Sequence of a cDNA coding for bovine pancreatic phospholipase A₂

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Submitted March 11, 1987

Accession no. Y00120

Phospholipase A₂ (PLA₂) from pancreas has the following interesting features. The enzyme preferably acts on aggregated phospholipid micell-like structures, requires Ca⁺⁺ for its activity, and is produced as a zymogen (1). To elucidate the relationship between these features and the structure of this enzyme, the gene encoding it and the expression system will be a useful tool. We have isolated a cDNA coding for bovine pancreatic PLA₂ from a pancreatic cDNA library. The cDNA encodes a 130 amino acids proPLA₂ with a 15 amino acids signal polypeptide. The deduced proPLA₂ amino acid sequence is consistent with the previously reported one except for the 122th Asn replaced with Lys, and the first residue pyroglutamic acid is encoded as Gln(-7th) by the cDNA (2,3). The sequence of the signal polypeptide is similar to that of other PLA₂ (4,5).

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      -22      -20      -10      -7
      M R L L V L A L L T V G A G Q A G L N S
ACCAACCTGACAAAGG ATG AGA CTC CTG GTG TTG GCT GCT CTG CTC ACA GTG GGC GCT GGC CAG GCC GGC CTC AAC TCG
-1  1      10      20      30      40      50
R A L W Q F N G M I K C K I P S S E P L L D F N N Y
AGG GCA TTA TGG CAG TTC AAC GGC ATG ATT AAG TGC AAG ATC CCC AGC AGT GAA CCA TTG CTG GAT TTC AAC AAC TAT
      60      70      80      90      100
G C Y C G L G G S G T P Y D D L D R C C Q T H D N C
GGC TGC TAT TGT GGC CTG GGT GGA TCA GGG ACC CCT GTG GAT GAT CTG GAC AGG TGC TGC CAG ACG CAC GAC AAC TGC
      110      120      130
Y K Q A K K L D S C K V L V D N P Y T N N Y S Y S C
TAC AAA CAA GCC AAG AAA CTG GAC AGC TGT AAA GTC CTC GTG GAC AAT CCC TAC ACC AAC AAC TAC TCC TAC TCA TGT
      140      150      160      170      180
S N N E I T C S S E N N A C E A F I C N C D R N A A
TCT AAC AAT GAG ATC ACC TGC AGC AGC GAA AAC AAT GCC TGT GAG GCC TTC ATC TGC AAC TGT GAC GGC AAT GCC GCC
      190      200      210      220      230
I C F S K V P Y N K E H K N L D K K K C
ATC TGC TTC TCA AAG GTG CCA TAC AAC AAG GAG CAC AAG AAC CTG GAC AAG AAG AAA TGC ATG ATCTGAGTATCTCTTGGG
AAATTAGGATTCCTTTGGGCCCATGGCTTTGACCTTATACCATGTCTTCCAATAAAGCACCCATTGAAG (546)

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Acknowledgment

We are grateful to Dr. M. Ikehara for his helpful advices.

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