

# Infevers - SLC29A3 (NM\_018344.6) - cDNA + Protein - 2023-02-09

AGTGGTCCTG	GCCGTGCGCC	GGAGGCAGCG	GCGGCGTGGC	GCAGCGGCGA	-2	
<u>CATG</u> GCCGTT	<u>GT</u> TCTCAGAGG	ACGACTTTCA	GCACAGTT <u>CA</u>	<u>AACT</u> CCACCT	49	<a href="#">M1?</a> <a href="#">V4D</a> <a href="#">S13*</a> <a href="#">S15Pfs*86</a>
MetAlaVal	ValSerGluA	spAspPheGl	nHisSerSer	AsnSerThrT	17	
<u>ACA</u> GAACCAC	AAGCAGCAGT	CTCCGAGCTG	ACCAGGAGGC	ACTGCTTGAG	99	<a href="#">R18G</a>
yrArgThrTh	rSerSerSer	LeuArgAlaA	spGlnGluAl	aLeuLeuGlu	33	
AAGCTGCTGG	ACCGCCCGCC	<u>CC</u> TGGCCTG	CAGAGGCC <u>CG</u>	AGGACCGCTT	149	<a href="#">P41Lfs*60</a> <a href="#">E47Rfs*54</a>
LysLeuLeuA	spArgProPr	oProGlyLeu	GlnArgProG	luAspArgPh	50	
CTGTGGCACA	TACATCATCT	TCTTCAGCCT	<u>GGC</u> CATTGGC	AGTCTACTGC	199	<a href="#">G61V</a>
eCysGlyThr	TyrIleIleP	hePheSerLe	uGlyIleGly	SerLeuLeuP	67	
CATGGAACTT	CTTTATCACT	GCCAAGGAGT	ACTGGATGTT	<u>CAA</u> ACTCCGC	249	<a href="#">K81Nfs</a>
roTrpAsnPh	ePheIleThr	AlaLysGluT	yrTrpMetPh	eLysLeuArg	83	
AACTCCTCCA	GCCCAGCCAC	CGGGGAGGAC	CCTGAGGGCT	CAGACATCCT	299	
AsnSerSerS	erProAlaTh	rGlyGluAsp	ProGluGlyS	erAspIleLe	100	
<u>GAA</u> CTACTTT	GAGAGCTACC	<u>TTGCC</u> GTTGC	CTCCACCGTG	<u>CCCTCCA</u> TGC	349	<a href="#">c.302_303insCTACTTTGAGAGCTACC</a> <a href="#">F103X</a> <a href="#">V109I</a> <a href="#">M116R</a>
uAsnTyrPhe	GluSerTyrL	euAlaValAl	aSerThrVal	ProSerMetL	117	
TGTGCCTGGT	GGCCAACTTC	CTGCTTGTC	ACAGGGTTGC	AGTCCACATC	399	
euCysLeuVa	lAlaAsnPhe	LeuLeuValA	snArgValAl	aValHisIle	133	
<u>CG</u> TGTCCTGG	<u>CCT</u> CAC <u>T</u> GAC	GGTCATCCTG	GCCATCTTCA	TGGTGATAAC	449	<a href="#">R133C</a> <a href="#">R134H</a> <a href="#">L139P</a>
ArgValLeuA	laSerLeuTh	rValIleLeu	AlaIlePheM	etValIleTh	150	
TGCACTGGTG	AAGGTGGACA	CTTCCTCCTG	GACCCGTGGC	TTTTTTGCGG	499	
rAlaLeuVal	LysValAspT	hrSerSerTr	pThrArgGly	PhePheAlaV	167	
TCACCATTGT	CTGCATGGTG	ATCCTCAGCG	GTGCCTCC <u>A</u> C	TGTCTTCAGC	549	<a href="#">T180A</a>
alThrIleVa	lCysMetVal	IleLeuSerG	lyAlaSerTh	rValPheSer	183	
<u>AG</u> CAGCATCT	ACGGCATGAC	CGGCTCCTTT	CCTATGAGGA	ACTCCAGGC	599	<a href="#">S184R</a>
SerSerIleT	yrGlyMetTh	rGlySerPhe	ProMetArgA	snSerGlnAl	200	

ACTGATATCA GGAGGAGCCA TGGGCGGGAC GGTACAGGCC GTGGCCTCAT 649 [S203P](#) [c.625G>A](#)  
 aLeuIleSer GlyGlyAlaM etGlyGlyTh rValSerAla ValAlaSerL 217

TGGTGGACTT GGCTGCATCC AGTGATGTGA GGAACAGCGC CCTGGCCTTC 699 [D225G](#) [A230T](#)  
 euValAspLe uAlaAlaSer SerAspValA rgAsnSerAl aLeuAlaPhe 233

TTCCTGACGG CCACTGTCTT CCTCGTGCTC TGCATGGGAC TCTACCTGCT 749 [T236M](#) [T236T](#)  
 PheLeuThrA laThrValPh eLeuValLeu CysMetGlyL euTyrLeuLe 250

GCTGTCCAGG CTGGAGTATG CCAGGTACTA CATGAGGCCT GTTCTTGCGG 799  
 uLeuSerArg LeuGluTyrA laArgTyrTy rMetArgPro ValLeuAlaA 267

