

# Porcine IL-1 alpha cDNA nucleotide sequence

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A porcine alveolar macrophage cDNA library in λgt10 was screened by cross-species hybridization using a bovine IL-1 $\alpha$  cDNA probe (1). The porcine IL-1 $\alpha$  cDNA encodes a protein of 270 amino acids with a predicted molecular weight of 30,788. The amino acid sequence exhibits 90%, 82% and 75% similarity with bovine, human and murine IL-1 $\alpha$ , respectively. A protein with IL-1 activity was secreted by COS-7 cells transfected with the porcine IL-1 $\alpha$  cDNA (data not shown).

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## REFERENCE

- Maliszewski,C.R. et al. (1988) *Molec. Immunol.* **25**, 429.

TTTGTGCTCCAGCCAGCACAGAAGTGAAGATGGCAAAGTCCCTGACCTCTTGAAGACCTGAAGAACTGCTACAGTAAAATGAAGAAATACAGTTCTGATAATCGACCATCTC	114
M A K V P D L F E D L K N C Y S E N E E Y S S D I D H L	28
TCTCTGAATCAGAAGTCCCTCATGATGCCAGCTATGAGCCACTTCCTGGGGACGGCATGGATAAAATTATGCCCTTGAGTACCTCTAAACCTCTAAGACATCCAGGCTAAC	228
S L N Q K S F Y D A S Y E P L P G D G M D K F M P L S T S K T S R L N	66
TTCAGGGACAGTGTGGTGAATGGCAGCAGCCAAAGGGAAAGATTCTGAAGAAGAGACGGTTGAGTTAAATCAGTTCATCACCGATGACGACCTGGAAAGCCATTGCCAATGACACA	342
F K D S V V M A A A N G K I L K K R R L S L N Q F I T D D D D L E A I A N D T	104
GAAGAAGAAATCATCAAGCCCAGATCAGCAACATACAGCTTCCAGAGCAACATGAAATACAACCTCATGAGGGTCATCAACCACCGATGCACTCTGAATGATGCCGCAATCAA	456
E E E I I K P R S A T Y S F Q S N M K Y N F M R V I N H Q C I L N D A R N Q	142
AGCATCATTGAGACCCGTCAGGTCAATACCTCATGGCTGCTGTGCTAAATAACCTGGATGAGGAGTGAATTTCACATGGCTGCCTATACATCAATGATGATTCGCAACTT	570
S I I R D P S G Q Y L M A A V L N N L D E A V K F D M A A Y T S N D D S Q L	180
CCTGTGACTCTAAGAATCTCAGAAACCGACTGTTGTGAGTGCTAAACAGAAGACGAACCCGTTGCTGAAGGAGCTGCCCTGAGACACCCAAAACCATCAAAGATGAGACC	684
P V T L R I S E T R L F V S A Q N E D E P V L L K E L P E T P K T I K D E T	218
AGTCTCTCTTCTGGAAAAGCATGGCAATATGGACTACTTCAAATCAGCCGCCATCCAAGTTGTTATTCGCAAGGCAGGAAAAACTGGTGCACATGGCACCGGGG	798
S L L F F W E K H G N M D Y F K S A A H P K L F I A T R Q E K L V H M A P G	256
CTGCCCTCTGCACTGACTTTCAAGATACTGGAAAACCAGTCCTGACTCTGGTGCTACTTACCTGTGAAGTGTGACAGGCCGTATGTACATGTACATGAAGGAGTTAATCT	912
L P S V T D F Q I L E N Q S 270	
TTCACTCTTAGTCACTCGCTGAGCATGTGCTGAGC 947 .....PolyA	