

Infevers - STING1 (NM_198282.4) - cDNA + Protein - 2023-06-01

GTTCAATTTTT	CACTCCTCCC	TCCTAGGTCA	CACTTTTCAG	AAAAAGAATC	-253	
TGCATCCTGG	AAACCAGAAG	AAAAATATGA	GACGGGGAAT	CATCGTGTGA	-203	
TGTGTGTGCT	GCCTTTGGCT	GAGTGTGTGG	AGTCCTGCTC	AGGTGTTAGG	-153	
TACAGTGTGT	TTGATCGTGG	TGGCTTGAGG	GGAACCCGCT	GTTCAGAGCT	-103	
GTGACTGCGG	CTGCACTCAG	AGAAGCTGCC	CTTGGCTGCT	CGTAGCGCCG	-53	
GGCCTTCTCT	CCTCGTCATC	ATCCAGAGCA	GCCAGTGTCC	GGGAGGCAGA	-3	
AGATG CCCCA	CTCCAGCCTG	CATCCATCCA	TCCCCTGTCC	CAGGGGTCAC	48	
MetProHi	sSerSerLeu	HisProSerI	leProCysPr	oArgGlyHis	16	
GGGGCCCAGA	AGGCAGCCTT	GGTTCTGCTG	AGTGCCTGCC	TGGTGACCCT	98	
GlyAlaGlnL	ysAlaAlaLe	uValLeuLeu	SerAlaCysL	euValThrLe	33	
TTGGGGGCTA	GGAGAGCCAC	CAGAGCACAC	TCTCCGGTAC	CTGGTGCTCC	148	
uTrpGlyLeu	GlyGluProP	roGluHisTh	rLeuArgTyr	LeuValLeuH	50	
ACCTAGCCTC	CCTGCAGCTG	GGACTGCTGT	TAAACGGGGT	CTGCAGCCTG	198	
isLeuAlaSe	rLeuGlnLeu	GlyLeuLeuL	euAsnGlyVa	lCysSerLeu	66	
GCTGAGGAGC	TGCGC C ACAT	CCACTCCAGG	TACCGGGGCA	GCTACTGGAG	248	<u>H72N</u>
AlaGluGluL	euArgHisIl	eHisSerArg	TyrArgGlyS	erTyrTrpAr	83	
GACTGTGCGG	GCCTGCCTGG	GCTGCCCCCT	CC G CCGTGGG	GCCCTGTTGC	298	<u>R94H</u>
gThrValArg	AlaCysLeuG	lyCysProLe	uArgArgGly	AlaLeuLeuL	100	
TGCTGTCCAT	CTATTTCTAC	TACTCCCTCC	CAAATGCGGT	CGGCCCGCCC	348	
euLeuSerIl	eTyrPheTyr	TyrSerLeuP	roAsnAlaVa	lGlyProPro	116	
TTCACTTGGA	TGCTTGCCCT	CCTGGGCCTC	TCGCAGGCAC	TGAACATCCT	398	
PheThrTrpM	etLeuAlaLe	uLeuGlyLeu	SerGlnAlaL	euAsnIleLe	133	
CCTGGGCCTC	AAGGGCCTGG	CCCCAGCTGA	GATCTCTGCA	<u>G</u> TGTGTGAAA	448	<u>V147L</u> <u>V147M</u>
uLeuGlyLeu	LysGlyLeuA	laProAlaGl	uIleSerAla	ValCysGluL	150	
AAGGGAAT T	CA A CGTGGCC	CATG G GCTGG	CATGGTCATA	TTACATCG G A	498	<u>F153V</u> <u>F153I</u> <u>N154S</u> <u>V155M</u> <u>G158A</u> <u>G166E</u>
ysGlyAsnPh	eAsnValAla	HisGlyLeuA	laTrpSerTy	rTyrIleGly	166	
TATCTGCGGC	TGATCCTGCC	AGAGCTCCAG	GCCCGGATTC	GAACCTACAA	548	

