
The nucleotide sequence for the cDNA of bovine interleukin-1 alpha

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The bovine interleukin-1 alpha cDNA was obtained by screening a bovine macrophage cDNA library under low stringency with a murine IL-1 alpha cDNA probe (1). The cDNA encodes a precursor protein of 268 amino acids which exhibits 73% similarity with murine IL-1 alpha and 82% similarity with human IL-1 alpha (2). The presumed cleavage between the signal and mature sequences is marked with an arrow. The mature protein encoded by this cDNA has been expressed in *E. coli* and exhibits authentic IL-1 activity.

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1      Met Ala Lys Val Pro Asp Leu Phe Glu Asp Leu
1      1 TGTGCTAGCTCGGTTTCAGCAAAGAAGTGAAG      ATG GCC AAA GTC CCT GAC CTC TTT GAA GAC CTG

12 Lys Asn Cys Tyr Ser Glu Asn Glu Asp Tyr Ser Ser Glu Ile Asp His Leu Ser Leu Asn
66 AAG AAC TGT TAC AGT GAA AAT GAA GAC TAC AGT TCT TCT GAA ATT GAC CAC CTC TCT CTC AAT

32 Gln Lys Ser Phe Tyr Asp Ala Ser Tyr Glu Pro Leu Arg Glu Asp Gln Met Asn Lys Phe
126 CAG AAG TCC TTC TAT GAT GCA AGC TAT GAG CCA CTT CGT GAG GAC CAG ATG AAT AAG TTT

52 Met Ser Leu Asp Thr Ser Glu Thr Ser Lys Thr Ser Lys Leu Ser Phe Lys Glu Asn Val
186 ATG TCC CTG GAT ACC TCG GAA ACC TCT AAG ACA TCC AAG CTT AGC TTC AAG GAG AAT GTG

72 Val Met Val Ala Ala Ser Gly Lys Ile Leu Lys Lys Arg Arg Leu Ser Leu Asn Gln Phe
246 GTG ATG GTG GCA GCC AGT GGG AAG ATT CTG AAG AAG AGA CGG TTG AGT TTA AAT CAG TTC

92 Ile Thr Asp Asp Asp Leu Glu Ala Ile Ala Asn Asn Thr Glu Glu Glu Ile Ile Lys Pro
306 ATC ACC GAT GAT GAC CTG GAA GCC ATT GCC AAT AAT ACA GAA GAA GAA ATC AAG CCC

112 Arg Ser Ala His Tyr Ser Phe Gln Ser Asn Val Lys Tyr Asn Phe Met Arg Val Ile His
366 AGA TCA GCA CAT TAC AGC TTC CAG AGT AAC GTG AAA TAC AAC TTT ATG AGA GTC ATC CAC

132 Gln Glu Cys Ile Leu Asn Asp Ala Leu Asn Gln Ser Ile Ile Arg Asp Met Ser Gly Pro
426 CAG GAA TGC ATC CTG AAC GAC GCC CTC AAT CAA AGT ATA ATT CGA GAT ATG TCA GGT CCA

152 Tyr Leu Thr Ala Thr Thr Leu Asn Asn Leu Glu Glu Ala Val Lys Phe Asp Met Val Ala
486 TAC CTG ACG GCT ACT ACA TTA AAT AAT CTG GAG GAG GCA GTG AAA TTT GAC ATG GTT GCT

172 Tyr Val Ser Glu Glu Asp Ser Gln Leu Pro Val Thr Leu Arg Ile Ser Lys Thr Gln Leu
546 TAT GTA TCA GAA GAG GAT TCT CAG CTT CCT GTG ACT CTA AGA ATC TCA AAA ACT CAA CTG

192 Phe Val Ser Ala Gln Asn Glu Asp Glu Pro Val Leu Leu Lys Glu Met Pro Glu Thr Pro
606 TTT GTG AGT GCT CAA AAT GAA GAC GAA CCC GTG TTT CTA AAG GAG ATG CCT GAG ACA CCC

212 Lys Ile Ile Lys Asp Glu Thr Asn Leu Leu Phe Phe Trp Glu Lys His Gly Ser Met Asp
666 AAA ATC ATC AAA GAT GAG ACC AAC CTC CTC TTC TTC TGG GAA AAG CAT GGC TCT ATG GAC

232 Tyr Phe Lys Ser Val Ala His Pro Lys Leu Phe Ile Ala Thr Lys Gln Glu Lys Leu Val
726 TAC TTC AAA TCA GTT GCC CAT CCA AAG TTG TTT ATT GCC ACA AAG CAA GAA AAA TTG GTG

252 His Met Ala Ser Gly Pro Pro Ser Ile Thr Asp Phe Gln Ile Leu Glu Lys
786 CAC ATG GCA AGT GGG CCG CCC TCG ATC ACT GAC TTT CAG ATA TTG GAA AAA TAG CCTGAC

847 TGTGCACTCTACTTACTTGTAAAGTGGTGACCATCCGTATGTACTATGTACATGAAGGAGTCGAGCCCTTACTGTTAG
926 TCACTCGCTGAGCATGTGCTGAGCTTTTGTAAATTCCTAAATGAATGTTTACTCTCTTTGTGAAGAGAGAACAACAAGTCCA
1005 --poly-A tail
  
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REFERENCES

(1) Lomedico, P. T. et al. (1984) *Nature* 312, 458. (2) March, C. J. et al. (1985) *Nature* 315, 641.