



AP1S3 (NM_001039569.2) - cDNA + Protein - 2024-05-18

ATTGTGGGAA GCAGCCATGG TCTAAGCCGG GCGCCTCACC TGTCAGCCGC -83
ACCGGCTCCA GCGCTCGCCT CTCGCCCTCG CTTCTCCAGC GCTCCTTGCT -33
CGCAAGGCGG GGGAGGCGGC GGCCCAGCCA CGATGATACA TTICATATTG 18 F4C
MetIleHi sPheIleLeu 6

CTCTTCAGTC GACAAGGGAA ATTACGGCTA CAGAAATGGT ACATCACTCT 68
LeuPheSerA rgGlnGlyLy sLeuArgLeu GlnLysTrpT yrIleThrLe 23

CCCTGATAAA GAGAGGAAGA AGATCACC CG GGAAATTGTT CAGATTATTC 118 I31I I32I R33W R33Q
uProAspLys GluArgLysL ysIleThrAr gGluIleVal GlnIleIleL 40

TCTCCCGTGG TCACAGGACA AGCAGTTTTG TTGACTGGAA GGAGCTAAAA 168
euSerArgGl yHisArgThr SerSerPheV aLaspTrpLy sGluLeuLys 56

CTTGTTTATA AAAGGTATGC TAGTTTATAT TTTTGCTGTG CAATAGAAAA 218
LeuValTyrL ysArgTyrAl aSerLeuTyr PheCysCysA laIleGluAs 73

TCAGGACAAT GAGCTCITGA CGCTAGAGAT TGTGCATCGT TACGTGGAGC 268 L79V I83T
nGlnAspAsn GluLeuLeuT hrLeuGluIl eValHisArg TyrValGluL 90

TGCTGGACAA ATATTTTGGG AATGTCTGTG AGCTGGATAT TATCTTTAAI 318 N106K
euLeuAspLy sTyrPheGly AsnValCysG luLeuAspIl eIlePheAsn 106

TTTGAAAAGG CTTATTTTCAT CCTGGACGAG TTTATAATAG GTGGGGAAAT 368
 PheGluLysA laTyrPheIl eLeuAspGlu PheIleIleG lyGlyGluIl 123

TCAGGAAACA TCCAAGAAAA TTGCTGTCAA AGCCATTGAA GACTCTGATA 418
 eGlnGluThr SerLysLysI leAlaVally sAlaIleGlu AspSerAspM 140

TGTTACAGGA GACAATGGAA GAATACATGA ACAAGCCTAC ATTTTAACTG *3
 etLeuGlnGl uThrMetGlu GluTyrMeta snLysProTh rPheStop

GAAATCTACT TGAAGACTCC AGCACTACAT GTTATGAAGC TGTAATAAAG *53
 CAACGCCTCC CATCCGGTTT TTTGATGGAG CCTCAGGCAC CATGCCAAAA *103
 ATAATTTAAA GGGATTCTTT GTTAACTAAC AAAGTTAAAG TTGTTTAACA *153
 TATTTATAAT TACTATGTGT CTGTATTATT AAAAAAATT ATGTGTCTGT *203
 GTTATACTGT ATAGGTACTT GTAGCTCTAA ATGTTTAAAG TAACTACCAC *253
 CTAACCCAAC AGACAATATT TGTAATGTAT TAACTCCATG TTATGTTTTT *303
 AAGCTGGTTT AGATACATTA GCTGCAATTT TTTTGCATT TGACACAATA *353
 TTGTAATAAT CCATGATTTT GAATGTAAAG TATATATGAT GTCATTAATA *403
 CTTTTTCTAA ATGTTTAGTT TTCTAAATTG TATAATAATT CAAAATTATG *453
 TTAATAGTGC AGAGTTTATA TGTAATGCTA GACATTTTTT ATACACTTAA *503
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 TCTATGAAC TATATTTTAT TAAGGTTTAT AGAGACCTAG AGATACAGCA *753
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AATCCCAGCA CTTTGGGAGG CCGAGGCAGG TGGATCACTT GAGGTCAGGA *1203
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AGACATATTT AGGGAAAACA GCAAAGCAAG CAGGAGAACA AAGGGAAAAA *2003
TTCACCAATT CCTCAATATA ACCATTGTTC AAAGGAAATA ACTCAGATTA *2053
GCATATAAAA TAATCATTAG GCTTTTACTA TCCAATATTT CTTCAGGTTA *2103
CCATGTAATT ACAATTATGG CATCAGCTTG AAGTTTATCA TGTATGATTG *2153
ACCACTGTGT TTACTTTAGC TAACCTTCAG TTTTGTGGTT TAACTTTTTA *2203
ATGTGTTAGA ATTTTTTCTT TCTTTTTTTC TTTCTTTCTT TCTTTTCTTT *2253
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TATAAACTA CCAAGAGAAA GACAGTAAAT GTTAAATTC TATAAACTT *3353
CCAAAATAAA ATGTTTTAAC ATGTTTTAAT GAGGAA

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