



PSMB4 (NM_002796.3) - cDNA + Protein - 2026-06-24

GCTACCGTGA CTAAGATGGA AGCGTTTTTG GGGTCGCGGT CCGGACTTTG 35 c.-9G>A MIT

MetG1 uAlaPheLeu GlySerArgS erGlyLeuTr 12

GGCGGGGGGT CCGGCCCCAG GACAGTTTTA CCGCATTCCG TCCACTCCCC 85 G15R p.P16Sfs*45

pAlaGlyGly ProAlaProG lyGlnPheTy rArgIlePro SerThrProA 29

ATTCCTTCAT GGATCCGGCG TCTGCACTTT ACAGAGGTCC AATCACGCGG 135

spSerPheMe tAspProAla SerAlaLeuT yrArgGlyPr oIleThrArg 45

ACCCAGAACC CCATGGTGAC CGGGACCTCA GTCCTCGGCG TTAAGTTCGA 185

ThrGlnAsnP roMetValTh rGlyThrSer ValLeuGlyV alLysPheGl 62

GGGCGGAGTG GTGATTGCCG CAGACATGCT GGGATCCTAC GGCTCCTTGG 235 p.(Leu78Trpfs?31)

uGlyGlyVal ValIleAlaA laAspMetLe uGlySerTyr GlySerLeuA 79

CTCGTTTCCG CAACATCTCT CGCATTATGC GAGTCAACAA CAGTACCATG 285

laArgPheAr gAsnIleSer ArgIleMetA rgValAsnAs nSerThrMet 95

CTGGGTGCCT CTGGCGACTA CGCTGATTTT CAGTATTTGA AGCAAGTTCT 335

LeuGlyAlas erGlyAspTy rAlaAspPhe GlnTyrLeuL ysGlnValLe 112

CGGCCAGATG GTGATTGATG AGGAGCTTCT GGGAGATGGA CACAGCTATA 385

uGlyGlnMet ValIleAspG luGluLeuLe uGlyAspGly HisSerTyrS 129

GTCCTAGAGC TATTCATTCA TGGCTGACCA GGGCCATGTA CAGCCGGCGC 435

erProArgAl aIleHisSer TrpLeuThrA rgAlaMetTy rSerArgArg 145

TCGAAGATGA ACCCTTTGTG GAACACCATG GTCATCGGAG GCTATGCTGA 485 [Y160C](#)

SerLysMetA snProLeuTr pAsnThrMet ValIleGlyG lyTyrAlaAs 162

TGGAGAGAGC TTCTTCGGTT ATGTGGACAT GCTTGGTGTA GCCTATGAAG 535

pGlyGluSer PheLeuGlyT yrValAspMe tLeuGlyVal AlaTyrGluA 179

CCCCCTCGCT GGCCACTGGT TATGGTGCAT ACTTGGCTCA GCCTCTGCTG 585

laProSerLe uAlaThrGly TyrGlyAlaT yrLeuAlaGl nProLeuLeu 195

CGAGAAGTTC TGGAGAAGCA GCCAGTGCTA AGCCAGACCG AGGCCCGCGA 635 [p.D212_V214del](#)

ArgGluValL euGluLysGl nProValLeu SerGlnThrG luAlaArgAs 212

CTTAGTAGAA CGCTGCATGC GAGTGCTGTA CTACCGAGAT GCCCGTTCTT 685 [Y222X](#)

pLeuValGlu ArgCysMetA rgValLeuTy rTyrArgAsp AlaArgSerT 229

ACAACCGGTT TCAAATCGCC ACTGTCACCG AAAAAGGTGT TGAAATAGAG 735

yrAsnArgPh eGlnIleAla ThrValThrG luLysGlyVa lGluIleGlu 245

GGACCATTTGT CTACAGAGAC CAACTGGGAT ATTGCCCACA TGATCAGTGG 785 [P247S](#)

GlyProLeuS erThrGluTh rAsnTrpAsp ileAlaHisM etIleSerGl 262

CTTTGAATGA AATACAGATG CATTATCCAG AACTGAAGTT GCCCTACTTT *40

yPheGluSto p

TAACTTTGAA CTTGGCTAGT TCAAAGATAG ACTCTTCTTT TGTAAGTAA *90 *45delT
ATAAATTCTT CAAAATGC

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