



PSMB9 (NM_002800.5) - cDNA + Protein - 2024-05-17

AGTGCCCCAG GCGGCGAGGA GAGCGGTGCC TTGCAGGGAT GCTGCGGGCG 12

Me tLeuArgAla 4

GGAGCACCAA CCGGGGACTT ACCCGGGGCG GGAGAAGTCC ACACCGGGAC 62

GlyAlaProT hrGlyAspLe uProArgAla GlyGluValH isThrGlyTh 21

CACCATCATG GCAGTGGAGT TTGACGGGGG CGTTGTGATG GGTTCGTATT 112 V32I

rThrIleMet AlaValGluP heAspGlyGl yValValMet GlySerAspS 38

CCCGAGTGTC TGCAGGCGAG GCGGTGGTGA ACCGAGTGT TGACAAGCTG 162

erArgValSe rAlaGlyGlu AlaValValA snArgValPh eAspLysLeu 54

TCCCCGCTGC ACGAGCGCAT CTACTGTGCA CTCTCTGGTT CAGCTGCTGA 212 R60C

SerProLeuH isGluArgIl eTyrCysAla LeuSerGlyS erAlaAlaAs 71

TGCCCCAAGCC GTGGCCGACA TGGCCGCCTA CCAGCTGGAG CTCCATGGGA 262

pAlaGlnAla ValAlaAspM etAlaAlaTy rGlnLeuGlu LeuHisGlyI 88

TAGAACTGGA GGAACCTCCA CTTGTTTTGG CTGCTGCAAA TGTGGTGAGA 312

leGluLeuGl uGluProPro LeuValLeuA laAlaAlaAs nValValArg 104

AATATCAGCT ATAAATATCG AGAGGACTTG TCTGCACATC TCATGGTAGC 362

AsnIleSerT yrLysTyrAr gGluAspLeu SerAlaHisL euMetValAl 121

TGGCTGGGAC CAACGTGAAG GAGGTCAGGT ATATGGAACC CTGGGAGGAA 412

aGlyTrpAsp GlnArgGluG lyGlyGlnVa lTyrGlyThr LeuGlyGlyM 138

TGCTGACTCG ACAGCCTTTT GCCATTGGTG GCTCCGGCAG CACCTTTATC 462

etLeuThrAr gGlnProPhe AlaIleGlyG lySerGlySe rThrPheIle 154

TATGTTATG TGGATGCAGC ATATAAGCCA GGATGTCTC CCGAGGAGTG 512 [G156D](#) [G165D](#)

TyrGlyTyrV aLaspAlaAl aTyrLysPro GlyMetSerP roGluGluCy 171

CAGGCGCTTC ACCACAGACG CTATTGCTCT GGCCATGAGC CGGGATGGCT 562 [R173C](#)

sArgArgPhe ThrThrAspA laIleAlaLe uAlaMetSer ArgAspGlyS 188

CAAGCGGGGG TGTCATCTAC CTGGTCACTA TTACAGCTGC CGGTGTGGAC 612

erSerGlyGl yValIleTyr LeuValThrI leThrAlaAl aGlyValAsp 204

CATCGAGTCA TCTTGGGCAA TGAAGTCCA AAATTCTATG ATGAGTGAAC *2

HisArgValI leLeuGlyAs nGluLeuPro LysPheTyrA spGluStop

CTTCCCCAGA CTTCTCTTTC TTATTTTGTG ATAAACTCTC TAGGGCCAAA *52

ACCTGGTATG GTCATTGGGA AATGAGTGCT CAGGGAGATG GAGCTTAGGG *102

GAGGTGGGTG CTTCCCTCCT AGATGTCAGC ATACACTCTT TCTTCTTTTG *152

TCCCAGGTCT AAAACATCTT TCCTAGAGAA AACAAAAGGG ACTAAACTAG *202

AAATATAAAG AGCCCTATAC ATGACAGGTG ATCACGTACT GAATGATTTT *252

GAAGTAGTAC AAACAATAAA AATTCTCATT CCGCATCATC ATGCGGTCCA *302

TGATGATGAG GCCGCAA

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