



ELF4 (NM_001421.4) - cDNA + Protein - 2025-02-13

ACTTCTCCTT TCGCCGGCGC CGAGTTCCTG GCGCCGCTCG CCCGGCCCCG -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 AGAAAGCCCC ACAGCTCTGG AGGGCTCTGA -33
TAATCCCATT GTCAGCTCTC TGAAAAGACA GCATGGCTAT TACCCTACAG 18

MetAlaI1 eThrLeuGln 6

CCCAGTGACC TGATCTTTGA GTTCGCAAGC AACGGGATGG ATGATGATAT 68
ProSerAspL euIlePheG1 uPheAlaSer AsnGlyMetA spAspAspI1 23

CCACCAGCTG GAAGACCCCT CTGTGTTCCC AGCTGTGATC GTGGAGCAGG 118 p.(Q39X)
eHisGlnLeu GluAspProS erValPhePr oAlaValIle ValGluGlnV 40

TACCCTACCC TGATTTACTG CATCTGTACT CGGGACTGGA GTTGGACGAC 168
alProTyrPr oAspLeuLeu HisLeuTyrS erGlyLeuG1 uLeuAspAsp 56

GTTCAATG GCATCATAAC AGACGGGACC TTGTGCATGA CGCAGGATCA 218
ValHisAsnG lyIleIleTh rAspGlyThr LeuCysMetT hrGlnAspG1 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 CTTCACTACC TCCGAAATGC TTCCAGACTC 368
IleLeuAspG luLysGlnIl ePheSerThr SerGluMetL euProAspSe 123

GGACCCTGCA CCAGCTGTCA CTCTGCCCAA CTACCTGTTT CCTGCCTCTG 418
rAspProAla ProAlaValT hrLeuProAs nTyrLeuPhe ProAlaSerG 140

AGCCCGATGC CCTGAACAGG GCGGGTGACA CTAGTGACCA GGAGGGGCAT 468 [p.\(G148Vfs*113\)](#) [p.\(H156Ifs*105\)](#)
luProAspAl aLeuAsnArg AlaGlyAspT hrSerAspGl nGluGlyHis 156

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

ATCAAAGAAG AGAATCCGGA AGACCAAGGG CAACCGAAGT ACCTCACCTG 568 [p.\(R185X\)](#)
sSerLysLys ArgIleArgL ysThrLysGl yAsnArgSer ThrSerProV 190

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

AGCACCATCT ATCTGTGGGA GTTCCTCCTG GCTCTTCTGC AAGACAGAAA 668 [p.\(W212C\)](#)
SerThrIleT yrLeuTrpGl uPheLeuLeu AlaLeuLeuG lnAspArgAs 223

CACCTGTCCC AAGTACATCA AGTGGACCCA GCGAGAGAAA GGCATCTTCA 718 [p.W231R](#) [p.\(R234X\)](#)

nThrCysPro LysTyrIleL ysTrpThrGl nArgGluLys GlyIlePheL 240

AACTGGTGGG CTCCAAAGCT GTGTCCAAGC TGTGGGGGAA GCAGAAAAAC 768 [p.\(S248F\)](#) [p.W251S](#)

ysLeuValAs pSerLysAla ValSerLysL euTrpGlyLy sGlnLysAsn 256

AAGCCTGACA TGAACTATGA GACAATGGGG CGGGCACTAA GATACTACTA 818

LysProAspM etAsnTyrGl uThrMetGly ArgAlaLeuA rgTyrTyrTy 273

CCAAAGAGGC ATACTGGCCA AAGTGGGAAGG 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

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hrGlnLeuVa lLeuGlnSer ValProAlaA laSerThrPh eLysAspThr 456

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AlaGlyProA laGlyProSe rSerGlnPro ProGlyThrV alIleAlaAl 523

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nAlaHisLeu GlnProLeuP roThrGlnVa lValSerArg GlySerHisA 590

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

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ValGlyLeuT hrProValAl aGluLeuGlu LeuSerSerG lySerGlySe 623

CCTGCTGATG GCTGAGCCTA GTGTGACCAC ATCTGGGAGC CTTCTGACAA 1918
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GATCCCCCAC CCCAGCCCCT TTCTCCCCAT TCAACCCTAC TTCCCTCATT 1968
rgSerProTh rProAlaPro PheSerProP heAsnProTh rSerLeuIle 656

AAGATGGAGC CCCATGACAT ATAAGCAAAG GGGTCAGGGC AAGTGTGACC *26
LysMetGluP roHisAspIl eStop

CACCAGGCAA AATTGAGCAG CATTTCATA GGGACCGACT TCAGTAGCAC *76
ACCTGCCCCT GCATTCAGT GGGATGTCAA TACACTTGAC CCCAAGTCCC *126
CCGGCCCTGC CTGGTGTAC TGTGGCCAAA CAGTGCCAG CTTAAGCATC *176
CCTGGCATCA GACTATGGCC TTCAAGAGCA CTAGGCATA TGCTTTTGGC *226

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ACCGGCCCCC CGCCAGACAA TAGCCTTTGC TGACACCCCA GCCTACTTCC *1026
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