Nucleotide sequence of human prostatic acid phosphatase determined from a full-length cDNA clone

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Submitted July 11, 1990 EMBL accession no. X53605

In this report we present the complete nucleotide sequence of the human prostatic acid phosphatase cDNA isolated from a human prostate cDNA library. A lambda gt11 human prostate cDNA library was screened using oligonucleotide probes synthesized from the known N-terminal protein sequence of PAP (Lin *et al.*, 1983) and/or using an anti-PAP monoclonal antibody (Patel *et al.*, 1986). The complete nucleotide sequence of one of our cDNA clones, PAP1−1B, is shown below. Our sequence differs from those published by Vihko *et al.* (1988) and Sherief *et al.* (1989) at several bases. There were 13 nucleotide substitutions in our clone, out of these 6 occurred in the coding region, three of which resulted in an amino acid change. At nucleotide 232, Trp to Arg and at 506 Pro to Arg, resulted in changes from aromatic amino acids to basic amino acids. At nucleotide 670, Ala to Pro resulted in a change from a neutral amino acid to an aromatic amino acid. The advantage of our clone from the other published clones is that it is a full-length clone. The sequence contains a complete open reading frame that can encode a polypeptide of 342 amino acid residues with a calculated M.W. of 50,000 DA. At present we are trying to express this cDNA in various cell lines.

ACKNOWLEDGEMENT

Supported in part by a grant from the Medical Research Council of Canada.

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   1  GCTCCTAACTCCTGGCCAGAAACAGCTCTCCTCAACATGAGAGCTGCACCCCTCCTCCTGGCCAGGGCAG   70
  71  CAAGCTTAGCCTTTGCTTCTTGTTTCTGCTTTTTTTGCTGGCTAGACCGAAGTGTACTAGCCAAGGAGTT  140
 141  GAAGTTTGTGACTTTGGTGTTTCGGCATGGACACCGAAGTCCCATTGACACCTTTCCCACTGACCCCATA  210
 211  AAGGAATCCTCATGGCCACAAAGGATTTGGCCAACTCACCCAGCTGGCATGGAGCAGCATTATGAACTTG  280
 281  GAGAGTATATAAGAAAGAGATATAGAAAATTCTTGAATGAGTCCTATAAACATGAACAGGTTTATATTCG  350
 351  AAGCACAGACGTTGACCGGACTTTGATGAGTGCTATGACAAACCTGGCAGCCCTGTTTCCCCCAGAAGGT  420
 421  GTCAGCATCTGGAATCCTATCCTACTCTGGGAGCCCATCCCGGTGCACACAGTTCCTCTTTCTGAAGATC  490
 491  AGTTGCTATACCTGCGTTTCAGGAACTGCCCTCGTTTTCAAGAACTTGAGAGTGAGACTTTGAAATCAGA  560
 561  GGAATTCCAGAAGAGGCTGCACCCTTATAAGGATTTTATAGCTACCTTGGGAAAACTTTCAGGATTACAT  630
 631  GGCCAGGACCTTTTTGGAATTTGGAGTAAAGTCTACGACCCTTTATATTGTGAGAGTGTTCACAATTTCA  700
 701  CTTTACCCTCCTGGGCCACTGAGGACACCATGACTAAGTTGAGAGAATTGTCAGAATTGTCCCTCCTGTC  770
 771  CCTCTATGGAATTCACAAGCAGAAAGAGAAATCTAGGCTCCAAGGGGGTGTCCTGGTCAATGAAATCCTC  840
 841  AATCACATGAAGAGAGCAACTCAGATACCAAGCTACAAAAAACTCATCATGTATTCTGCGCATGACACTA  910
 911  CTGTGAGTGGCCTACAGATGGCGCTAGATGTTTACAACGGACTCCTTCCTCCCTATGCTTCTTGCCACTT  980
 981  GACGGAATTGTACTTTGAGAAGGGGGAGTACTTTGTGGAGATGTACTACCGGAATGAGACGCAGCACGAG 1050
1051  CCGTATCCCCTCATGCTACCTGGATGCAGCCCCAGCTGTCCTCTGGAGAGGTTTGCTGAGCTGGTTGGCC 1120
1121  CTGTGATCCCTCAAGACTGGTCCACGGAGTGTATGACCACAAACAGCCATCAAGGTACTGAGAACAGTAC 1190
1191  AGATTAGTGTGCACAGAGATCTCTGTAGAAGGAGTAGCTGCCCTTTCTCAGGGCAGATGATGCTTTGAGA 1260
1261  ACGTACTTTGGCCATTACCCCCCAGCTTTGAGGAAAATGGGCTTTGGATGATTATTTTATGTTTTAGGGA 1330
1331  CCCCCAACCTCAGGCAATTCCTACCTCTTCACCTGACCCTGCCCCCACTTGCCATAAAACTTAGCTAAGT 1400
1401  TTTGTTTTGTTTTTCAGCGTTAATGTAAAGGGGCAGCAGTGCCAAAATATAATCAGAGATAAAGCTTAGG 1470
1471  TCAAAGTTCATAGAGTTCCCATGAACTATATGACTGGCCACACAGGATCTTTTGTATTTAAGGATTCTGA 1540
1541  GATTTTGCTTGAGCAGGATTAGACAAGCCTGTTCTTTAAATTGCTGAAATGGAACAGATTTCAAAAAAAA 1610
1611  CGCCCACAATCTAGGGTGGGAACAAGGAAGGAAAGATGTGAATAGGCTGATGGGCAAAAAACCAATTTAC 1680
1681  CCATCAGTTCCAGCCTTCTCTCAAGGAGAGGCAAAGAAAGGAGATACAGTGGAGACATCTGGAAAGTTTT 1750
1751  CTCCACTGGAAAACTGCTACTATCTGTTTTTATATTTCTGTTAAAATATATGAGGCTACAGAACTAAAAA 1820
1821  TTAAAACCTCTTGGTGTCCCTTGGTCCTGGAACATTTATGTTCCTTTTAAAGAAACAAAAATCAAACTTT 1890
1891  ACAGAAAGATTTGATGTATGTAATACATATAGCAGCTCTTGAAGTATATATATCATAGCAAATAAGTCAT 1960
1961  CTGATGAGAACAAGCTATTTGGGCACAACACATCAGGAAAGAGAGCACCACGTGATGGAGTTTCTCCAGA 2030
2031  AGCTCCAGTGATAAGAAGTGTTGACTCTAAAGTTGATTTAAGGGCAGGCATGGTGGTTTACGCCTATAAT 2100
2101  CCCAGCATTTTGGGAGTCCGAGGTGGGCAGATCACTTGAGCTCAGGAGGTCAAGATCAGCCTGGGCAACA 2170
2171  TGGTGAAACCTTGGCTCTACATAAAATACAAAAACTTAGATGGGCATGGTGGTGTGTGCCTATAGTCCAC 2240
2241  TACTTGTGGGGCTAAGGCAGGAGGATCACTTGAGCCCCGGAGGTCGAGGCTACAGTGAGCCAAGAGTGCA 2310
2311  CTACTGTACTCCAGCCAGGGCAAGAGAGCGAGACCCTGTCTCAATAAATAAATAAATAAATAAATAAATA 2380
2381  AATAAATAAATAAAAAAAAAAA 2403
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