PSMB9 (NM_002800.5) - cDNA + Protein - 2026-05-07

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AGTGCCCCAG GCGGCGAGGA GAGCGGTGCC TTGCAGGGAT GCTGCGGGCG 12
                                         Me tLeuArgAla 4

GGAGCACCAA CCGGGGACTT ACCCCGGGCG GGAGAAGTCC ACACCGGGAC 62
GlyAlaProT hrGlyAspLe uProArgAla GlyGluValH isThrGlyTh 21

CACCATCATG GCAGTGGAGT TTGACGGGGG CGTTGTGATG GGTTCTGATT 112  V32I
rThrIleMet AlaValGluP heAspGlyGl yValValMet GlySerAspS 38

CCCGAGTGTC TGCAGGCGAG GCGGTGGTGA ACCGAGTGTT TGACAAGCTG 162
erArgValSe rAlaGlyGlu AlaValValA snArgValPh eAspLysLeu 54

TCCCCGCTGC ACGAGCGCAT CTACTGTGCA CTCTCTGGTT CAGCTGCTGA 212  R60C
SerProLeuH isGluArgIl eTyrCysAla LeuSerGlyS erAlaAlaAs 71

TGCCCAAGCC 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
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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

TATGGTTATG TGGATGCAGC ATATAAGCCA GGCATGTCTC 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 TGAACTGCCA AAATTCTATG ATGAGTGAAC *2
HisArgValI leLeuGlyAs nGluLeuPro LysPheTyrA spGluStop

CTTCCCCAGA CTTCTCTTTC TTATTTTGTA 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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