



PSMB8 (NM_148919.4) - cDNA + Protein - 2024-12-06

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

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

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

CACAGAATTC TTCCAGTCCC TGGGTGGGGA CGGAGAAAGG AACGTTCAGA 199
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 R91W A92T A94P
ValIleAlaA laValAspSe rArgAlaSer AlaGlySerT yrIleSerAl 100

CTTACGGGTG AACAGGTGA TTGAGATTAA CCCTTACCTG CTTGGCACCA 349 K105Q M117Y
aLeuArgVal AsnLysValI leGluIleAs nProTyrLeu LeuGlyThrM 117

TGTC**TGGCTG** TGCAGCA**GAC** TGTC**AGTACT** GGGAG**CGCCT** GCTGGCCAAG 399 D123N Q125P R129C

etSerGlyCy sAlaAlaAsp CysGlnTyrT rpGluArgLe uLeuAlaLys 133

GAATGCAGGC TGTACTATCT GCGAAATGGA GAACGTATTT CAGTGT**CGGC** 449 G135X

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

TyrTyrValA spGluHisGl yThrArgLeu SerGlyAsnM etPheSerTh 200

GG**G**TAGTGGG AACACTTATG CCTACGGGGT CATGGACAGT GGCTATCGGC 649 G201V

rGlySerGly AsnThrTyrA laTyrGlyVa lMetAspSer GlyTyrArgP 217

CTAATCTTAG CCCTGAAGAG GCCTATGACC TTGGCCGCAG GGCTATTGCT 699

roAsnLeuSe rProGluGlu AlaTyrAspL euGlyArgAr gAlaIleAla 233

TA**T**GGCCACTC ACAGAGACAG CTAT**T**CTGGA GCGGT**T**GTCA ATATGTACCA 749 Y234C

TyrAlaThrH isArgAspSe rTyrSerGly GlyValValA snMetTyrHi 250

CATGAAGGAA GATGGTTGGG TGAAAGTAGA AAGTACAGAT GTCAGTGACC 799

sMetLysGlu AspGlyTrpV alLysValGl uSerThrAsp ValSerAspL 267

TGCTGCACCA GTACCGGGAA GCCAATCAAT **AATGGTGGT**G 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 CATTTCCTCC AGGGAAGTTT CTGGGTGCC CACTAAGTAG *218

AATAAAGAAA AACGGTTATA AATA

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