CCCATGTGTT TTCTGGTGAA GAGGAGCTTC CCCAGGACTC CCTCAGTGCC 849  
 laHisValPh eSerGlyGlu GluGluLeuP roGlnAspSe rLeuSerAla 283

CCTTCGGTGG CCTCCAGATT CATTGATTCC CACACACCCC CTCTCCGCCC 899  
 ProSerValA laSerArgPh eIleAspSer HisThrProP roLeuArgPr 300

CATCCTGAAG AAGACGGCCA GCCTGGGCTT CTGTGTCACC TACGTCTTCT 949 [C310X](#) [Y314Tfs](#) [F316V](#)  
 oIleLeuLys LysThrAlaS erLeuGlyPh eCysValThr TyrValPheP 317

TCATCACCAG CCTCATCTAC CCGCCATCT GCACCAACAT CGAGTCCCTC 999 [P324S](#) [P324L](#) [I326V](#)  
 heIleThrSe rLeuIleTyr ProAlaIleC ysThrAsnIl eGluSerLeu 333

AACAAAGGGTT CGGGCTCACT GTGGACCACC AAGTTTTTCA TCCCCCTCAC 1049 [c.1045delC](#)  
 AsnLysGlyS erGlySerLe uTrpThrThr LysPhePheI leProLeuTh 350

TACCTTCTC CTGTACAACT TTGCTGACCT ATGTGGCCGG CAGCTCACCG 1099 [c.1087C>T](#) [R363Q](#) [A367T](#)  
 rThrPheLeu LeuTyrAsnP heAlaAspLe uCysGlyArg GlnLeuThrA 367

CCTGGATCCA GGTGCCAGGG CCCAATAGCA AGGCGCTCCC AGGGTTCGTG 1149  
 laTrpIleGl nValProGly ProAsnSerL ysAlaLeuPr oGlyPheVal 383

CTCCTCGGGA CCTGCCTCAT CCCCCTCTTC GTGCTCTGTA ACTACCAGCC 1199 [R386W](#) [R386Q](#) [c.1172C>A](#)  
 LeuLeuArgT hrCysLeuIl eProLeuPhe ValLeuCysA snTyrGlnPr 400

CCGCGTCCAC CTGAAGACTG TGGTCTTCCA GTCCGATGTG TACCCCGCAC 1249  
 oArgValHis LeuLysThrV alValPheGl nSerAspVal TyrProAlaL 417

TCCTCAGCTC CCTGCTGGG CTCAGCAAC GCTACCTCAG CACCCTGGCC 1299 c.1269\_1270delinsA G427S  
 euLeuSerSe rLeuLeuGly LeuSerAsnG lyTyrLeuSe rThrLeuAla 433

CTCCTCTACG GGCCTAAGAT TGTGCCCAGG GAGCTGGCTG AGGCCACGGG 1349 G437R E444X c.1339G>A T449R  
 LeuLeuTyrG lyProLysIl eValProArg GluLeuAlaG luAlaThrGl 450

AGTGGTGATG TCCTTTTATG TGTGCTTG CTTAACACTG GGCTCAGCCT 1399  
 yValValMet SerPheTyrV alCysLeuGl yLeuThrLeu GlySerAlaC 467

GCTCTACCCCT CCTGGTGCAC CTCATCTAGA AGGGAGGACA CAAGGACATT \*21  
 ysSerThrLe uLeuValHis LeuIleStop

GGTGCTTCAG AGCCTTTGAA GATGAGAAGA GAGTGCAGGA GGGCTGGGGG \*71  
 CCATGGAGGA AAGGCCTAAA GTTTCACCTG GGGACAGAGA GCAGAGCACA \*121  
 CTCGGGCCCTC ATCCCTCCCA AGATGCCAGT GAGCCACGTC CATGCCCATT \*171  
 CCGTGCAAGG CAGATATTCC AGTCATATTA ACAGAACACT CCTGAGACAG \*221  
 TTGAAGAAGA AATAGCACAA ATCAGGGGTA CTCCCTTCAC AGCTGATGGT \*271  
 TAACATTCCA CCTTCTTTCT AGCCCTTCAA AGATGCTGCC AGTGTTTCGCC \*321  
 CTAGAGTTAT TACAAAGCCA GTGCCAAAAC CCAGCCATGG GCTCTTTGCA \*371  
 ACCTCCCAGC TGCCTCATT CCAGCTGACA GCGAGATGCA AGCAAATGCT \*421 c.1893G>A  
 CAGCTCTCCT TACCCTGAAG GGGTCTCCCT GGAATGGAAG TCCCCTGGCA \*471  
 TGGTCAGTCC TCAGGCCCAA GACTCAAGTG TGCACAGACC CCTGTGTTCT \*521  
 GTGGGTGAAC AACTGCCCAC TAACCAGACT GGAAAACCCA GAAAGATGGG \*571  
 CCTTCCATGA ATGCTTCATT CCAGAGGGAC CAGAGGGCCT CCCTGTGCAA \*621  
 GGGATCAAGC ATGTCTGGCC TGGGTTTTCA AAAAAAGAGG GATCCTCATG \*671  
 ACCTGGTGGT CTATGGCCTG GGTCAAGATG AGGGTCTTTC AGTGTTCTCTG \*721  
 TTTACAACAT GTCAAAGCCA TTGGTTCAAG GCGTAATAA ATACTTGCGT \*771  
 ATTCAA

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