



AP1M2 (NM_005498.5) - cDNA + Protein - 2026-04-30

GCTTCCGCAG GAAGAAGGAA GCGGCGCCGC CATCGCCTCC CGGCGCTCCC -32

TCCCCGACTC CTAAGTCCTT CGGCCGCCAC **CATG**TCCGCC TCGGCTGTCT 19

MetSerAla SerAlaValP 7

TCATTCTGGA CGTTAAGGGC AAGCCATTGA TCAGCCGCAA CTACAAGGGC 69

heIleLeuAs pValLysGly LysProLeuI leSerArgAs nTyrLysGly 23

GATGTGGCCA TGAGCAAGAT TGAGCACTTC ATGCCTTTGC TGGTACAGCG 119

AspValAlaM etSerLysIl eGluHisPhe MetProLeuL euValGlnAr 40

GGAGGAGGAA GCGGCCCTGG CCCCCTGCT GAGCCACGGC CAGGTCCACT 169

gGluGluGlu GlyAlaLeuA laProLeuLe uSerHisGly GlnValHisP 57

TCCTATGGAT CAAACACAGC AACCTCTACT TGGTGGCCAC CACATCGAAG 219

heLeuTrpIl eLysHisSer AsnLeuTyrL euValAlaTh rThrSerLys 73

AATGCCAATG CCTCCCTGGT GTACTCCTTC CTGTATAAGA CAATAGAGGT 269

AsnAlaAsnA laSerLeuVa lTyrSerPhe LeuTyrLysT hrIleGluVa 90

ATTCTGCGAA TACTTCAAGG AGCTGGAGGA GGAGAGCATC CGGGACAACT 319

lPheCysGlu TyrPheLysG luLeuGluGl uGluSerIle ArgAspAsnP 107

TTGTCATCGT CTACGAGTTG CTGGACGAGC TCATGGACTT TGGCTTCCCG 369

heValIleVa lTyrGluLeu LeuAspGluL euMetAspPh eGlyPhePro 123

CAGACCACCG ACAGCAAGAT CCTGCAGGAG TACATCACTC AGCAGAGCAA 419

GlnThrThrA spSerLysIl eLeuGlnGlu TyrIleThrG lnGlnSerAs 140

CAAGCTGGAG ACGGGCAAGT CACGGGTGCC ACCCACTGTC ACCAACGCTG 469

nLysLeuGlu ThrGlyLysS erArgValPr oProThrVal ThrAsnAlaV 157

TGTCCTGGCG CTCCGAGGGT ATCAAGTATA AGAAGAACGA GGTCTTCATT 519

alSerTrpAr gSerGluGly IleLysTyrL ysLysAsnGl uValPheIle 173

GATGTCATAG AGTCTGTCAA CCTGCTGGTC AATGCCAACG GCAGCGTCCT 569

AspValIleG luSerValAs nLeuLeuVal AsnAlaAsnG lySerValLe 190

TCTGAGCGAA ATCGTCGGTA CCATCAAGCT CAAGGTGTTT CTGTCAGGAA 619

uLeuSerGlu ileValGlyT hrIleLysLe uLysValPhe LeuSerGlyM 207

TGCCAGAGCT GCGGCTGGGC CTCAATGACC GCGTGCTCTT CGAGCTCACT 669

etProGluLe uArgLeuGly LeuAsnAspA rgValLeuPh eGluLeuThr 223

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GlyArgSerL ysAsnLysSe rValGluLeu GluAspValL ysPheHisGl 240

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nCysValArg LeuSerArgP heAspAsnAs pArgThrIle SerPheIleP 257

CGCCTGATGG TGACTTTGAG CTCATGTCAT ACCGCCTCAG CACCCAGGTC 819

roProAspGl yAspPheGlu LeuMetSerT yrArgLeuSe rThrGlnVal 273

AAGCCACTGA TCTGGATTGA GTCTGTCATT GAGAAGTTCT CCCACAGCCG 869

LysProLeuI leTrpIleGl uSerValIle GluLysPheS erHisSerAr 290

CGTGGAGATC ATGGTCAAGG CCAAGGGGCA GTTTAAGAAA CAGTCAGTGG 919

gValGluIle MetValLysA laLysGlyGl nPheLysLys GlnSerValA 307

CCAACGGTGT GGAGATATCT GTGCCGTGAC CCAGCGATGC CGACTCCCCC 969

laAsnGlyVa lGluIleSer ValProValP roSerAspAl aAspSerPro 323

AGATTCAAGA CCAGTGTGGG CAGCGCCAAG TATGTGCCGG AGAGAAACGT 1019

ArgPheLysT hrSerValGl ySerAlaLys TyrValProG luArgAsnVa 340

CGTGATTTGG AGTATTAAGT CTTTCCCGGG GGGCAAGGAG TACTTGATGC 1069

lValIleTrp SerIleLysS erPheProGl yGlyLysGlu TyrLeuMetA 357

GAGCCCACTT TGGCCTCCCC AGTGTGGAAA AGGAAGAGGT GGAGGGCCGG 1119

rgAlaHisPh eGlyLeuPro SerValGluL ysGluGluVa lGluGlyArg 373

CCCCCATCG GGGTCAAGTT TGAGATCCCC TACTTCACCG TCTCTGGGAT 1169

ProProIleG lyValLysPh eGluIlePro TyrPheThrV alSerGlyIl 390

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eGlnValArg TyrMetLysI leIleGluLy sSerGlyTyr GlnAlaLeuP 407

CCTGGGTTTCG CTACATCACC CAGAGTGGCG ATTACCAACT TCGTACCAGC 1269

roTrpValAr gTyrIleThr GlnSerGlyA spTyrGlnLe uArgThrSer 423

TAGAAGGGAG AAGAGATGGG GGCTTGAACA CGGGGCTTCC TTACAGCCCC *47

Stop

GGATGCAGAT TTTAGAGGGA GGGCAGGTGC GGGCTGTGTG TGTCTGTGTG *97

AGGGCAGGTC CTGGACTTGG CAGTTTCTTG CTCCCAGCAC CCGCCCCTTC *147

CTCACCTCTT CTTATTCCA TAGGCTGGGA GAGAACTCT CTCTGCTTCC *197

CTCGCCCTTG GAGCTTTCCC CATCCCCCTG ATTTTATATG AAGAAATAGA *247

AGAGGGGCTT GAAGTCCTCC TCGCGAGTGC CTTCTTGCAA TTACCTGCCT *297

TAGCGGGTGT TCGGGGTCCC TCCTTCACAG CCGCTGAGCC CAGAGGTCCC *347

GCTGGCCCCT CCTCTGAATT TTAGGATGTC ATTAAAAAGA TGAATCTA

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