

Sequence of MyD116 cDNA: a novel myeloid differentiation primary response gene induced by IL6

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cDNA clones of myeloid differentiation primary response (MyD) genes activated in the absence of protein synthesis in M1 myeloblastic leukemia cells induced for terminal differentiation by IL6, have been isolated (1). Here we report the full length nucleotide and deduced amino-acid sequences of MyD116, a novel MyD gene, which exhibits biphasic kinetics of expression, with an early peak (1 hr) and a decline followed by increased levels of steady state mRNA in terminally differentiated M1 cells (1). MyD116 expression was observed also in murine bone-marrow, but not in non-myeloid tissues (1). MyD116 encodes for a 2.5 kb mRNA, having a very short 3' untranslated region with multiple AT₃ motifs (underlined), implicated in mRNA destabilization (2). The MyD116 encoded protein (657aa) harbors 419 almost perfect 38aa long repeats (underlined), each containing a PEST region, characteristic of short lived proteins (3). The

MyD116 protein does not contain protein secretory signals, transmembrane domains or known protein-DNA binding motifs; it contains, however, potential protein kinase phosphorylation sites (position 4, 181), amidation site (position 653), and 19 casein kinase II phosphorylation sites, including 3 in each repeat.

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GCTCTGAGTTTGTGGAGATTACATCGGATATCCCGCGGACCCCGCATCCCTTTGCCGGCCGGGACAGCCTTTGCTACAGCCTGTGAAACATTGCGTCCCGGA 104
GCCCCACGCTGAGGGCGACATGAACCCCTGGCTTCGCGAGCAGTCCGGACCCACGATCGCTTTGGCAACCAGAACCCGGCTTCAGCCCCGGGGTGACGT 208
      M A P S P R P Q H V L H W R D A H N F Y L L S P L M G L
GCAGCCCCCGCCAGACACATGGCCCCGAGCCCAAGACCCAGCATGTCTCTGCATGGAGGGACGCCCAACTTCTATCTCCTGTCCCCACTGATGGGCTTG 312
L S R A W S R L R G P E V P E A W L A K T V T G A D Q I E A A A L L T
CTCAGTCGGGCTGAGCCCGCTGAGGGGCCCAAGTCCAGAGGCGATGGCTGGCAAAACAGTAACAGGAGCAGATCAGATAGAAGCTGGCGCTCTGCTGAC 416
P T P V S Q N L L P H G E T E E S G S P E Q S Q A A Q R L C L V E A
ACCTACCCCTGTCTGTGTAACCTCCTCCCTCATGGGGAGACTGAAGAAGTGGATCTCCTGAACAGAGTCAAGCAGCCAGAGGCTCTGCTTGTGGAAAGCTG 520
E S S P P E T W G L S N V D E Y N A K P G Q D D L R E K E M E R T A G
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K A T L Q P A G L Q G A D K R L G E V V A R E E G V A E P A Y P T S Q
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L E G G F A E N E E D G E T V K T Y Q A S A A S I A P G Y K P S T P
GCTGGAGGGTGGTCCAGATGAAAGAGGATGGAGAAACAGTGAAGACTTACCAAGCTTCTGCTTCCATAGCTCCGGGATACAAACCCAGCACCCTG 832
V P F L G E A E H Q A T E E K G T E N K A D P S N S P S S G S H S R A
TGCCTTTCTGGGGGAGGCAGAACATCAAGCCCGGAAAGAAAGGAACAGAAACAGGCTGACCCCTCCAACCTCTCTTCTCAGGCTCCCACTCCAGAGCC 936
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G G P E T T F V C T G N A F L K A W V Y R P G E D T E E E D N S D S
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Q P Q R C L P G E K T K G R G E E P P L F Q V A F Y L P G E K P E S
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P W A A P K L P L R L Q R R L R L F K A P T R D Q D P E I P L K A R K
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R F A R I A Q A E E K L G P Y L T P D S R A R A W A R L R N P S L
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G G R R G *** 657
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AAAAAA 2295

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