

ELF4 (NM_001421.4) - cDNA + Protein - 2026-11-14

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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 AGAAAGCCCC ACAGCTCTGG AGGGCTCTGA -33
TAATCCCGTT GTCAGCTCTC TGAAAAGACA GCATGGCTAT TACCCTACAG 18
                                  MetAlaIl eThrLeuGln 6

CCCAGTGACC TGATCTTTGA GTTCGCAAGC AACGGGATGG ATGATGATAT 68
ProSerAspL euIlePheGl uPheAlaSer AsnGlyMetA spAspAspIl 23

CCACCAGCTG GAAGACCCCT CTGTGTTCCC AGCTGTGATC GTGGAGCAGG 118  p.(Q39X)
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  p.L80*
nIleLeuGlu GlySerPheL euLeuThrAs pAspAsnGlu AlaThrSerH 90

ACACCATGTC AACCGCGGAA GTCTTACTCA ATATGGAGTC TCCCAGCGAT 318
isThrMetSe rThrAlaGlu ValLeuLeuA snMetGluSe rProSerAsp 106

ATCCTGGATG AGAAGCAGAT CTTCAGTACC TCCGAAATGC TTCCAGACTC 368  p.L108fs*3 p.E110Gfs*35
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 AGAAGGCCTC CAGAGAGGAA AGTGCCAAGA AGACTGGGAA 518
SerLeuGluG luLysAlaSe rArgGluGlu SerAlaLysL ysThrGlyLy 173
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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.I229V I229M p.W231R p.(R234X)
nThrCysPro LysTyrIleL ysTrpThrGl nArgGluLys GlyIlePheL 240

AACTGGTGGA CTCCAAAGCT GTGTCCAAGC TGTGGGGGAA GCAGAAAAAC 768  p.(S248F) p.W251S
ysLeuValAs pSerLysAla ValSerLysL euTrpGlyLy sGlnLysAsn 256

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LysProAspM etAsnTyrGl uThrMetGly ArgAlaLeuA rgTyrTyrTy 273

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rGlnArgGly IleLeuAlaL ysValGluGl yGlnArgLeu ValTyrGlnP 290

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heLysGluMe tProLysAsp LeuValValI leGluAspGl uAspGluSer 306

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

TGCCAGTACC ACCCGGCGAA CCAGCTCCAG GGTCTCATCC AGATCTGCCC 1018 p.A339fs
rAlaSerThr ThrArgArgT hrSerSerAr gValSerSer ArgSerAlaP 340

CCCAGGGCAA GGGCAGCTCT TCTTGGGAGA AGCCAAAAAT TCAGCATGTC 1068
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ysLeuThrLy sAlaValSer AlaSerSerV alProSerAs nIleHisLeu 406

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PheThrLeuG lnAlaSerPh eProLeuAsn AlaSerPheG lnAspSerGl 473

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LysMetGluP roHisAspIl eStop

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ACCTGCCCCT GCATTTCAGT GGGATGTCAA TACACTTGAC CCCAAGTCCC *126
CCGGCCCTGC CTGGTGTCAC TGTGGCCAAA CAGTGCCCAG CTTAAGCATC *176
CCTGGCATCA GACTATGGCC TTCAAGAGCA CTAGGGCATA TGCTTTTGGC *226
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CTTAGTTTCT TTGGGGAGGA CAGGGCTGTA GCTGTGAGGT CTTGTCTCCA *476

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