PSMB8 (NM_148919.4) - cDNA + Protein - 2026-06-24

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GCTTTCACTT CCTCCTCCGA GAGCGGACAG ATCTCTGGGT GCTGGGCGGT -2
CATGGCGCTA CTAGATGTAT GCGGAGCCCC CCGAGGGCAG CGGCCGGAAT 49    G8R
 MetAlaLeu LeuAspValC ysGlyAlaPr oArgGlyGln ArgProGluS 17

CGGCTCTCCC GGTTGCGGGA AGCGGGCGTC GCTCGGACCC AGGACACTAC 99
erAlaLeuPr oValAlaGly SerGlyArgA rgSerAspPr oGlyHisTyr 33

AGTTTCTCTA TGCGATCTCC AGAGCTCGCT TTACCCCGGG GAATGCAGCC 149   Q49K
SerPheSerM etArgSerPr oGluLeuAla LeuProArgG lyMetGlnPr 50

CACAGAATTC TTCCAGTCCC TGGGTGGGGA CGGAGAAAGG AACGTTCAGA 199   E55*
oThrGluPhe PheGlnSerL euGlyGlyAs pGlyGluArg AsnValGlnI 67

TTGAGATGGC CCATGGCACC ACCACGCTCG CCTTCAAGTT CCAGCATGGA 249   T74S T74I T75M F80L
leGluMetAl aHisGlyThr ThrThrLeuA laPheLysPh eGlnHisGly 83

GTGATTGCAG CAGTGGATTC TCGGGCCTCA GCTGGGTCCT ACATTAGTGC 299   S90F R91W R91P A92T A94P
ValIleAlaA laValAspSe rArgAlaSer AlaGlySerT yrIleSerAl 100

CTTACGGGTG AACAAGGTGA TTGAGATTAA CCCTTACCTG CTTGGCACCA 349   K105Q M117V
aLeuArgVal AsnLysValI leGluIleAs nProTyrLeu LeuGlyThrM 117
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TGTCTGGCTG TGCAGCAGAC TGTCAGTACT GGGAGCGCCT GCTGGCCAAG 399  S118P D123N Q125P R129C c.389delT
etSerGlyCy sAlaAlaAsp CysGlnTyrT rpGluArgLe uLeuAlaLys 133

GAATGCAGGC TGTACTATCT GCGAAATGGA GAACGTATTT CAGTGTCGGC 449  C135X
GluCysArgL euTyrTyrLe uArgAsnGly GluArgIleS erValSerAl 150

AGCCTCCAAG CTGCTGTCCA ACATGATGTG CCAGTACCGG GGCATGGGCC 499
aAlaSerLys LeuLeuSerA snMetMetCy sGlnTyrArg GlyMetGlyL 167

TCTCTATGGG CAGTATGATC TGTGGCTGGG ATAAGAAGGG TCCTGGACTC 549
euSerMetGl ySerMetIle CysGlyTrpA spLysLysGl yProGlyLeu 183

TACTACGTGG ATGAACATGG GACTCGGCTC TCAGGAAATA TGTTCTCCAC 599  Y184* E188K T200A
TyrTyrValA spGluHisGl yThrArgLeu SerGlyAsnM etPheSerTh 200

GGGTAGTGGG AACACTTATG CCTACGGGGT CATGGACAGT GGCTATCGGC 649  G201V G209R G209R_GC
rGlySerGly AsnThrTyrA laTyrGlyVa lMetAspSer GlyTyrArgP 217

CTAATCTTAG CCCTGAAGAG GCCTATGACC TTGGCCGCAG GGCTATTGCT 699
roAsnLeuSe rProGluGlu AlaTyrAspL euGlyArgAr gAlaIleAla 233

TATGCCACTC ACAGAGACAG CTATTCTGGA GGCGTTGTCA ATATGTACCA 749  Y234C A235D G243R
TyrAlaThrH isArgAspSe rTyrSerGly GlyValValA snMetTyrHi 250

CATGAAGGAA GATGGTTGGG TGAAAGTAGA AAGTACAGAT GTCAGTGACC 799
sMetLysGlu AspGlyTrpV alLysValGl uSerThrAsp ValSerAspL 267

TGCTGCACCA GTACCGGGAA GCCAATCAAT AATGGTGGTG GTGGCAGCTG *18  *8G>A
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euLeuHisGl nTyrArgGlu AlaAsnGlnS top

GGCAGGTCTC CTCTGGGAGG TCTTGGCCGA CTCAGGGACC TAAGCCACGT *68  *20G>C
TAAGTCCAAG GAGAAGAAGA GGCCTAGCCT GAGCCAAAGA GAGAGTACGG *118
GCTCAGCAGC CAGAGGAGGC CGGTGAAGTG CATCTTCTGC GTGTTCTCTA *168
TTTGAACAAG CATTTCCCCC AGGGAAGTTT CTGGGTGCCC CACTAAGTAG *218
AATAAAGAAA AACGGTTATA AATA
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