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Nucleotide sequence of the cDNA from the mouse leukocyte adhesion protein CD18

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We screened a mouse thymus cDNA library with a nucleotide probe derived from the human CD18 full-length cDNA sequence (1,2). Four unique clones were isolated; the longest was characterized further, and the sequence is presented here. Clone 17.4 consisted of 2856 bp, containing a 2313 bp open reading frame beginning with ATG at bp 82 and ending with TAG at bp 2394. The murine nucleotide sequence shows 81% overall identity to the human CD18 sequence over the coding region. The only conserved sequence outside the coding region was a 62 bp sequence in the 3'-untranslated region (bp 2650-2711) which shows 87% identity to the human sequence (bp 2652-2713) and contains the 8*mer* TTATTTAT which has been reported to be a possible regulatory consensus sequence conserved in the 3'-untranslated region of human and mouse inflammatory protein mRNAs (3). The open reading frame translates to a predicted 770 amino acid product (one residue longer than the human homologue) which is 82% identical to the predicted human amino acid sequence. The predicted mouse protein shows 100% conservation of the 56 cysteine residues in the mature human protein.

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1     CGAGGCCCCT GGCAAGAAGT AGGCAAAGAC ATCTCCAGTC AGATTCTCGG AGTGGAGGCT TCCTGGGACT GAGAGGGGGA CATGCTGGGC CCACACTCAC
101   TGCTGCTTGC CCTAGCTGGA CTGTTCTTCC TGGGATCTGC TGTGTCCCAG GAATGCACCA AGTACAAAGT CAGCAGTTGC CGGGACTGTA TCCAGTCGGG
201   GCCTGGCTGT TCCTGGTGCC AGAAGCTGAA CTTCACTGGA CCAGGAGAAC CTGACTCCTT GCGCTGTGAC ACACGGGCAC AGCTGCTGCT GAAGGGTTGT
301   CCAGCCGATG ATATCATGGA CCCCAGGAGC ATCGCTAATC CTGAGTTCGA CCAACGGGGG CAACGGAAAC AGCTATCTCC ACAAAAAGTG ACACTTTACT
401   TGCGACCAGG ACAGGCTGCC GCATTCAATG TGACTTTCCG GCGGGCCAAG GGATACCCCA TTGATCTGTA CTACCTCATG GATCTCTCCT ACTCCATGCT
501   TGATGACCTC AACAACGTCA AGAAGCTGGG CGGGGACTTG CTGCAGGCCC TCAACGAGAT CACCGAGTCT GGCCGCATCG GCTTTGGGTC GTTTGTGGAC
601   AAGACGGTGC TGCCTTTTGT TAACACCCAT CCTGAGAAGC TGAGGAACCC ATGTCCCAAC AAGGAGAAGG CCTGCCAGCC CCCATTTGCC TTTCGGCACG
701   TGCTCAAGTT AACCGACAAC TCCAACCAGT TTCAGACAGA GGTCGGCAAG CAACTGATTT CCGGAAACCT GGACGCCCCT GAGGGTGGGC TGGATGCCAT
801   AATGCAAGTT GCTGCATGTC CGGAGGAAAT TGGCTGGCGC AATGTCACGA GGCTGCTGGT GTTTGCCACA GACGATGGCT TCCACTTTGC TGGTGATGGC
