

Infevers - PSMB8 (NM_148919.4) - cDNA + Protein - 2023-02-09

GCTTTCACTT	CCTCCTCCGA	GAGCGGACAG	ATCTCTGGGT	GCTGGGCGGT	-2	
CATGGCGCTA	CTAGATGTAT	GC <u>G</u> GAGCCCC	CCGAGGGCAG	CGGCCGGAAT	49	<u>G8R</u>
MetAlaLeu	LeuAspValC	ysGlyAlaPr	oArgGlyGln	ArgProGluS	17	
CGGCTCTCCC	GGTTGCGGGA	AGCGGGCGTC	GCTCGGACCC	AGGACACTAC	99	
erAlaLeuPr	oValAlaGly	SerGlyArgA	rgSerAspPr	oGlyHisTyr	33	
AGTTTCTCTA	TGCGATCTCC	AGAGCTCGCT	TTACCCCGGG	GAATG <u>C</u> AGCC	149	<u>Q49K</u>
SerPheSerM	etArgSerPr	oGluLeuAla	LeuProArgG	lyMetGlnPr	50	
CACAGAATTC	TTCCAGTCCC	TGGGTGGGGA	CGGAGAAAGG	AACGTTCAGA	199	
oThrGluPhe	PheGlnSerL	euGlyGlyAs	pGlyGluArg	AsnValGlnI	67	
TTGAGATGGC	CCATGGCACC	A <u>C</u> CAC <u>G</u> CTCG	CCTTCAAGTT	C <u>C</u> AGCATGGA	249	<u>T74S T74I T75M F80L</u>
leGluMetAl	aHisGlyThr	ThrThrLeuA	laPheLysPh	eGlnHisGly	83	
GTGATTGCAG	CAGTGGATTC	T <u>C</u> GG <u>G</u> CCTCA	G <u>T</u> GGGTCCT	ACATTAGTGC	299	<u>R91W A92T A94P</u>
ValIleAlaA	laValAspSe	rArgAlaSer	AlaGlySerT	yrIleSerAl	100	
CTTACGGGTG	AAC <u>A</u> AGGTGA	TTGAGATTAA	CCCTTACCTG	CTTGGCACCA	349	<u>K105Q M117V</u>
aLeuArgVal	AsnLysValI	leGluIleAs	nProTyrLeu	LeuGlyThrM	117	
TGTCTGGCTG	TGCAGCAGAC	TGTC <u>A</u> GTACT	GGGAG <u>C</u> GCCT	GCTGGCCAAG	399	<u>D123N Q125P R129C</u>
etSerGlyCy	sAlaAlaAsp	CysGlnTyrT	rpGluArgLe	uLeuAlaLys	133	
GAATG <u>C</u> AGGC	TGTACTIONTCT	GCGAAATGGA	GAACGTATTT	CAGTGTCCGC	449	<u>C135X</u>
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	

GGCTAGTGGG 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 GCGGTTGTCA ATATGTACCA 749 Y234C
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
euLeuHisGl 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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