

Infevers - OTULIN (NM_138348.6) - cDNA + Protein - 2023-02-09

GGAAACCGCC	CCGGCGGCTG	AGAGGCTGCG	GCCACTGCCT	GGCACCCCGA	-59	
CGGGAGGGGC	TCCGGATCGT	TCGGAGCCGG	CTGAACCCCT	TCGGCCGCGA	-9	
CGCACC G AT	G AGTCGGGGG	ACTATGCCCC	AGCCCGAAGC	GTGGCCAGGC	42	
Me	tSerArgGly	ThrMetProG	lnProGluAl	aTrpProGly	14	
GCGAGCTGCG	CCGAGACGCC	GGCGCGGGAG	GCGGCGGCCA	CGGCGCGGGA	92	
AlaSerCysA	laGluThrPr	oAlaArgGlu	AlaAlaAlaT	hrAlaArgAs	31	
CGGCGGGAAG	GCGGCGGCCA	GCGGGCAGCC	GCGGCCCGAG	ATGCAGTGCC	142	<u>Q40R</u>
pGlyGlyLys	AlaAlaAlaS	erGlyGlnPr	oArgProGlu	MetGlnCysP	48	
CGGCCGAGCA	TGAGGAGGAC	ATGTACCGTG	CTGCAGATGA	AATAGAAAAG	192	
roAlaGluHi	sGluGluAsp	MetTyrArgA	laAlaAspGl	uIleGluLys	64	
GAGAAAGAAT	TGCTTATACA	TGAAAGAGGG	GCATCAGAAC	CGAGATTAAG	242	<u>I70T</u>
GluLysGluL	euLeuIleHi	sGluArgGly	AlaSerGluP	roArgLeuSe	81	
CGTAGCTCCT	GAAATGGATA	TCATGGACTA	CTGCAAAAAA	GAATGGAGAG	292	<u>V82I M86I</u>
rValAlaPro	GluMetAspI	leMetAspTy	rCysLysLys	GluTrpArgG	98	
GAAATACACA	GAAAGCAACG	TGTATGAAAA	TGGGCTATGA	AGAGGTTTCT	342	
lyAsnThrGl	nLysAlaThr	CysMetLysM	etGlyTyrGl	uGluValSer	114	
CAGAAGTTCA	CCTCCATACG	GCGAGTCCGT	GGTGATAATT	A C TGTGCACT	392	<u>Q115H p.Leu131 Arg132insLeuCysThrGlu</u>
GlnLysPheT	hrSerIleAr	gArgValArg	GlyAspAsnT	yrCysAlaLe	131	
GAGGGCCACG	CTGTTCCAGG	CCATGAGCCA	GGCTGTGGGG	CTGCCGCCCT	442	
uArgAlaThr	LeuPheGlnA	laMetSerGl	nAlaValGly	LeuProProT	148	
GGCTGCAGGA	CCCGGAGCTC	ATGCTGTTAC	CAGAAAAACT	CATAAGCAAA	492	
rpLeuGlnAs	pProGluLeu	MetLeuLeuP	roGluLysLe	uIleSerLys	164	
TACAACTGGA	TCAAGCAATG	GAAAC C TTGGA	CTGAAATTTG	ATGGGAAGAA	542	<u>W167S G174Dfs*2</u>
TyrAsnTrpI	leLysGlnTr	pLysLeuGly	LeuLysPheA	spGlyLysAs	181	
TGAGGACCTG	GTTGATAAAA	TTAAAGAGTC	CCTTACTCTG	CTGAGGAAGA	592	
nGluAspLeu	ValAspLysI	leLysGluSe	rLeuThrLeu	LeuArgLysL	198	

AGTGGGCAGG CTTGCTGAA ATGAGAACTG CTGAAGCAAG ACAGATAGCT 642 L202F
 ysTrpAlaGl yLeuAlaGlu MetArgThrA laGluAlaAr gGlnIleAla 214

TGTGATGAAC TATTCACAAA TGAGGCGGAG GAATATAGCC TCTATGAAGC 692
 CysAspGluL euPheThrAs nGluAlaGlu GluTyrSerL euTyrGluAl 231

TGTAATAATT CTAATGCTAA ACAGAGCCAT TGAACTATAT AATGATAAAG 742 Y244C
 aValLysPhe LeuMetLeuA snArgAlaIl eGluLeuTyr AsnAspLysG 248

AGAAAGGAAA GGAAGTACCA TTTTTCTCTG TGCTTCTGTT TGCTCGGGAC 792
 luLysGlyLy sGluValPro PhePheSerV alLeuLeuPh eAlaArgAsp 264

ACATCAAATG ACCCAGGACA GCTTCTGAGG AACCACCTCA ACCAGGTGGG 842 L272P G281R
 ThrSerAsnA spProGlyGl nLeuLeuArg AsnHisLeuA snGlnValGl 281

ACACACTGGT GGTCTTGAAC AGGTTGAAAT GTTCCTTCTT GCCTATGCTG 892
 yHisThrGly GlyLeuGluG lnValGluMe tPheLeuLeu AlaTyrAlaV 298

TGCGCCACAC CATCCAGGTG TACCGGCTCT CCAAGTACAA CACGGAAGAA 942
 alArgHisTh rIleGlnVal TyrArgLeuS erLysTyrAs nThrGluGlu 314

TTCATCACAG TCTACCCAC CGACCCACCC AAGGACTGGC CAGTGGTAAC 992
 PheIleThrV alTyrProTh rAspProPro LysAspTrpP roValValTh 331

GCTCATTGCT GAGGACGATC GGCACATAAA CATCCCCGTC AGAGTGTGTG 1042
 rLeuIleAla GluAspAspA rgHisTyrAs nIleProVal ArgValCysG 348

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 luGluThrSe rLeuStop

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