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

```
GCTACCGTGA CTAAGATGGA AGCGTTTTTG GGGTCGCGGT CCGGACTTTG 35    c.-9G>A  M1T
                MetGl uAlaPheLeu GlySerArgS erGlyLeuTr 12

GGCGGGGGGT CCGGCCCCAG GACAGTTTTA CCGCATTCCG TCCACTCCCG 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 CGCTGATTTC CAGTATTTGA AGCAAGTTCT 335
LeuGlyAlaS erGlyAspTy rAlaAspPhe GlnTyrLeuL ysGlnValLe 112

CGGCCAGATG GTGATTGATG AGGAGCTTCT GGGAGATGGA CACAGCTATA 385
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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 TTCCTCGGTT ATGTGGACAT GCTTGGTGTA GCCTATGAAG 535
pGlyGluSer PheLeuGlyT yrValAspMe tLeuGlyVal AlaTyrGluA 179

CCCCTTCGCT 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

GGACCATTGT CTACAGAGAC CAACTGGGAT ATTGCCCACA TGATCAGTGG 785  P247S
GlyProLeuS erThrGluTh rAsnTrpAsp IleAlaHisM etIleSerGl 262

CTTTGAATGA AATACAGATG CATTATCCAG AACTGAAGTT GCCCTACTTT *40
yPheGluSto p
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TAACTTTGAA CTTGGCTAGT TCAAAGATAG ACTCTTCTTT TGTAAAGTAA ***90** *45delT

ATAAATTCTT CAAAATGC

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