

Nucleotide sequence of the bovine bactericidal permeability increasing protein (BPI)

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BPI is a bactericidal protein originally found in human neutrophils (1). It is speculated that BPI is a member of a gene family of lipopolysaccharide binding proteins (LBP). A clone for bovine BPI has been isolated by screening a bovine bone marrow cDNA library with human BPI probes and by PCR of random primed first strand cDNA using a 5′ human and 3′ bovine BPI primer. A 1745 bp clone was isolated from the library but was 150 bp short at the 5′ end. The missing sequence was obtained by PCR and the complete sequence derived from analyzing 6 clones is presented below. The cDNA encodes a protein with a putative 26 amino acid signal peptide followed by a 456-residue mature protein. Analysis of the sequence flanking the ATG initiator codon at base 6 (**GACATGG**) suggests the sequence is an efficient ribosome binding site. There is moderate conservation of both the nucleotide (75%) and amino acid (63%) sequences between bovine and human BPI. The proposed site where elastase cleaves the holoprotein into the 25kD fragment is conserved. Further evidence that BPI and LBP are members of a gene family is exemplified by bovine BPIs' primary sequence identity with rabbit (42%) and human (45%) LBP. The mature proteins of bovine BPI and rabbit LBP start with the same amino acids TNPG.

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REFERENCES

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2. Kozak,M. (1986) *Cell* **44**, 283–292.
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                                                                    1
  1 AAGACATGGC CAGAGGCCCT GACACCGCGC GGAGGTGGGC AACCCTGGTG GTGCTGGCCG CCCTGGGCAC GGCTGTGACG ACTACCAACC CTGGCATTGT GGCCAGGATC ACCCAGAAGG
-26      M  A  R  G  P  D  T  A  R  R  W  A  T  L  V  V  L  A  A  L  G  T  A  V  T  T  T  N  P  G  I  V  A  R  I  T  Q  K  G

121 GCCTGGACTA CGCCTGCCAG CAGGGAGTGC TTACTCTGCA GAAGGAGTTG GAGAAGATAA CAATTCCCAA TTTCTCAGGA AACTTTAAGA TAAAGTACCT CGGGAAAGGG CAATACAGCT
 14  L  D  Y  A  C  Q  Q  G  V  L  T  L  Q  K  E  L  E  K  I  T  I  P  N  F  S  G  N  F  K  I  K  Y  L  G  K  G  Q  Y  S  F

241 TCTTCAGCAT GGTTATTCAA GGATTCAATC TTCCCAATTC CCAGATAAGA CCGTTGCCAG ATAAGGGCCT TGATCTCTCT ATCAGAGATG CCAGTATCAA GATCAGAGGA AAATGGAAGG
 54  F  S  M  V  I  Q  G  F  N  L  P  N  S  Q  I  R  P  L  P  D  K  G  L  D  L  S  I  R  D  A  S  I  K  I  R  G  K  W  K  A

361 CACGAAAGAA TTTCATCAAA CTCGGTGGCA ACTTTGACCT GAGTGTGGAG GGCATCTCTA TTTTGGCGGG TCTGAATCTG GGCTATGATC CTGCCTCGGG CCACTCCACT GTTACCTGCT
 94  R  K  N  F  I  K  L  G  G  N  F  D  L  S  V  E  G  I  S  I  L  A  G  L  N  L  G  Y  D  P  A  S  G  H  S  T  V  T  C  S

481 CCAGCTGCAG CAGTGGCATC AACACCGTCC GCATACACAT CTCTGGCAGC AGCCTGGGGT GGCTGATCCA ACTCTTCCGC AAACGAATCG AGTCTTTGCT CCAAAAGTCC ATGACCAGAA
134  S  C  S  S  G  I  N  T  V  R  I  H  I  S  G  S  S  L  G  W  L  I  Q  L  F  R  K  R  I  E  S  L  L  Q  K  S  M  T  R  K

601 AGATCTGCGA GGTGGTGACT AGTACCGTGT CCTCCAAGCT GCAGCCTTAT TTCCAGACGC TGCCAGTGAC AACCAAACTA GACAAAGTGG CTGGGGTCGA TTACTCACTG GTGGCACCTC
174  I  C  E  V  V  T  S  T  V  S  S  K  L  Q  P  Y  F  Q  T  L  P  V  T  T  K  L  D  K  V  A  G  V  D  Y  S  L  V  A  P  P

