

Infervers - ELF4 (NM_001421.4) - cDNA + Protein - 2023-02-09

ACTTCTCCTT	TCGCCGGCGC	CGAGTTCCTG	GCGCCGCTCG	CCCGGCCCGG	-333
CTTCCGAGGG	GAGAGGACGG	GCTGGCGGGG	CTGGGGACCC	GCGTCTCGGC	-283
CCCCGGAGCG	GGGACCACGG	AGACAGACCC	CGGCCCGGCG	ACCGAGCTGG	-233
GCCCGTGAGC	CACTCGGCCT	CAGGTCGCTC	CTGTGGTTGG	TCCAGCCCAG	-183
AATGCAGCCT	TGAGCCTGGC	TTAGGCCACC	ACCTACTCCA	GCTCTCTCCA	-133
CCCCCTATTT	TACTGCAGCT	CAGGGGGTAG	GCTCTAGGCT	CCAAAGTACC	-83
TGGGTATTGT	CCCTTCATCA	AGAAAAGCCC	ACAGCTCTGG	AGGGCTCTGA	-33
TAATCCCGTT	GTCAGCTCTC	TGAAAAGACA	GCATGGCTAT	TACCCTACAG	18
			MetAlaI1	eThrLeuGln	6
CCCAGTGACC	TGATCTTTGA	GTTTCGCAAGC	AACGGGATGG	ATGATGATAT	68
ProSerAspL	euIlePheGl	uPheAlaSer	AsnGlyMetA	spAspAspI1	23
CCACCAGCTG	GAAGACCCCT	CTGTGTTCCC	AGCTGTGATC	GTGGAGCAGG	118
eHisGlnLeu	GluAspProS	erValPhePr	oAlaValIle	ValGluGlnV	40
TACCCTACCC	TGATTTACTG	CATCTGTACT	CGGGACTGGA	GTTGGACGAC	168
alProTyrPr	oAspLeuLeu	HisLeuTyrS	erGlyLeuGl	uLeuAspAsp	56
GTTCACAATG	GCATCATAAC	AGACGGGACC	TTGTGCATGA	CGCAGGATCA	218
ValHisAsnG	lyIleIleTh	rAspGlyThr	LeuCysMetT	hrGlnAspGl	73
GATCCTGGAA	GGCAGTTTTT	TGCTGACAGA	TGACAATGAG	GCCACCTCGC	268
nIleLeuGlu	GlySerPheL	euLeuThrAs	pAspAsnGlu	AlaThrSerH	90
ACACCATGTC	AACCGCGGAA	GTCTTACTCA	ATATGGAGTC	TCCCAGCGAT	318
isThrMetSe	rThrAlaGlu	ValLeuLeuA	snMetGluSe	rProSerAsp	106
ATCCTGGATG	AGAAGCAGAT	CTTCAGTACC	TCCGAAATGC	TTCCAGACTC	368
IleLeuAspG	luLysGlnI1	ePheSerThr	SerGluMetL	euProAspSe	123
GGACCCTGCA	CCAGCTGTCA	CTCTGCCCAA	CTACCTGTTT	CCTGCCTCTG	418
rAspProAla	ProAlaValT	hrLeuProAs	nTyrLeuPhe	ProAlaSerG	140
AGCCCGATGC	CCTGAACAGG	GCGGGTGACA	CTAGTGACCA	GGAGGGGCAT	468
luProAspAl	aLeuAsnArg	AlaGlyAspT	hrSerAspGl	nGluGlyHis	156

TCTCTGGAGG AGAAGGCCTC CAGAGAGGAA AGTGCCAAGA AGACTGGGAA 518
SerLeuGluG luLysAlaSe rArgGluGlu SerAlaLysL ysThrGlyLy 173

ATCAAAGAAG AGAATCCGGA AGACCAAGGG CAACCGAAGT ACCTCACCTG 568
sSerLysLys ArgIleArgL ysThrLysGl yAsnArgSer ThrSerProV 190

TCACTGACCC CAGCATCCCC ATTAGGAAGA AATCAAAGGA TGGCAAAGGC 618
alThrAspPr oSerIlePro ileArgLysL ysSerLysAs pGlyLysGly 206

AGCACCATCT ATCTGTGGGA GTTCCTCCTG GCTCTTCTGC AAGACAGAAA 668
SerThrIleT yrLeuTrpGl uPheLeuLeu AlaLeuLeuG lnAspArgAs 223

CACCTGTCCC AAGTACATCA AGTGGACCCA GCGAGAGAAA GGCATCTTCA 718 [p.W231R](#)
nThrCysPro LysTyrIleL ysTrpThrGl nArgGluLys GlyIlePheL 240

AACTGGTGGA CTCCAAAGCT GTGTCCAAGC TGTGGGGGAA GCAGAAAAAC 768 [p.W251S](#)
ysLeuValAs pSerLysAla ValSerLysL euTrpGlyLy sGlnLysAsn 256