TyrLeuArgL euIleLeuPr oGluLeuGln AlaArgIleA rgThrTyrAs 183
TCAGCATTAC AACAACTGC TACGGGGTGC AGTGAGCCAG CGGCTGTATA 598
nGlnHisTyr AsnAsnLeuL euArgGlyAl aValSerGln ArgLeuTyrI 200
TTCTCCTCCC ATTGGACTGT GGGTGCCTG ATAACCTGAG TATGGCTGAC 648 [C206G](#) [C206Y](#) [G207E](#)
leLeuLeuPr oLeuAspCys GlyValProA spAsnLeuSe rMetAlaAsp 216
CCCAACATTC GCTTCCTGGA TAAACTGCCC CAGCAGACCG GTGACCATGC 698
ProAsnIleA rgPheLeuAs pLysLeuPro GlnGlnThrG lyAspHisAl 233
TGGCATCAAG GATCGGGTTT ACAGCAACAG CATCTATGAG CTTCTGGAGA 748
aGlyIleLys AspArgValT yrSerAsnSe rIleTyrGlu LeuLeuGluA 250
ACGGGCAGCG GCGGGCACC TGTGTCCTGG AGTACGCCAC CCCCTTGACG 798
snGlyGlnAr gAlaGlyThr CysValLeuG luTyrAlaTh rProLeuGln 266
ACTTTGTTTG CCATGTCACA ATACAGTCAA GCTGGCTTTA GCCGGGAGGA 848 [F279L](#) [R281W](#) [R281Q](#)
ThrLeuPheA laMetSerGl nTyrSerGln AlaGlyPheS erArgGluAs 283
TAGCCTTGAG CAGGCCAAAC TCTTCTGCCG GACACTTGAG GACATCCTGG 898 [R284G](#) [R284S](#)
pArgLeuGlu GlnAlaLysL euPheCysAr gThrLeuGlu AspIleLeuA 300
CAGATGCCCC TGAGTCTCAG AACAACTGCC GCCTCATTGC CTACCAGGAA 948
laAspAlaPr oGluSerGln AsnAsnCysA rgLeuIleAl aTyrGlnGlu 316
CCTGCAGATG ACAGCAGCTT CTCGCTGTCC CAGGAGGTTT TCCGGCACCT 998
ProAlaAspA spSerSerPh eSerLeuSer GlnGluValL euArgHisLe 333
CGGCAGGAG GAAAAGGAAG AGGTTACTGT GGCAGCTTG AAGACCTCAG 1048 [K338Rfs*9](#)
uArgGlnGlu GluLysGluG luValThrVa lGlySerLeu LysThrSerA 350
CGGTGCCAG TACCTCCAG ATGTCCCAAG AGCCTGAGCT CCTCATCAGT 1098
laValProSe rThrSerThr MetSerGlnG luProGluLe uLeuIleSer 366
GGAATGGAAA AGCCCCTCCC TCTCCGCACG GATTTCTCTT GAGACCCAGG *8
GlyMetGluL ysProLeuPr oLeuArgThr AspPheSerS top
GTCACCAGGC CAGAGCCTCC AGTGGTCTCC AAGCCTCTGG ACTGGGGGCT *58

CTCTTCAGTG GCTGAATGTC CAGCAGAGCT ATTTCTTCC ACAGGGGGCC *108
TTGCAGGGAA GGGTCCAGGA CTTGACATCT TAAGATGCGT CTTGTCCCCT *158
TGGGCCAGTC ATTTCCCCTC TCTGAGCCTC GGTGTCTTCA ACCTGTGAAA *208
TGGGATCATA ATCACTGCCT TACCTCCCTC ACGGTTGTTG TGAGGACTGA *258
GTGTGTGGAA GTTTTTCATA AACTTTGGAT GCTAGTGTAC TTAGGGGGTG *308
TGCCAGGTGT CTTTCATGGG GCCTTCCAGA CCCACTCCCC ACCCTTCTCC *358
CCTTCCTTTG CCCGGGGACG CCGAACTCTC TCAATGGTAT CAACAGGCTC *408
CTTCGCCCTC TGGCTCCTGG TCATGTTCCA TTATTGGGGA GCCCCAGCAG *458
AAGAATGGAG AGGAGGAGGA GGCTGAGTTT GGGGTATTGA ATCCCCGGC *508
TCCCACCTG CAGCATCAAG GTTGCTATGG ACTCTCCTGC CGGGCAACTC *558
TTGCGTAATC ATGACTATCT CTAGGATTCT GGCACCACTT CCTTCCCTGG *608
CCCCTTAAGC CTAGCTGTGT ATCGGCACCC CCACCCCACT AGAGTACTCC *658
CTCTCACTTG CGGTTTCCTT ATACTCCACC CCTTTCTCAA CGGTCCTTTT *708
TTAAAGCACA TCTCAGATTA

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