

**5' nucleotide sequence of a putative human placental alkaline phosphatase-like gene**L.-P. Shen, H. Liu, Y. W. Kan<sup>1</sup> and W. KamDepartment of Medicine and <sup>1</sup>Howard Hughes Medical Institute, University of California, San Francisco CA, USA

Submitted May 9, 1988

Accession no. X07247

The multigene family of human alkaline phosphatase (EC 3.1.3.1) is a good model to study tumor-associated (re)expression including the placental alkaline phosphatase (PLAP, Regan), PLAP-like (Nagao), intestinal alkaline phosphatase (IAP) and IAP-like (Kasahara) forms (1). A form of these putative PLAP or IAP-like genes was isolated by using a 1.9 kb PLAP cDNA KpnI fragment (2) to screen the EMBL3 lambda human genomic library kindly provided by Dr. J. Nathans (3). Based on the 5' sequence presented here with closer homology to the PLAP gene than to the IAP gene (4) we propose this as a PLAP-like gene. Arrows above the sequence indicate unique repeats. The TATA box and Spl binding sites are well-conserved. The putative PLAP-like mRNA was found in human placental tissue by Northern analysis (unpublished data).

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CACAGTGAGCAGGGTTGGGGAGGCCCTCGGCGGAGATGCACA→CTCGACTATACCCAAAATCCACCCTTCCT 72
GGGACACCTGGTCCCACCC→TAAAGCTGCCTTTCTCAGACCCCAGCCCCAGCCAGCCAGCCACACCCCTGCCA 144
CTCCCTTCAGCCAGTGGCTTCAGGTCAAGAGGCTGGGCGGGTCAAGGTGGTAAACAAGGGGAGGGGCCAG 216
GACACAGTTTCCCTGATTTAAACCAGGCAGCCTGGAGTGCAGCTCATACTCCATACCTGGGATTTCCGCC 288
TCGCGCTCTCCGACTGCTTCCAGAC ATG CAG GGG CCC TGG GTG CTG CTC CTG CTG GGC 347
                                     Exon 1 M Q G P W V L L L L G
CTG AGG CTA CAG CTC TCC CTG GGC ATC ATC CCA G]GTAATGAGGCTCCCCAGCTGGCCCT 407
L R L Q L S L G I I P
ACACACACACACACAGGGCACC→CCCCAGCCAGGCTGACCTGATCTTTGCTCTCCCCCTGGCCAG 476
2]TT GAG GAG GAG AAC CCG GAC TTC TGG AAC CGC CAG GCA GCC GAG GCC CTG GGT 529
V E E E N C D F W N R Q A A E A L G
GCC GCC AAG AAG CTG CAG CCT GCA CAG ACA GCC GCC AAG AAC CTC ATC ATC TTC 583
A A K K L Q P A Q T A A K N L I I F
CTG GGT GAC G]GTGAGTGAGCCAGGCCCTCCAGCCCGCAGCCCTGACAGCCCGGGCCCGGACCCTC 651
L G D                                     3
AGTGGTTCCAGGACAGCCCTGGGGAGCAAGCCTCACACACTTCTGCTCCTTACG [GG ATG GGG GTG 716
                                     G M G V
TCT ACG GTG ACA GCT GCC AGG ATC CTA AAA GGG CAG AAG AAG GAC AAA CTG GGG 770
S T V T A A R I L K G Q K K D K L G
CCT GAG ACC TTC CTG GCC ATG GAC CGC TTC CCG TAC GTG GCT CTG TCC AAG]GTAA 825
P E T F L A M D R F P Y V A L S K
GTGCTGGGCTACCTTTAGAGTCTCCAAGCAGAGAAGGGGAATCTGGCTATGGAGTGTGGTAGGAGGGAGGGA 897
CCCTAAACAGCTGGGGCTCCAATAAGGAGCTGGAGGCAGTTGGAATCCCAGAGGACAGAGATCAGGGTCTTG 969
TTTGTCTGCCCCAGAGAAGAGCTCAGAGTGTCTCTGTCCCAG]ACA TAC AGT GTA GAC AAG CAT 1032
                                     4 T Y N V D K H
GTG CCA GAC AGT GGA GCC ACA GCC ACG GCC TAC CTG TGC GGG GTC AAG GGC AAC 1086
V P D S G A T A T A Y L C G V K G N
TTC CAG ACC ATT GGC TTG AGT GCA GCC CGC TTT AAC CAG TGC AAC ACG ACA 1140
F Q T I G L S A A A R F N Q C N T T
CGC GGC AAC GAG GTC ATC TCC GTG ATG AAT CGG GCC AAG AAA 1182
R G N E V I S V M N R A K K

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**Acknowledgements:** LP S is a visiting scientist from the Shanghai Institute of Biochemistry, LH is a Cheng Scholar. Supported in part by NIH grant DK16666. We thank S.P. Cai for her technical assistance.

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