Volume 16 Number 9 1988 Nucleic Acids Research

Nucleotide sequence of the gene encoding the monocyte differentiation antigen, CD14

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Submitted February 11, 1988 Accession no.X06882

We report here the nucleotide sequence of the gene encoding the monocyte cell surface differentiation antigen CD14. CD14 is expressed by monocytes, macrophages and activated granulocytes (1,2). A cDNA clone encoding CD14 was isolated from a cDNA expression library (3), sequenced and used to isolate the CD14 gene from a genomic phage library. The initiation codon is flanked by a sequence which shows homology to the consensus sequence C(C)ACCATGG for a translation initiation site defined by Kozak (4) and is separated from the rest of the coding region by an 88bp intron. The cDNA polyadenylation signal (ATTAAA) is overlined.

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CAGAATGACATCCCAGGATTACATAAACTGTCAGAGGCAGCCGAAGAGTTCACAAGTGTGAAGCCTGGAAGCCGGCGGGTGCCGCTGTGTAGGAAAGAA
GCTAAAGCACTTCCAGAGCCTGTCCGGAGCTCAGAGGTTCGGAAGACTTATCGACCATGGTGAGTGTAGGGTCTTGGGGTCGAACGCGTGCCACTCGGG
                                                  Met
                                                  -19
AGCCACAGGGGTTGGATGGGGCCTCCTAGACCTCTGCTCTCTCCCCAGGAGCGCGCGTCCTGCTTGTTGCTGCTGCTGCTGCCGCTGGTGCACGTCTCT
                                              GluArgAlaSerCysLeuLeuLeuLeuLeuProLeuValHisValSer
                                              -18                 -10
GCGACCACGCCAGAACCTTGTGAGCTGGACGATGAAGATTTCCGCTGCGTCTGCAACTTCTCCGAACCTCAGCCCGACTGGTCCGAAGCCTTCCAGTGT
AlaThrThrProGluProCysGluLeuAspAspGluAspPheArgCysValCysAsnPheSerGluProGlnProAspTrpSerGluAlaPheGlnCys
 -1 +1                  10                  20                  30
GTGTCTGCAGTAGAGGTGGAGATCCATGCCGGCGGTCTCAACCTAGAGCCGTTTCTAAAGCGCGTCGATGCGGACGCCGACCCGCGGCAGTATGCTGAC
ValSerAlaValGluValGluIleHisAlaGlyGlyLeuAsnLeuGluProPheLeuLysArgValAspAlaAspAlaAspProArgGlnTyrAlaAsp
                    40                  50                  60
ACGGTCAAGGCTCTCCGCGTGCGGCGGCTCACAGTGGGAGCCGCACAGGTTCCTGCTCAGCTACTGGTAGGCGCCCTGCGTGTGCTAGCGTACTCCCGC
ThrValLysAlaLeuArgValArgArgLeuThrValGlyAlaAlaGlnLeuLeuValGlyAlaLeuArgValLeuAlaTyrSerArg
            70                  80                  90
CTCAAGGAACTGACGCTCGAGGACCTAAAGATAACCGGCACCATGCCTCCGCTGCCTCTGGAAGCCACAGGACTTGCACTTTCCAGCTTGCGCCTACGC
LeuLysGluLeuThrLeuGluAspLeuLysIleThrGlyThrMetProProLeuProLeuGluAlaThrGlyLeuAlaLeuSerSerLeuArgLeuArg
   100                 110                 120                 130
AACGTGTCGTGGGCGACAGGGCGTTCTTGGCTCGCCGAGCTGCAGCAGTGGCTCAAGCCAGGCCTCAAGGTACTGAGCATTGCCCAAGCACACTCGCCT
AsnValSerTrpAlaThrGlyArgSerTrpLeuAlaGluLeuGlnGlnTrpLeuLysProGlyLeuLysValLeuSerIleAlaGlnAlaHisSerPro
                140                 150                 160
GCCTTTTCCTACGAACAGGTTCGCGCCTTCCCGGCCCTTACCAGCCTAGACCTGTCTGACAATCCTGGACTGGGCGAACGCGGACTGATGGCGGCTCTC
AlaPheSerTyrGluGlnValArgAlaPheProAlaLeuThrSerLeuAspLeuSerAspAsnProGlyLeuGlyGluArgGlyLeuMetAlaAlaLeu
            170                 180                 190
TGTCCCCACAAGTTCCCGGCCATCCAGAATCTAGCGCTGCGCAACACAGGAATGGAGACGCCCACAGGCGTGTGCGCCGCACTGGCGGCGGCAGGTGTG
CysProHisLysPheProAlaIleGlnAsnLeuAlaLeuArgAsnThrGlyMetGluThrProThrGlyValCysAlaAlaLeuAlaAlaAlaGlyVal
      200                 210                 220                 230
CAGCCCCACAGCCTAGACCTCAGCCACAACTCGCTGCGCGCCACCGTAAACCCTAGCGCTCCGAGATGCATGTGGTCCAGCGCCCTGAACTCCCTCAAT
GlnProHisSerLeuAspLeuSerHisAsnSerLeuArgAlaThrValAsnProSerAlaProArgCysMetTrpSerSerAlaLeuAsnSerLeuAsn
                240                 250                 260
CTGTCGTTCGCTGGGCTGGAACAGGTGCCTAAAGGACTGCCAGCCAAGCTCAGAGTGCTCGATCTCAGCTGCAACAGACTGAACAGGGCGCCGCAGCCT
LeuSerPheAlaGlyLeuGluGlnValProLysGlyLeuProAlaLysLeuArgValLeuAspLeuSerCysAsnArgLeuAsnArgAlaProGlnPro
            270                 280                 290
GACGAGCTGCCCGAGGTGGATAACCTGACACTGGACGGGAATCCCTTCCTGGTCCCTGGAACTGCCCTCCCCCACGAGGGCTCAATGAACTCCGGCGTG
AspGluLeuProGluValAspAsnLeuThrLeuAspGlyAsnProPheLeuValProGlyThrAlaLeuProHisGluGlySerMetAsnSerGlyVal
      300                 310                 320
GTCCCAGCCTGTGCACGTTCGACCCTGTCGGTGGGGGTGTCGGGAACCCTGGTGCTGCTCCAAGGGGCCCGGGGCTTTGCCTAAGATCCAAGACAGAAT
ValProAlaCysAlaArgSerThrLeuSerValGlyValSerGlyThrLeuValLeuLeuGlnGlyAlaArgGlyPheAla·
330                 340                 350
AATGAATGGACTCAAACTGCCTTGGCTTCAGGGGAGTCCCGTCAGGACGTTGAGGACTTTTCGACCAATTCAACCCTTTGCCCCACCTTTATTAAAATC
TTAAACAACGGTTCCGTGTCATTCATTTAACAGACCTTTATTGGATGTCTGCTATGTGCTGGGCACAGTACTGGATGGGGAATTC
                                                                                    1570**
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