901   AAACTGGGTG CCATCCTGAC CCCCAATGAT GGCCGCTGCC ACCTGGAGGA TAACATGTAC AAGAGGAGCA ATGAGTTCGA CTACCCATCC GTGGGTCAGC
1001  TGGCACACAA ACTTTCCGAG AGCAACATCC AGCCCATCTT TGCGGTGACA AAGAAGATGG TGAAAACGTA TGAGAAACTC ACGGAGATCA TCCCCAAGTC
1101  AGCAGTGGGG GAACTGTCTG ACGACTCCAG CAACGTGGTG CAGCTCATCA AGAATGCCTA CTATAAACTC TCCTCTAGAG TCTTCCTGGA CCACAGCACC
1201  CTCCCGGACA CCCTGAAAGT CACCTATGAC TCCTTCTGCA GTAATGGAGC ATCGAGTATA GGCAAATCCC GTGGGGACTG TGATGGCGTA CAGATCAACA
1301  ACCCGGTCAC CTTCCAGGTA AAGGTCATGG CTTCCGAGTG TATCCAGGAG CAGTCCTTTG TCATCCGGGC ACTGGGTTTC ACTGATACAG TGACCGTGCA
1401  GGTCCGTCCC CAGTGTGAGT GTCAGTGCCG GGACCAGAGT CGGGAGCAGA GTCTCTGTGG AGGCAAGGGA GTCATGGAGT GTGGTATCTG CAGGTGTGAG
1501  TCTGGCTACA TTGGGAAAAA CTGTGAGTGC CAGACTCAGG GTCGGAGCAG CCAGGAGCTG GAGAGAAACT GTCGGAAGGA CAATAGTTCC ATCGTGTGCT
1601  CAGGGCTTGG GGACTGCATC TGTGGGCAGT GTGTATGCCA TACCAGTGAC GTCCCCAACA AAGAGATCTT TGGGCAATAC TGCGAGTGTG ACAATGTCAA
1701  CTGTGAGAGA TATAACAGCC AAGTCTGCGG TGGCTCAGAT CGGGGTTCCT GCAACTGTGG CAAATGTAGT TGCAAGCCCG GTTACGAGGG CTCGGCCTGC
1801  CAGTGTCAGA GGTCCACCAC GGGCTGTCTG AATGCACGGC TGGTAGAGTG CAGTGGCCGT GGCCACTGCC AATGCAACAG GTGCATATGT GACGAAGGCT
1901  ACCAGCCACC GATGTGTGAG GATTGTCCCA GCTGTGGCTC GCACTGCAGG GACAACCACA CCTCTTGTGC CGAGTGCCTG AAGTTTGATA AGGGCCCTTT
2001  TGAGAAGAAC TGTAGTGTTC AGTGTGCTGG TATGACGCTG CAGACTATCC CTTTGAAGAA AAAGCCCTGC AAGGAGAGGG ACTCGGAAGG CTGTTGGATA
2101  ACTTACACTT TGCAGCAGAA GGACGGAAGG AACATTTACA ACATCCATGT GGAGGACAGT CTAGAGTGTG TGAAGGGCCC CAATGTGGCT GCCATCGTAG
2201  GGGGCACCGT GGTAGGTGTC GTACTGATTG GTGTCCTCCT CCTGGTCATC TGGAAGGCCC TGACCCACCT GACTGACCTC AGGGAGTACA GGCGCTTTGA
2301  GAAGGAGAAA CTCAAGTCCC AATGGAACAA TGACAACCCC CTCTTCAAGA GTGCTACGAC AACGGTCATG AACCCCAAGT TTGCTGAAAG CTAGAGCATG
2401  AGTTATCATA ATCAAGCAGA TGTGACCCCC TCAGACCACG CCTCCTCCCC TCTGCAAACA CAACGTGGCT TACAGCTCAC CCCAGTGCTG CCAAGGATCC
2501  AAAAGCCTGC TCGGTTTCTT TCCGCCATTA TATCAAGTCT GCCAGGGTTT CCAGGGACTT GTCTTCCGAC CTGCACAATC TTGCCGCAGA GCCCTAAGAA
2601  TTGTCCCGAG TCCCAAGAGG TTCCACCCAC ATTTTCTTGC ATAAAGGAAG ACAGCAGTCT CAGTAAAGGT GGCCCCAACT TATTTATATT TAAACTTGTC
2701  AGAGTATAAA ACTCCTATTA TATTGTTAAC ATCCCATCTG TTGTATTATA TGTGAGTATA AAAACTATAT CCAACGTATT ATTTCATAAT CATGTATGAA
2801  AAATAATAAA GCTTCCATCC ATGCTGTCAA AAAAAAAAAA AAAAAAAAAA AAAAAA
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