AAGCCTGACA TGAACTATGA GACAATGGGG CGGGCACTAA GATACTACTA 818
LysProAspM etAsnTyrGl uThrMetGly ArgAlaLeuA rgTyrTyrTy 273

CCAAAGAGGC ATACTGGCCA AAGTGGAAGG GCAGAGGCTG GTGTACCAGT 868
rGlnArgGly ileLeuAlaL ysValGluGl yGlnArgLeu ValTyrGlnP 290

TTAAGGAGAT GCCCAAGGAC CTGGTGGTCA TTGAAGATGA GGATGAGAGC 918
heLysGluMe tProLysAsp LeuValValI leGluAspGl uAspGluSer 306

AGCGAAGCCA CAGCAGCCCC ACCTCAGGCC TCCACGGCCT CTGTGGCCTC 968
SerGluAlaT hrAlaAlaPr oProGlnAla SerThrAlaS erValAlaSe 323

TGCCAGTACC ACCCGGCGAA CCAGCTCCAG GGTCTCATCC AGATCTGCC 1018 [p.A339fs](#)
rAlaSerThr ThrArgArgT hrSerSerAr gValSerSer ArgSerAlaP 340

CCCAGGGCAA GGGCAGCTCT TCTTGGGAGA AGCCAAAAAT TCAGCATGTC 1068
roGlnGlyLy sGlySerSer SerTrpGluL ysProLysIl eGlnHisVal 356

GGTCTCCAGC CATCTGCGAG TCTGGAATTG GGACCGTCGC TAGACGAGGA 1118
GlyLeuGlnP roSerAlaSe rLeuGluLeu GlyProSerL euAspGluGl 373

GATCCCCACT ACCTCCACCA TGCTCGTCTC TCCAGCAGAG GGCCAGGTCA 1168
 uIleProThr ThrSerThrM etLeuValSe rProAlaGlu GlyGlnValL 390

AGCTCACCAA AGCTGTGAGT GCATCTTCAG TGCCCAGCAA CATCCACCTA 1218
 ysLeuThrLy sAlaValSer AlaSerSerV alProSerAs nIleHisLeu 406

GGAGTGGCCC CCGTGGGGTC GGGCTCGGCC CTGACCCTGC AGACGATCCC 1268
 GlyValAlaP roValGlySe rGlySerAla LeuThrLeuG lnThrIlePr 423

ACTGACCACG GTGCTGACCA ATGGGCCTCC TGCCAGTACT ACTGCTCCCA 1318
 oLeuThrThr ValLeuThrA snGlyProPr oAlaSerThr ThrAlaProT 440

CTCAGCTCGT TCTCCAGAGT GTTCCAGCGG CCTCTACTTT CAAGGACACC 1368
 hrGlnLeuVa lLeuGlnSer ValProAlaA laSerThrPh eLysAspThr 456

TTCACTTTGC AGGCCTCTTT CCCCCTGAAC GCCAGTTTCC AAGACAGCCA 1418
 PheThrLeuG lnAlaSerPh eProLeuAsn AlaSerPheG lnAspSerGl 473

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 nValAlaAla ProGlyAlaP roLeuIleLe uSerGlyLeu ProGlnLeuL 490

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 euAlaGlyAl aAsnArgPro ThrAsnProA laProProTh rValThrGly 506

GCTGGACCAG CAGGGCCCAG CTCTCAGCCC CCTGGGACTG TCATTGCTGC 1568
 AlaGlyProA laGlyProSe rSerGlnPro ProGlyThrV alIleAlaAl 523

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 aPheIleArg ThrSerGlyT hrThrAlaAl aProArgVal LysGluGlyP 540

CACTGAGGTC CTCCTCCTAT GTTCAGGGTA TGGTGACGGG GGCCCCCATG 1668
 roLeuArgSe rSerSerTyr ValGlnGlyM etValThrGl yAlaProMet 556

GAGGGGCTGC TGGTTCCTGA AGAGACCCTG AGGGAGCTCC TGAGAGATCA 1718
 GluGlyLeuL euValProGl uGluThrLeu ArgGluLeuL euArgAspGl 573

GGCTCATCTT CAGCCACTTC CAACCCAGGT GGTTCAGG GGTTCACCA 1768
 nAlaHisLeu GlnProLeuP roThrGlnVa lValSerArg GlySerHisA 590

ATCCGAGCCT TCTGGGCAAC CAGACTTTGT CTCCTCCCAG CCGCCCCACT 1818
 snProSerLe uLeuGlyAsn GlnThrLeuS erProProSe rArgProThr 606

GTTGGGCTGA CCCCAGTGGC TGAAC TTGAG CTCTCCTCAG GCTCAGGGTC 1868
 ValGlyLeuT hrProValAl aGluLeuGlu LeuSerSerG lySerGlySe 623

CCTGCTGATG GCTGAGCCTA GTGTGACCAC ATCTGGGAGC CTTCTGACAA 1918
 rLeuLeuMet AlaGluProS erValThrTh rSerGlySer LeuLeuThrA 640

