



TREX1 (NM_033629.6) - cDNA + Protein - 2026-10-17

ACTTCCCGCC ACTGCTGCCA GCGAGAGCCG CGGGAGAGTG TGCAGCCGAG -57

TCACTACTGC CTGCCTGCCT GCCTGCTACG GCTCAGCAGC AGGTACGTAC -7

CCAACCATGG GCTCGCAGGC CCTGCCCCCG GGGCCCATGC AGACCCTCAT 44

MetG lySerGlnAl aLeuProPro GlyProMetG lnThrLeuIl 15

CTTTTTCGAC ATGGAGGCCA CTGGCTTGCC CTTCTCCCAG CCCAAGGTCA 94

ePhePheAsp MetGluAlaT hrGlyLeuPr oPheSerGln ProLysValT 32

CGGAGCTGTG CCTGCTGGCT GTCCACAGAT GTGCCCTGGA GAGCCCCCCC 144

hrGluLeuCy sLeuLeuAla ValHisArgC ysAlaLeuGl uSerProPro 48

ACCTCTCAGG GGCCACCTCC CACAGTTCCT CCACCACCGC GTGTGGTAGA 194

ThrSerGlnG lyProProPr oThrValPro ProProProA rgValValAs 65

CAAGCTCTCC CTGTGTGTGG CTCCGGGGAA GGCCTGCAGC CCTGCAGCCA 244

pLysLeuSer LeuCysValA laProGlyLy sAlaCysSer ProAlaAlaS 82

GCGAGATCAC AGGTCTGAGC ACAGCTGTGC TGGCAGCGCA TGGGCGTCAA 294

erGluIleTh rGlyLeuSer ThrAlaValL euAlaAlaHi sGlyArgGln 98

TGTTTTGATG ACAACCTGGC CAACCTGCTC CTAGCCTTCC TCGGGCGCCA 344

CysPheAspA spAsnLeuAl aAsnLeuLeu LeuAlaPheL euArgArgGl 115

GCCACAGCCC TGGTGCCTGG TGGCACACAA TGGTGACCGC TACGACTTCC 394
nProGlnPro TrpCysLeuV aAlaHisAs nGlyAspArg TyrAspPheP 132

CCCTGCTCCA AGCAGAGCTG GCTATGCTGG GCCTCACCAG TGCTCTGGAT 444
roLeuLeuGl nAlaGluLeu AlaMetLeuG lyLeuThrSe rAlaLeuAsp 148

GGTGCCTTCT GTGTGGATAG CATCACTGCG CTGAAGGCCC TGGAGCGAGC 494
GlyAlaPheC ysValAspSe rIleThrAla LeuLysAlaL euGluArgAl 165

AAGCAGCCCC TCAGAACACG GCCCAAGGAA GAGCTATAGC CTAGGCAGCA 544
aSerSerPro SerGluHisG lyProArgLy sSerTyrSer LeuGlySerI 182

TCTACACTCG CCTGTATGGG CAGTCCCCTC CAGACTCGCA CACGGCTGAG 594
leTyrThrAr gLeuTyrGly GlnSerProP roAspSerHi sThrAlaGlu 198

GGTGATGTCC TGGCCCTGCT CAGCATCTGT CAGTGGAGAC CACAGGCCCT 644
GlyAspValL euAlaLeuLe uSerIleCys GlnTrpArgP roGlnAlaLe 215

GCTGCGGTGG GTGGATGCTC ACGCCAGGCC TTTCGGCACC ATCAGGCCCA 694
uLeuArgTrp ValAspAlaH isAlaArgPr oPheGlyThr IleArgProM 232

TGTATGGGGT CACAGCCTCT GCTAGGACCA AGCCAAGACC ATCTGCTGTC 744
etTyrGlyVa lThrAlaSer AlaArgThrL ysProArgPr oSerAlaVal 248

ACAACCACTG CACACCTGGC CACAACCAGG AACACTAGTC CCAGCCTTGG 794
ThrThrThrA laHisLeuAl aThrThrArg AsnThrSerP roSerLeuGl 265

AGAGAGCAGG GGTACCAAGG ATCTTCCTCC AGTGAAGGAC CCTGGAGCCC 844

yGluSerArg GlyThrLysA spLeuProPr oValLysAsp ProGlyAlaL 282

TATCCAGGGA GGGGCTGCTG GCCCCACTGG GTCTGCTGGC CATCCTGACC 894

euSerArgGl uGlyLeuLeu AlaProLeuG lyLeuLeuAl aIleLeuThr 298

TTGGCAGTAG CCACACTGTA TGGACTATCC CTGGCCACAC CTGGGGAGTA 944

LeuAlaValA laThrLeuTy rGlyLeuSer LeuAlaThrP roGlyGluSt 315

GGCCAAGAAG GAAAATCTGA CGAATAAAGA CCCCCGCTGC CCCATA

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