGTTACCCAGAGCAGTGGCCCCCTTCCCACTGCTCTCAGG 720
ACATAGGTGTGGGACCCATATACACCAAGTGGGTTTAGGGGACGACGCCACCCAGTGTGCTCTCTTACACTCTCTTGGGGCTGTGACATTACGAACCCCTAACCCGGGCTGTC 840
CTAGGCTGTGTGTTTCCAGCTCTCCCTCTTCAACCTTGAATGAGGTGAATGAAGGAGTGGCAACGCTCTCCCAAGACACTGTGAGGACCAACCCAGTCCCTTCCCTTCAGCAAGC 960
                                     Sp1          CAAT Box          TATA Box
TTGGCTTCAGGTCACAGGACTGGGCGGGTCAAGATGGACACACAGGGGTGTTGGGGAGGACGTGGAGCATTACAGCCAGGGGCAACAGTCTCCCTGATTAAACCCAGGCGCTG 1080
                                     Exon I
CGCTCGAGCGGTTCTGGTGTCCCACTTGCCTCCCTCTGCTGCCCCAAGACATGCAGGGGCCCCGGGTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCTGGGCGTCACTC 1200
                                     MetGlnGlyProTrpValLeuLeuLeuGlyLeuArgLeuGlnLeuSerLeuGlyValIleP
CAGGTAATGAGGCTCCCCAAGCTGTTCCACACACAGGGGACCCCTCAGCCAGGCTGACCTGATCTCTACTCTCCCTCGGCCACTGAGGAGGAGAACCCGGGCTTCTGGAACCCGCA 1320
roA                                     1aGluGluGluAsnProAlaPheTrpAsnArgGln
GCAGCTGAGGCCCCGATGCTGCCAAGAAGTGCAGCCCATCCAGAAGTGCAGCAAGCTCATCTCTCTCTGGGCGATGGTGAGTGAGCAAGGCTGTCCAGGCCCCGTAGTCTCTAC 1440
Ala1aGluAlaLeuAspAla1aLysLysLeuGlnProIleGlnLysValAlaLysAsnLeuIleLeuPheLeuGlyAsp
AGCTCCGCAACCCGGGACCTTCAGTGTTCCAGGACAACCTTGGGGCCAGGACTCACACATTTCTGCTCTTCAGGGTTGGGGGTGCCACGGTGACAGCCACCGAGATCTTAAGGGG 1560
                                     1yLeuGlyValProThrValThrAlaThrArgIleLeuLysGly
CAGAAGATGGCAACTGGGGCTGAGACGCCCTGGCCATGGACCGCTTCCCATACCTGGCTCTGCTCAAGGTAAGGGCTGGGCACCTCAGAGTCTCTCAAGCAGAGGAGAGGGATCAA 1680
GlnLysAsnGlyLysLeuGlyProGluThrProLeuAlaMetAspArgPheProTyrLeuAlaLeuSerLys
GGATATGGAGTGGCAGGAGGGGAGGACCGAGGACAGCTG 1721

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