



PSMB8 (NM_148919.4) - cDNA + Protein - 2026-05-02

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

CACAGAATTC TTCAGTCCC 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 CAGTGGATT CCGGCCTCA GCTGGGTCCT ACATTAGTGC 299 S90F R91W A92T A94P
ValIleAlaA laValAspSe rArgAlaSer AlaGlySerT yrIleSerAl 100

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

TGICTGGCTG TGCAGCAGAC TGTCAGTACT GGGAGCGCCT GCTGGCCAAG 399 S118P D123N Q125P R129C c.389delT
etSerGlyCy sAlaAlaAsp CysGlnTyrT rpGluArgLe uLeuAlaLys 133

GAATGCAGGC TGTACTATCT GCGAAATGGA GAACGTATTT CAGTGTCCGC 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 CTATTCGGGA GGC GTTGTCA ATATGTACCA 749 Y234C A235D
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

euLeuHisG1 nTyrArgGlu AlaAsnGlnS top

GCAGGTCTC 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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