



PSMB10 (NM_002801.4) - cDNA + Protein - 2026-05-25

AGACGTGAAG CCTAGCAGAG GACTTTTTAG CTGCTCACTG GCCCCGCTTG -52
TCTGGCCGAC TCATCCGCC GCGACCCCTA ATCCCCTCTG CCTGCCCAA -2
GATGCTGAAG CCAGCCCTGG AGCCCCGAGG GGGCTTCTCC T~~T~~CGAGAACT 49 F14S
MetLeuLys ProAlaLeuG luProArgGl yGlyPheSer PheGluAsnC 17

GCCAAAGAAA TGCATCATTG GAACGCGTCC TCCCGGGGCT CAAGGTCCCT 99
ysGlnArgAs nAlaSerLeu GluArgValL euProGlyLe uLysValPro 33

CACGCACGCA AGACCGGGAC CACCATCGCG GGCCTGGTGT TCCAAGACGG 149
HisAlaArgL ysThrGlyTh rThrIleAla GlyLeuValP heGlnAspGl 50

GGTCATTCTG GGCGCCGATA CGCGAGCCAC TAACGATTCG GTCGTGGCGG 199 D56H
yValIleLeu GlyAlaAspT hrArgAlaTh rAsnAspSer ValValAlaA 67

ACAAGAGCTG CGAGAAGATC CACTTCATCG CCCCCAAAAT C~~T~~ACTGCTGT 249
spLysSerCy sGluLysIle HisPheIleA laProLysIl eTyrCysCys 83

GGGGCTGGAG TAGCCGCGGA CGCCGAGATG ACCACACGGA TGGTGGCGTC 299
GlyAlaGlyV aAlaAlaAs pAlaGluMet ThrThrArgM etValAlaSe 100

CAAGATGGAG CTACACGCGT TATCTACGGG CCGCGAGCCC CGCGTGGCCA 349
rLysMetGlu LeuHisAlaL euSerThrGl yArgGluPro ArgValAlaT 117

CGGTCACTCG CATCCTGCGC CAGACGCTCT TCAGGTACCA GGGCCACGTG 399

hrValThrAr gIleLeuArg GlnThrLeuP heArgTyrGl nGlyHisVal 133

GGTGCATCGC TGATCGTGGG CGGCGTAGAC CTGACTGGAC CGCAGCTCTA 449

GlyAlaSerL euIleValGl yGlyValAsp LeuThrGlyP roGlnLeuTy 150

CGGTGTGCAT CCCCATGGCT CCTACAGCCG TCTGCCCTTC ACAGCCCTGG 499

rGlyValHis ProHisGlyS erTyrSerAr gLeuProPhe ThrAlaLeuG 167

GCTCTGGTCA GGACGCGGCC CTGGCGGTGC TAGAAGACCG GTTCCAGCCG 549 G167D

lySerGlyGl nAspAlaAla LeuAlaValL euGluAspAr gPheGlnPro 183

AACATGACGC TGGAGGCTGC TCAGGGGCTG CTGGTGAAG CCGTCACCGC 599

AsnMetThrL euGluAlaAl aGlnGlyLeu LeuValGluA laValThrAl 200

CGGGATCTTG GGTGACCTGG GCTCCGGGG CAATGTGGAC GCATGTGTGA 649 G201R GA G201R G209R

aGlyIleLeu GlyAspLeuG lySerGlyGl yAsnValAsp AlaCysValI 217

TCACAAAGAC TGGCGCCAAG CTGCTGCGGA CACTGAGCTC ACCCACAGAG 699

leThrLysTh rGlyAlaLys LeuLeuArgT hrLeuSerSe rProThrGlu 233

CCCGTGAAGA GGTCTGGCCG CTACCACTTT GTGCCTGGAA CCACAGCTGT 749

ProValLysA rgSerGlyAr gTyrHisPhe ValProGlyT hrThrAlaVa 250

CCTGACCCAG ACAGTGAAGC CACTAACCTT GGAGCTAGTG GAGGAAACTG 799

lLeuThrGln ThrValLysP roLeuThrLe uGluLeuVal GluGluThrV 267

TGCAGGCTAT GGAGGTGGAG TAAGCTGAGG CTTAGAGCTT GGAACAAGGG *27

alGlnAlaMe tGluValGlu Stop

GGAATAAACC CAGAAAATAC AGTTAAA

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