



*AP1M2* (NM\_005498.5) - cDNA - 2026-04-30

GCTTCCGCAG GAAGAAGGAA GCGGCGCCGC CATCGCCTCC CGGCGCTCCC -32  
TCCCCGACTC CTAAGTCCTT CGGCCGCCAC **CATG**TCCGCC TCGGCTGTCT 19  
TCATTCTGGA CGTTAAGGGC AAGCCATTGA TCAGCCGCAA CTACAAGGGC 69  
GATGTGGCCA TGAGCAAGAT TGAGCACTTC ATGCCTTTGC TGGTACAGCG 119  
GGAGGAGGAA GGCGCCCTGG CCCCCTGTCT GAGCCACGGC CAGGTCCACT 169  
TCCTATGGAT CAAACACAGC AACCTCTACT TGGTGGCCAC CACATCGAAG 219  
AATGCCAATG CCTCCCTGGT GTACTCCTTC CTGTATAAGA CAATAGAGGT 269  
ATTCTGCGAA TACTTCAAGG AGCTGGAGGA GGAGAGCATC CGGGACAACT 319  
TTGTCATCGT CTACGAGTTG CTGGACGAGC TCATGGACTT TGGCTTCCCG 369  
CAGACCACCG ACAGCAAGAT CCTGCAGGAG TACATCACTC AGCAGAGCAA 419  
CAAGCTGGAG ACGGGCAAGT CACGGGTGCC ACCCACTGTC ACCAACGCTG 469  
TGTCC TGCGC CTCCGAGGGT ATCAAGTATA AGAAGAACGA GGTCCTCATT 519  
GATGTCATAG AGTCTGTCAA CCTGCTGGTC AATGCCAACG GCAGCGTCCT 569  
TCTGAGCGAA ATCGTCGGTA CCATCAAGCT CAAGGTGTTT CTGTCAGGAA 619  
TGCCAGAGCT GCGGCTGGGC CTCAATGACC GCGTGCTCTT CGAGCTCACT 669  
GGCCGCAGCA AGAACAAATC AGTAGAGCTG GAGGATGTAA AATTCCACCA 719  
GTGCGTGCGG CTCTCTCGCT TTGACAACGA CCGCACCATC TCCTTCATCC 769  
CGCCTGATGG TGACTTTGAG CTCATGTCAT ACCGCCTCAG CACCCAGGTC 819  
AAGCCACTGA TCTGGATTGA GTCTGTCTATT GAGAAGTTCT CCCACAGCCG 869  
CGTGGAGATC ATGGTCAAGG CCAAGGGGCA GTTTAAGAAA CAGTCAGTGG 919  
CCAACGGTGT GGAGATATCT GTGCCTGTAC CCAGCGATGC CGACTCCCCC 969  
AGATTCAAGA CCAGTGTGGG CAGCGCCAAG TATGTGCCGG AGAGAAACGT 1019

CGTGATTTGG AGTATTAAGT CTTTCCCGGG GGGCAAGGAG TACTTGATGC 1069  
GAGCCCACTT TGGCCTCCCC AGTGTGGAAA AGGAAGAGGT GGAGGGCCGG 1119  
CCCCCATCG GGGTCAAGTT TGAGATCCCC TACTTCACCG TCTCTGGGAT 1169  
CCAGGTCCGA TACATGAAGA TCATTGAGAA AAGTGGTTAC CAGGCCCTGC 1219  
CCTGGGTTTCG CTACATCACC CAGAGTGGCG ATTACCAACT TCGTACCAGC 1269  
TAGAAGGGAG AAGAGATGGG GGCTTGAACA CGGGGCTTCC TTACAGCCCC \*47  
GGATGCAGAT TTTAGAGGGA GGCAGGTGC GGGCTGTGTG TGTCTGTGTG \*97  
AGGGCAGGTC CTGGACTTGG CAGTTTCTTG CTCCAGCAC CCGCCCCTTC \*147  
CTCACCTCTT CCTTATTCCA TAGGCTGGGA GAGAACTCT CTCTGCTTCC \*197  
CTCGCCCTTG GAGCTTTCCC CATCCCCCTG ATTTTATATG AAGAAATAGA \*247  
AGAGGGGCTT GAAGTCCTCC TCGCGAGTGC CTTCTTGCAA TTACCTGCCT \*297  
TAGCGGGTGT TGCGGTCCC TCCTTCACAG CCGCTGAGCC CAGAGGTCCC \*347  
GCTGCCCCCT CCTCTGAATT TTAGGATGTC ATTA AAAAGA TGAATCTA

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