

Infevers - PSMB10 (NM_002801.4) - cDNA + Protein - 2023-02-09

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AGACGTGAAG CCTAGCAGAG GACTTTTTTAG CTGCTCACTG GCCCCGCTTG -52
TCTGGCCGAC TCATCCGCCC GCGACCCCTA ATCCCCTCTG CCTGCCCCAA -2
GATGCTGAAG CCAGCCCTGG AGCCCCGAGG GGGCTTCTCC TCGAGAACT 49 F14S
  MetLeuLys ProAlaLeuG luProArgGl yGlyPheSer PheGluAsnC 17

GCCAAAGAAA TGCATCATTG GAACGCGTCC TCCCGGGGCT CAAGGTCCCT 99
ysGlnArgAs nAlaSerLeu GluArgValL euProGlyLe uLysValPro 33

CACGCACGCA AGACCGGGAC CACCATCGCG GGCCTGGTGT TCCAAGACGG 149
HisAlaArgL ysThrGlyTh rThrIleAla GlyLeuValP heGlnAspGl 50

GGTCATTCTG GGCGCCGATA CGCGAGCCAC TAACGATTCTG GTCGTGGCGG 199
yValIleLeu GlyAlaAspT hrArgAlaTh rAsnAspSer ValValAlaA 67

ACAAGAGCTG CGAGAAGATC CACTTCATCG CCCCCAAAAT CTACTGCTGT 249
spLysSerCy sGluLysIle HisPheIleA laProLysIl eTyrCysCys 83

GGGGCTGGAG TAGCCGCGGA CGCCGAGATG ACCACACGGA TGGTGGCGTC 299
GlyAlaGlyV alAlaAlaAs pAlaGluMet ThrThrArgM etValAlaSe 100

CAAGATGGAG CTACACGCGT TATCTACGGG CCGCGAGCCC CGCGTGGCCA 349
rLysMetGlu LeuHisAlaL euSerThrGl yArgGluPro ArgValAlaT 117

CGGTCACTCG CATCCTGCGC CAGACGCTCT TCAGGTACCA GGGCCACGTG 399
hrValThrAr gIleLeuArg GlnThrLeuP heArgTyrGl nGlyHisVal 133

GGTGCATCGC TGATCGTGGG CGGCGTAGAC CTGACTGGAC CGCAGCTCTA 449
GlyAlaSerL euIleValGl yGlyValAsp LeuThrGlyP roGlnLeuTy 150

CGGTGTGCAT CCCCATGGCT CCTACAGCCG TCTGCCCTTC ACAGCCCTGG 499
rGlyValHis ProHisGlyS erTyrSerAr gLeuProphe ThrAlaLeuG 167

GCTCTGGTCA GGACGCGGCC CTGGCGGTGC TAGAAGACCG GTTCCAGCCG 549
lySerGlyGl nAspAlaAla LeuAlaValL euGluAspAr gPheGlnPro 183

AACATGACGC TGGAGGCTGC TCAGGGGCTG CTGGTGGAAG CCGTCACCGC 599
AsnMetThrL euGluAlaAl aGlnGlyLeu LeuValGluA laValThrAl 200

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CGGATCTTG GGTGACCTGG GCTCCGGGGG CAATGTGGAC GCATGTGTGA 649 G210R
aGlyIleLeu GlyAspLeuG lySerGlyGl yAsnValAsp AlaCysValI 217

TCACAAAGAC TGGCGCCAAG CTGCTGCGGA CACTGAGCTC ACCCACAGAG 699
leThrLysTh rGlyAlaLys LeuLeuArgT hrLeuSerSe rProThrGlu 233

CCCGTGAAGA GGTCTGGCCG CTACCACTTT GTGCCTGGAA CCACAGCTGT 749
ProValLysA rgSerGlyAr gTyrHisPhe ValProGlyT hrThrAlaVa 250

CCTGACCCAG ACAGTGAAGC CACTAACCTT GGAGCTAGTG GAGGAAACTG 799
lLeuThrGln ThrValLysP roLeuThrLe uGluLeuVal GluGluThrV 267

TGCAGGCTAT GGAGGTGGAG **TAAG**CTGAGG CTTAGAGCTT GGAACAAGGG *27
alGlnAlaMe tGluValGlu Stop

GGAATAAACC CAGAAAATAC AGTTAAA

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