

Cloning of cDNA encoding human placental protein 12 (PP12): binding protein for IGF I and somatomedin

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By N-terminal sequence comparison it was shown that the placental protein 12 (PP12)(1) is homologous to the IGF I (insulin-like growth factor) and somatomedin binding protein (2-4). Starting with an antibody raised against PP12 we have screened cDNA libraries from human placenta. Two cDNA clones were identified with an open reading frame encoding a hydrophobic leader peptide consisting of 25 aa and the mature protein of 234 aa (MW 25 270). The MW and the amino acids composition are in good agreement to the data of Bohn and Kraus. The protein sequence shows no N-linked glycosylation site. The cDNA encodes 18 Cys-residues, which may explain the wide discrepancy in the reported MW of the PP12 protein (25 200 to 34 000). The N-terminal protein sequence is identical to the sequence of Baxter et al., but different in residues 11 and 12 to Koistinen et al. . The 5' nontranslated region of PP12 cDNA extends 150 nt. The stop codon at position 928 is followed by 566 nt of untranslated region including the poly(A) addition site AATAAA 18 nt upstream of poly(A). The size of PP12 cDNA (1511 nt) agrees with a band of 1600 nt in northern blot analysis (not shown).

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10           30           50           70           90           110
CCCATCAGCGAGCATCTGCGCCGCGCCGCCACCTCCAGAGAGACTGGCCACCGCTCCACCATCACTTGCCAGAGTTGGGCCACCGCCGCCACCCAGGCCAGAGAGCA
130          150          170          190          210          230
TCGGCCCTGTCTGCTGCTCGCGCTGGAGATGTCAAGGTCCTCGCTCGCGCTGGCTGGTACTGCTCTGCTGACTGTCCAGGTCGGCGTGACAGCCGCGCTCCGGGGCAGTGC
M S E V P V A R V W L V L L L L L T V Q V G V T A G A P W Q C
-1 +1

250          270          290          310          330          350
GCGCCCTGCTCCGCCGAGAAGCTCGCGCTCGCCGCGCGTGTCCGCCCTGCTGCTCGGAGGTACCCGGTCCGGCTGCGGCTGCGGCTGTGGCCGATGTGCGCCCTGCCCTCTGGGCGCCG
A P C S A E K L A L C P F V S A S C S E V T R S A G G C C P M C A L P L G A A

370          390          410          430          450          470
TGGCGCTGGCGACTGACAGCTGCGCCCGGGGACTCAGTTGCGCCGCGCTCGCGGGGAGCAGCAACTCTGCACGCCCTCCCGCGGCCAAGGCGCCCTGGCTGCGAGGATCTGACGCC
C G V A T A R C A R G L S C R A L F G E Q Q P L H A L T R G Q G A C V Q E S D A

490          510          530          550          570          590
TCCGCTCCCGTCTGCGAGGACGAGCCCTGAAAGCCAGAGAGCAGCGAGATAAAGTGAAGGAGGCTCCTGGATAATTTCCATCTGATGGCCCTTCTGAAGAGGATCATTCCATC
S A P H A A E A G S P E S P E S T E I T E E E L L D N F H L M A P S E E D H S I

610          630          650          670          690          710
CTTTGGAGCCCATCAGTACCTATGATGGCTGCAAGGCTTCCATGTCAACACATCAAAAAATGGAAGGAGCCCTGCCGAATAGACTCTACAGAGTCGTAGAGAGTTTAGCCAAAGCA
L W D A I S T Y D G S K A L H V T N I K K W K E P C R I E L Y R V V E S L A K A

730          750          770          790          810          830
CAGGAGCATCAGGAGAAGAAATTTCAAAATTTTCCCTGCAAACTGCAACAAGAAATGGATTTTATCACAGCAGACAGTGTGAGACATCCATGGATGGAGAGCGGACCTGTCTGGTGC
Q E T S G E E I S R F Y L F N C N R N G F Y H S R Q C E T S M D G E A G L C W C

850          870          890          910          930          950
GTCTACCCCTTGAATGGGAAGAGGATCCCTGGGTCTCCAGAGATCAGGGGAGACCCCAACTGCCAGATATATTTAAATGTACAAAACGAAACCAGATGAAATATGTTCTGTCACTGTA
V Y P W N G K R I P G S P E I R G D P N C Q I Y F N V Q N

970          990          1010          1030          1050          1070
AATATTAGTATATAGTATATTTATACTCTAGAATGCACATTATATATATATATATATATATATATATATATATATATATATAGTAAGTACTTTTTTACTCCATACATAACTTGTATAGAAAGCTG
1090          1110          1130          1150          1170          1190
TTTATTATTCACGTAAAGTTTATTTTCTACAGTAAAAACTTGTAATGTAATAACTTGTCTATGTCAATTTGTATATCATGAAACACTTCTCATATATGTATGTAAGTAA
1210          1230          1250          1270          1290          1310
TTGCATTTCTGCTTCCAAAGCTCTCCGCTCTGTTTTAAAGAGCATGGAAAAAATCTGCTAGAAAATGCAAAATGAAATGAGAGAGAGTATTTTTTCAGCTAGTTTGAGGAGGAGC
1330          1350          1370          1390          1410          1430
GTAACTGTATATCCACCATTCACATTTGATGTACATGTGTAGGGAAGTTAAAGTGTGATTACATAATCAAAGTACTCTGGTGTATGTGGCCACTGTGTTAAATGACACTGTA
1450          1470          1490          1510
TATGTTGTTAAACAGCTGTCTATAATGAAAACATTTCATAAATAATTTCTGCATGGAAAAA
    
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