



PSMG2 (NM_020232.5) - cDNA + Protein - 2025-04-03

GCCTTCTTGC TGCCCTCGTT CTTGCCAGGG CCGCGGTTAG TCCCTGCTGG -17
CCACCCCACT GCGACCATGT TCGTTCCTG CGGGGAGTCG GCCCCCGACC 34
MetP heValProCy sGlyGluSer AlaProAspL 12

TTGCCGGCTT CACCCCTCCTA ATGCCAGCAG TATCTGTTGG AAATGTTGGC 84
euAlaGlyPh eThrLeuLeu MetProAlaV alSerValGl yAsnValGly 28

CAGCTTGCAA TGGATCTGAT TATTTCTACA CTGAATATGT CTAAGATTGG 134
GlnLeuAlaM etAspLeuIl eIleSerThr LeuAsnMetS erLysIleGl 45

TTACTTCTAT ACCGATTGTC TTGTGCCAAT GGTGGAAC AATCCATATG 184
yTyrPheTyr ThrAspCysL euValProMe tValGlyAsn AsnProTyrA 62

CGACCACAGA AGGAAATTCA ACAGAACTTA GCATAAATGC TGAAGTGTAT 234
laThrThrGl uGlyAsnSer ThrGluLeuS erIleAsnAl aGluValTyr 78

TCATTGCCTT CAAGAAAGCT GGTGGCTCTA CAGTTAAGAT CCATTTTTAT 284
SerLeuProS erArgLysLe uValAlaLeu GlnLeuArgS erIlePheIl 95

TAAGTATAAA TCAAAGCCAT TCTGTGAAAA ACTGCTTTCC TGGGTGAAAA 334
eLysTyrLys SerLysProP heCysGluLy sLeuLeuSer TrpValLysS 112

GCAGTGGCTG TGCCAGAGTC ATTGTTCTTT CAAGCAGTCA TTCATATCAG 384

erSerGlyCy sAlaArgVal IleValLeuS erSerSerHi sSerTyrGln 128

CGTAATGATC TGCAGCTTCG TAGTACTCCC TTCCGGTACC TACTTACACC 434

ArgAsnAspL euGlnLeuAr gSerThrPro PheArgTyrL euLeuThrPr 145

TTCCATGCAA AAAAGTGTTT AAAATAAAAT AAAGAGCCTT AACTGGGAAG 484

oSerMetGln LysSerValG lnAsnLysIl eLysSerLeu AsnTrpGluG 162

AAATGGAAAA AAGCCGGTGC ATTCCTGAAA TAGATGATTC CGAGTTTTGT 534

luMetGluLy sSerArgCys IleProGluI leAspAspSe rGluPheCys 178

ATCCGCATTC CGGGAGGAGG TATCACAAAA ACACTCTATG ATGAAAGCTG 584

IleArgIleP roGlyGlyGl yIleThrLys ThrLeuTyrA spGluSerCy 195

TTCTAAAGAA ATCCAAATGG CAGTTCCTGCT GAAATTTGTT TCAGAAGGGG 634

sSerLysGlu IleGlnMetA laValLeuLe uLysPheVal SerGluGlyA 212

ACAACATCCC AGATGCATTA GGTCTTGTTG AGTATCTTAA TGAGTGGCTT 684 [N213S](#) [Y223Sfs*2](#) [N225K](#)

spAsnIlePr oAspAlaLeu GlyLeuValG luTyrLeuAs nGluTrpLeu 228

CAGATACTCA AACCACTTAG CGATGACCCC ACAGTATCTG CCTCACGGTG 734

GlnIleLeuL ysProLeuSe rAspAspPro ThrValSerA laSerArgTr 245

GAAAATACCA AGTTCCTGGA GATTACTCTT TGGCAGTGGT CTTCCCCCTG 784

pLysIlePro SerSerTrpA rgLeuLeuPh eGlySerGly LeuProProA 262

CACTTTCTG ATCTAATTC TGTTTTATAC CTTATACCCA AAACACTTAC *39

laLeuPheSt op

TACCAACACA GCTGTAAAC ATTCTATACA AAAAAATTGT ATGATCTGGT *89
ATTAGGAAAT TACTTTCACA GTAAATATCA AAGAAAAAAG ATTAAGGGTC *139
TCTTTGCCAT GCTTTTCATC ATATGCACCA AATGTAAATT TTGTACAATA *189
AAATTTTATT TCCTAAGTAA

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