cDNA sequence of rabbit lipoprotein-associated coagulation inhibitor

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Plasma contains a lipoprotein-associated coagulation inhibitor (LACI) that inhibits activated factor X (Xa) directly, and inhibits VIIa/TF activity in a Xa-dependent fashion (1). cDNA sequence for human LACI has been previously reported (2, 3). Here we report the cDNA sequence for rabbit LACI. Deduced amino acid sequence shows that similar to human LACI, rabbit LACI contains a cluster of negatively charged amino acid residues at its NH₂-terminus followed by three tandem Kunitz-type protease inhibitory domains and a cluster of positively charged residues near its COOH-terminus. The three sites of possible N-linked glycosylation are located in identical positions in both rabbit and human LACI. The sequences of the polypeptide regions linking the Kunitz domains in rabbit LACI diverge considerably from

those in human LACI, suggesting that these regions may be involved in the species specificity of VIIa/TF inhibition by LACI. Of the Kunitz domains the sequence of the second Kunitz domain is the most highly conserved between rabbit and human LACI. Notably, rabbit LACI contains a glutamine at the P-1 residue of the active-site cleft of the third Kunitz domain instead of the arginine found in human LACI.

REFERENCES

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2. Wun, T.-C. *et al.* (1988) *J. Biol. Chem.* 263, 6001-6004.
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-90  ACCTGGAAGGGAAGACAAAACAGCCTCAACTCCGTTTGA AAAAATCTTTCCAAGACCTTTCTTCAGAGATTTTACTCAGTTGATCTACA
1   ATGAAGAAAGAACACATCTTTTGGACGCTCTATATGCGTCTGCTTGGTCTTGTCCCTGCCCTGTTAGCTCAGCGGCCGAGGAAGATGAA
   M K K E H I F W T S I C L L L G L V P A P V S S A A E E D E
91  GAATTCACAAACATTACAGATATTAACCGCCACTACAGAAGCCGACACACTCATTGTGCAATGAAGGTAGATGATGGGCCGTGCAGA
   E F T N I T D I K P P L Q K P T H S F C A M K V D D G P C R
181 GCATACATCAAGAGATTTTTTTTCAATATTCTCGCCCATCAGTGTGAAGAATTATATATGGAGGATGTAAGGGAACGAGAATCGATTG
   A Y I K R F F F N I L A H Q C E E F I Y G G C E G N E N R F
271  GAGAGTCTGGAAGAATGCAAGAAAAATGTGCACGAGATTATCAAAGATGACTACAAAGCTGACATTTCAAAAAGGAAAGCCTGATTTG
   E S L E E C K E K C A R D Y P K M T T K L T F Q K G K P D F
361  TGCTTTTGGGAAGAAGATCCTGGTATTTGTGCGAGGTTATATTACCAGATATTTTATAACAATCAATCAAAACATGTGAACGTTTCAAG
   C F L E E D P G I C R G Y I T R Y F Y N N Q S K Q C E R F K
451  TACGGTGGGTGCTTGGCAATCTAAACAACCTTGTAGTCATTGGAAGAATGCAAAAACACCTGTGAGAATCCAACGAGTGATTTCCAGGTG
   Y G G C L G N L N N F E S L E E C K N T C E N P T S D F Q V
541  GATGACCATAGAACCCAGCTCAATACTGTGAATAACACTTTAATTAACCGCCGACCAAGGCTCCAGACGTTGGGCATTTCAGGGCCCC
   D D H R T Q L N T V N N T L I N Q P T K A P R R W A F H G P
631  TACTGGTGTCTGCCCCAGCAGAACGAGGATTGTGTCAAGCCAATGAGATCAGATTCTTCTACAATGCAATCATCGGGAAATGCCGCCCA
   Y W C L P P A E R G L C Q A N E I R F F Y N A I I G K C R P
721  TTTAAGTACAGTGGATGTGGGGGAAATGAAAATAATTTCACTTCCAAAAAGCATGTATCACAGCTTGTA AAAAAGGTTTCATCCCGAAA
   F K Y S G C G G N E N N F T S K K A C I T A C K K G F I P K
811  TCTATCAAAGGAGGACTAATTAACCAAAAGGAAGAAAAAGAAGCAGCCAGTGAAAAATACTTATGTAGAACTTTTGTAAAAAGACA
   S I K G G L I K T K R K K K K Q P V K I T Y V E T F V K K T
901  TAAGTTTGTGTAATAGAAAAATTAATTCTACTAATCATTTTCTTTGAGTATTTCACTCTGATTATCTTG
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