GATCCCCCAC CCCAGCCCCT TTCTCCCCAT TCAACCCTAC TTCCCTCATT 1968
 rgSerProTh rProAlaPro PheSerProP heAsnProTh rSerLeuIle 656

AAGATGGAGC CCCATGACAT ATAAGCAAAG GGGTCAGGGC AAGTGTGACC *26
 LysMetGluP roHisAspIl eStop

CACCAGGCAA AATTGAGCAG CATT TTCATA GGGACCGACT TCAGTAGCAC *76
 ACCTGCCCTT GCAT TTCAGT GGGATGTCAA TACACTTGAC CCCAAGTCCC *126
 CCGGCCCTGC CTGGTGT CAC TGTGGCCAAA CAGTGCCCAG CTTAAGCATC *176
 CCTGGCATCA GACTATGGCC TTCAAGAGCA CTAGGGCATA TGCTTTTGGC *226
 AGCATAACGG GCTGACTTGG TGATGGAGGG AAAAAAGCCTT GAGCCAGGCA *276
 GAAGTTTGTG GCCAGGGTTT GTGCAGCAGC TTTGTGAGAA GAGCCCTTCT *326
 ACCTGGCTCT ATCTCACTGG CTGCATTCCC TACACAGGGA ATTTACTACC *376
 CTATATGTGA ATATCCCTGT ATGTACTTGT GTGTACTTGT TGGTCTGTAT *426
 CTTAGTTTCT TTGGGGAGGA CAGGGCTGTA GCTGTGAGGT CTTGTCTCCA *476
 AGGGTGTGTG TATGTCTCCG TGGATCAGCC ACAGGGATAG GGATTTTGT T *526
 TTTAAGGGAA AGCATTCTCT AATTCCCTTT GTTCATGCCG AGATT CAGTT *576
 GCTCTGAGAC TATGGGGTAC AAGTTTGATC CTCCGAATCT GGAGATGTTG *626
 TAGAGCTGGA ACGAGTGCAG AGTAGGAACG CTTTGATGCG CATGCACATT *676
 GGGGAAGATG CGCTCCTCAG GGACACAAAG GCCGAGTGGG GTAAAACCAC *726
 GAAGGGAGGG AAGGGAAAGTC AGCTCTGGGA GCAGCCCTCA CTGGCTGGAC *776
 CAAGGTA CT T TCCTGGAGT TTGCCGTGTT AGCAACCACA GTCACCTTGC *826
 AGTCAGGCTG GAATCTTGGG CCACCCCAA GTGCTTTGCT GAAGGATTTA *876
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 AGCTGAATTC ATTGAGTATT TGTGCCTAGG GCTTGGGCTG TTTGTGTGAT *976
 ACCGGCCCCC CGCCAGACAA TAGCCTTTGC TGACACCCCA GCCTACTTCC *1026
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 TGCAACTCAC CTCGAAGGCG GACCAGCCTG CCTCTGTGAT GACTGCAGCA *1226

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GCACCTCTCT CTCTTCGTGG CTCCCTGCTT CCCCCTTCCC TCTTTCCGAG *1376
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GATCTCCTCC CCTCTCCCTT CTTTAAACGA GCTTGCCTCC CTCCTGCCAA *1476
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GTAGCCCCGC CCCCACCTGA AAACCTGGTT CTGCCACCCC TACTCCAAC *1926
CCATGGAAAC TCATTGCTGG AAGGTCATCA ATGACCTCAT GGTGAAATCA *1976
AATGTCTTCT TCACAGTTCT CGGGCCCCCG TGAGCCCACA CTAGCTGGGC *2026
TCTCCTGCAT CCCCCATCAC CCTTTCCGGG GCTGGTTCTT CACCTACCAC *2076
TTCCAACGTG GCTGTTCAAG AATCTCATCC ATTTTGGGCT CATTTTGGCT *2126
CCTCGGAGAT GGGTCCTAAA TCTAGAGCTC CAGTCCCAAC CTTTCTCTTA *2176
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CTTGTCAGCT CCTTAAAGAT AGCCCCTCTA TCAACAATGT TTTTGTGTTG *2276
TCGTTTGTGTT TTGAGTCAGA GTCTTGCTCT GTCGGCTGGA GTGCAGTGGT *2326
GCAATCTCGG TTCACTGCAA CCTCTGCCTC CCAGGCTCAA GTGATTCTCC *2376
TGCCTCAGCC TCCTGAGTAG CTGGGAGTAC AGGCACATGC CACCATGCCC *2426
AGCTAATTTT TGTATTTTCA GTAGAGCCAG GGTTTCACCA TTTTCGGCCAG *2476
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TGGGTGCAGC AAACCACCAT GGCACATGTA TACCTATGTA ACAAACCTGC *2676
ACGTTCTGCA CATGTATCCC AGAACTTAAA GTATAATAAT AATAATAATA *2726
ATAATAATAA TAATAATAAT AAAAATCAAG CAAACAAAAA

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