



PSMB8 (NM_148919.4) - cDNA + Protein - 2024-05-19

GCTTCACTT CCTCCTCCGA GAGCGGACAG ATCTCTGGGT GCTGGGCGGT -2

CAT**G**GCGCTA CTAGATGTAT **GC**GAGCCCC CCGAGGGCAG CGGCCGGAAT 49 **G8R**

MetAlaLeu LeuAspValC ysGlyAlaPr oArgGlyGln ArgProGluS 17

CGGCTCTCCC GGTTGGGGGA AGCGGGCGTC GCTCGGACCC AGGACACTAC 99

erAlaLeuPr oValAlaGly SerGlyArgA rgSerAspPr oGlyHisTyr 33

AGTTTCTCTA TGCGATCTCC AGAGCTCGCT TTACCCGGG GAAT**G**CAGCC 149 **Q49K**

SerPheSerM etArgSerPr oGluLeuAla LeuProArgG lyMetGlnPr 50

CACAGAATTTC TTCCAGTCCC TGGGTGGGGGA CGGAGAAAGG AACGTTCAGA 199

oThrGluPhe PheGlnSerL euGlyGlyAs pGlyGluArg AsnValGlnI 67

TTGAGATGGC CCATGGCACC **A**CC**A**CGCTCG CCTTCAAGTT **C**CAGCATGGA 249 **T74S T74I T75M F80L**

leGluMetAl aHisGlyThr ThrThrLeuA laPheLysPh eGlnHisGly 83

GTGATTGCAG CAGTGGATTTC **T**CGGGCCTCA **G**CTGGGTCT ACATTAGTGC 299 **R91W A92T A94P**

ValIleAlaA laValAspSe rArgAlaSer AlaGlySerT yrIleSerAl 100

CTTACGGGTG **A**A**C**AGGTGA TTGAGATTAA CCCTTACCTG CTTGGCACCA 349 **K105Q M117V**

aLeuArgVal AsnLysValI leGluIleAs nProTyrLeu LeuGlyThrM 117

TGTCTGGCTG TGCAGCAGAC TGTCAGTACT GGGAGCGCCT GCTGGCCAAG 399 D123N Q125P R129C

etSerGlyCy sAlaAlaAsp CysGlnTyrT rpGluArgLe uLeuAlaLys 133

GAATGCAGGC TGTACTATCT GCGAAATGGA GAACGTATTT CAGTGTCCGGC 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 TGTTCTCAC 599

TyrTyrValA spGluHisGl yThrArgLeu SerGlyAsnM etPheSerTh 200

GGGTAGTGGG AACACTTATG CCTACGGGGT CATGGACAGT GGCTATCGGC 649 G201V

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

TyrAlaThrH isArgAspSe rTyrSerGly GlyValValA snMetTyrHi 250

CATGAAGGAA GATGGTTGGG TGAAAGTAGA AAGTACAGAT GTCAGTGACC 799

sMetLysGlu AspGlyTrpV allLysValGl uSerThrAsp ValSerAspL 267

TGCTGCACCA GTACCGGGAA GCCAATCAAT AATGGTGGTG GTGGCAGCTG *18 *8G>A

euLeuHisG1 nTyrArgGlu AlaAsnGlnS top

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

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