



*ELF4* (NM\_001421.4) - cDNA + Protein - 2025-04-03

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

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

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AlaGlyProA laGlyProSe rSerGlnPro ProGlyThrV alIleAlaAl 523

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aPheIleArg ThrSerGlyT hrThrAlaAl aProArgVal LysGluGlyP 540

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roLeuArgSe rSerSerTyr ValGlnGlyM etValThrGl yAlaProMet 556

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GluGlyLeuL euValProGl uGluThrLeu ArgGluLeuL euArgAspGl 573

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nAlaHisLeu GlnProLeuP roThrGlnVa lValSerArg GlySerHisA 590

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snProSerLe uLeuGlyAsn GlnThrLeuS erProProSe rArgProThr 606

GTTGGGCTGA CCCAGTGGC TGAACCTGAG 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 CATTTCATA GGGACCGACT TCAGTAGCAC \*76  
ACCTGCCCCT GCATTCAGT GGGATGTCAA TACACTTGAC CCCAAGTCCC \*126  
CCGGCCCTGC CTGGTGTAC TGTGGCCAAA CAGTGCCAG CTTAAGCATC \*176  
CCTGGCATCA GACTATGGCC TTCAAGAGCA CTAGGCATA TGCTTTTGGC \*226

AGCATAACGG GCTGACTTGG TGATGGAGGG AAAAAGCCTT 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 GGATTTTGTG \*526  
TTTAAGGGAA AGCATTCTCT AATTCCCTTT GTTCATGCCG AGATTCAGTT \*576  
GCTCTGAGAC TATGGGGTAC AAGTTTGATC CTCCGAATCT GGAGATGTTG \*626  
TAGAGCTGGA ACGAGTGCAG AGTAGGAACG CTTTGATGCG CATGCACATT \*676  
GGGGAAGATG CGCTCCTCAG GGACACAAAG GCCGAGTGGG GTAAAACCAC \*726  
GAAGGGAGGG AAGGGAAGTC AGCTCTGGGA GCAGCCCTCA CTGGCTGGAC \*776  
CAAGGTACTC TTCCTGGAGT TTGCCGTGTT AGCAACCACA GTCACCTTGC \*826  
AGTCAGGCTG GAATCTTGGG CCACCCAAA GTGCTTTGCT GAAGGATTTA \*876  
GACGGGGATG AAGTGCCCTC CAGCCTCAGA GCTAGCCACA AAGCCCCCAG \*926  
AGCTGAATTC ATTGAGTATT TGTGCCTAGG GCTTGGGCTG TTTGTGTGAT \*976  
ACCGGCCCCC CGCCAGACAA TAGCCTTTGC TGACACCCCA GCCTACTTCC \*1026  
CCGATCCTGG GCTCCCTCTT GATTACTTTT TGACATTTTC CAGCTGTCAG \*1076  
GCATCACTGC GGCTAGTCCG GCAGCGACCT AGATGGGGTC CACCCCATTT \*1126  
CCTGCTCAAG CATGGGCACC TACCACATGG TTTCTGCTGC TCAGCCTGCC \*1176  
TGCAACTCAC CTCGAAGGCG GACCAGCCTG CCTCTGTGAT GACTGCAGCA \*1226  
GACCTCCTTG GGTGTACCAA TGCCCTCAT CTCCACTTT CACACCTAAC \*1276  
CCTGACTCCT TCACCAAGAA GACGGGAGTC GGCAGCCAGG AGTTCCCGTG \*1326  
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CGCTCTTCTC TTCTTTGTTA AGCCAACAAC TATCACCCCTC TCCTACTCTT \*1676  
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AGGGTCACCA TTAATAAAAA ATTTTGCATA AAGGTGCTGC ATGGGTGGG \*1876  
GTAGCCCCGC CCCCACCTGA AAACCTGGTTT CTGCCACCCC TACTCCAAC \*1926  
CCATGGAAAC TCATTGCTGG AAGGTCATCA ATGACCTCAT GGTGAAATCA \*1976  
AATGTCTTCT TCACAGTTCT CGGGCCCCCG TGAGCCCACA CTAGCTGGGC \*2026  
TCTCCTGCAT CCCCATCAC CCTTCCGGG GCTGGTTCTT CACCTACCAC \*2076  
TTCCAACGTG GCTGTTCAAG AATCTCATCC ATTTTGGGCT CATTTTGGCT \*2126  
CCTCGGAGAT GGGTCCTAAA TCTAGAGCTC CAGTCCCAAC CTTTCTCTTA \*2176  
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CTTGTGAGCT CCTTAAAGAT AGCCCCCTA TCAACAATGT TTTTGTGTTG \*2276  
TCGTTTGTGTT TTGAGTCAGA GTCTTGCTCT GTCGGCTGGA GTGCAGTGGT \*2326  
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TGCCCTCAGCC TCCTGAGTAG CTGGGAGTAC AGGCACATGC CACCATGCCC \*2426  
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TTTAAATTAT TTCCACGCTC AAAAAAACC TTTCCAAGAT GACGGGTTGA \*2626  
TGGGTGCAGC AAACCACCAT GGCACATGTA TACCTATGTA ACAAACCTGC \*2676  
ACGTTCTGCA CATGTATCCC AGAACTTAAA GTATAATAAT AATAATAATA \*2726  
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