721 CAAGAGCCAC AGCCAATAAC CTGGATTGGC TGCTGAAGGG GGAGTTTTTC AGTCTGGCCC ACCGCAGCCC CCCGCCCTTT GCCCCGCCAG CGCTGGCCTT TCCCTCAGAC CACGATCGCA
214  R  A  T  A  N  N  L  D  W  L  L  K  G  E  F  F  S  L  A  H  R  S  P  P  P  F  A  P  P  A  L  A  F  P  S  D  H  D  R  M

841 TGGTGTACCT GGGCATCTCT GAGTATTTTT TCAACACGGC CGGGTTCGTG TATCAGAAGG CTGGAGCCCT GAATCTGACC CTCAGAGACG ACATGATTCC AAAGGAATCC AAGTTCCGCC
254  V  Y  L  G  I  S  E  Y  F  F  N  T  A  G  F  V  Y  Q  K  A  G  A  L  N  L  T  L  R  D  D  M  I  P  K  E  S  K  F  R  L

961 TGACAACCAA ATTCTTTGGA ATCCTGATAC CCCAGGTGGC CAAGATGTTC CCTGACATGC AGATGCAGCT CTTCATCTGG GCCTCTTTGC CTCCGAAACT CACCATGAAG CCCAGCAGCC
294  T  T  K  F  F  G  I  L  I  P  Q  V  A  K  M  F  P  D  M  Q  M  Q  L  F  I  W  A  S  L  P  P  K  L  T  M  K  P  S  S  L

1081 TTGACCTCAT CTTTGTCCTG GACACCCAGG CCTTTGCCAT CCTCCCAAAC TCCTCCTTGG ACCCCCTCTT CCTGCTTGAG ATGAACTTGA ACCTTTCTGT GGTTGTTGGT GCCAAGTCCG
334  D  L  I  F  V  L  D  T  Q  A  F  A  I  L  P  N  S  S  L  D  P  L  F  L  L  E  M  N  L  N  L  S  V  V  V  G  A  K  S  D

1201 ACAGACTTAT TGGAGAGCTC AGATTGGACA AGCTGCTCCT GGAACTGAAG CACTCAGACA TCGGCCCCTT CTCGGTTGAG TCGCTGCAGT CTGTCATCAA CTACGTTATG CCCACCATCG
374  R  L  I  G  E  L  R  L  D  K  L  L  L  E  L  K  H  S  D  I  G  P  F  S  V  E  S  L  Q  S  V  I  N  Y  V  M  P  T  I  V

1321 TGCTTCCCGT GATTAACAAG AAGCTACAGA AAGGCTTCCC TCTCCCGCTG CCCGCCTACA TCGAGCTCTT CAACCTGACC CTTCAGCCTT ACCAGGATTT CCTGCTGTTC GGTGCAGATG
414  L  P  V  I  N  K  K  L  Q  K  G  F  P  L  P  L  P  A  Y  I  E  L  F  N  L  T  L  Q  P  Y  Q  D  F  L  L  F  G  A  D  V

1441 TCCAGTACAG CTGAAGACCC CATGGGTGCC GGGGGCGTCA ATCAGGAGGT GCAGGGTTGT CAGCACCCGT TCCTGACACA CCCCTGGGCA CAGGCTGCCC CCTCTCTAGG CTTCCCTCTC
454  Q  Y  S  O

1561 TAGCTCAGGA CTCAGAGACT CTTGCAAACT TCTCTGAACT CAGATTCAGA AATGATCCAA ACATGAAACT TGGTCTTTTG GAAAACTGAG AGGTGTGTAT TTTAGGAATT GTTTCTTCCA

1681 AGGGCTAAGG CTGCAGGGAC ATTTCCTCCA AGAATTGCAT TTCAATGGTA ATCACAATAT TTCTCTTTGT GCTTCATACT ACATTAAAAA AAAAAAAAAC ACCTTTTTTT TTTCTTTGAA

1801 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAA
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Figure 1. Nucleotide sequence and numbered translation of bovine BPI. Elastase cleavage site is underlined.

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