



TBXAS1 (NM_001061.7) - cDNA + Protein - 2026-04-29

ACTCCATGTG ATGTTTGCTT GGTTCCTGT TCCCTTTTCT ACCTGCAGAG -78

CACGGTTCCC ATAAGGGCGG CGAGATCAGC CTCCTGTCTC ATCTGGAAGA -28

CCACCACTCT GGGGTCTCAG AGGAATGATG GAAGCCTTGG GGTTCCTAAA 23

Met GluAlaLeuG lyPheLeuLy 8

ATTGGAAGTG AATGGCCCCA TGGTGACGGT GGCCCTGTCA GTGGCTCTCT 73

sLeuGluVal AsnGlyProM etValThrVa lAlaLeuSer ValAlaLeuL 25

TGGCCCTCCT GAAATGGTAC TCCACATCAG CATTCTCAAG ACTGGAGAAG 123

euAlaLeuLe uLysTrpTyr SerThrSerA laPheSerAr gLeuGluLys 41

TTAGGCCTCA GACATCCCAA GCCTTCTCCT TTCATTGGAA ACTTGACATT 173

LeuGlyLeuA rgHisProLy sProSerPro PheIleGlyA snLeuThrPh 58

TTTCCGCCAG GGTTTTTGGG AAAGCCAAAT GGAGCTCAGA AAGCTGTATG 223 [R60Pfs*33](#) [R71Efs*25](#)

ePheArgGln GlyPheTrpG luSerGlnMe tGluLeuArg LysLeuTyrG 75

GACCTCTGTG TGGGTACTAT CTTGGTCGTC GGATGTTTAT TGTTATTTCT 273 [p.L77Cfs*19](#)

lyProLeuCy sGlyTyrTyr LeuGlyArgA rgMetPheIl eValIleSer 91

GAGCCAGACA TGATCAAGCA GGTGTTGGTT GAGAACTTCA GTAACCTTAC 323

GluProAspM etIleLysGl nValLeuVal GluAsnPheS erAsnPheTh 108

CAACAGAATG GCGTCGGGTT TGGAGTTCAA GTCGGTAGCC GACAGCGTTC 373
rAsnArgMet AlaSerGlyL euGluPheLy sSerValAla AspSerValL 125

TGTTTTTACG TGACAAAAGA TGGGAAGAGG TCAGAGGTGC CCTGATGTCT 423
euPheLeuAr gAspLysArg TrpGluGluV alArgGlyAl aLeuMetSer 141

GCTTTCAGTC CTGAAAAGCT GAACGAGATG GTTCCCCTCA TCAGCCAAGC 473
AlaPheSerP roGluLysLe uAsnGluMet ValProLeuI leSerGlnAl 158

CTGCGACCTT CTCCTGGCTC ATTTAAAACG CTATGCGGAA TCTGGGGACG 523
aCysAspLeu LeuLeuAlaH isLeuLysAr gTyrAlaGlu SerGlyAspA 175

CATTTGACAT CCAGAGGTGC TACTGCAATT ACACCACAGA TGTGGTTGCC 573
laPheAspIl eGlnArgCys TyrCysAsnT yrThrThrAs pValValAla 191

AGCGTCGCCT TTGGCACCCC GGTGGACTCC TGGCAGGCCC CTGAGGATCC 623
SerValAlaP heGlyThrPr oValAspSer TrpGlnAlaP roGluAspPr 208

CTTTGTGAAA CACTGCAAGC GTTTCTTCGA ATTCTGCATC CCCAGACCTA 673
oPheValLys HisCysLysA rgPhePheGl uPheCysIle ProArgProI 225

TCCTGGTTTT ACTCTTATCA TTTCCATCCA TAATGGTCCC ACTGGCCCGG 723
leLeuValLe uLeuLeuSer PheProSerI leMetValPr oLeuAlaArg 241

ATTTTGCCCA ATAAGAACCG AGACGAACTG AATGGCTTTT TTAACAAACT 773
IleLeuProA snLysAsnAr gAspGluLeu AsnGlyPheP heAsnLysLe 258

CATTAGGAAT GTGATTGCCT TGCGGGACCA GCAAGCTGCC GAAGAGAGGC 823
uIleArgAsn ValIleAlaL euArgAspGl nGlnAlaAla GluGluArgA 275

GGAGAGACTT CCTCCAAATG GTCCTGGATG CCCGACATTC TGCAAGTCCC 873
rgArgAspPh eLeuGlnMet ValLeuAspA laArgHisSe rAlaSerPro 291

ATGGGCGTGC AAGACTTTGA CATCGTCAGA GACGTTTTCT CCTCTACTGG 923
MetGlyValG lnAspPheAs pIleValArg AspValPheS erSerThrGl 308

GTGCAAGCCG AACCCCTCCC GGCAACACCA GCCCAGCCCT ATGGCCAGGC 973
yCysLysPro AsnProSerA rgGlnHisGl nProSerPro MetAlaArgP 325

CTTTGACTGT GGATGAGATT GTGGGCCAGG CCTTCATCTT CCTCATCGCT 1023
roLeuThrVa lAspGluIle ValGlyGlnA laPheIlePh eLeuIleAla 341

GGCTATGAAA TCATCACCAA CACACTTTCT TTTGCCACCT ACCTACTGGC 1073
GlyTyrGluI leIleThrAs nThrLeuSer PheAlaThrT yrLeuLeuAl 358

CACCAACCCT GACTGCCAAG AGAAGCTTCT GAGAGAGGTA GACGTTTTTA 1123
aThrAsnPro AspCysGlnG luLysLeuLe uArgGluVal AspValPheL 375

AGGAGAAACA CATGGCCCCCT GAGTTCTGCA GCCTCGAGGA AGGCCTGCCC 1173
ysGluLysHi sMetAlaPro GluPheCysS erLeuGluGl uGlyLeuPro 391

TATCTGGACA TGGTGATTGC AGAGACGCTG AGGATGTACC CGCCAGCTTT 1223
TyrLeuAspM etValIleAl aGluThrLeu ArgMetTyrP roProAlaPh 408

CAGATTCACA CGGGAGGCAG CTCAGGACTG CGAGGTGCTG GGGCAGCGCA 1273

eArgPheThr ArgGluAlaA laGlnAspCy sGluValLeu GlyGlnArgI 425

TCCCCGCAGG CGCTGTGCTA GAGATGGCCG TGGGTGCCCT GCACCATGAC 1323
leProAlaGl yAlaValLeu GluMetAlaV alGlyAlaLe uHisHisAsp 441

CCTGAGCACT GGCCAAGCCC GGAGACCTTC AACCCTGAAA GGTTCACGGC 1373
ProGluHist rpProSerPr oGluThrPhe AsnProGluA rgPheThrAl 458

TGAGGCCCGG CAGCAGCACC GGCCCTTCAC GTACCTGCCC TTCGGGGCCG 1423
aGluAlaArg GlnGlnHisA rgProPheTh rTyrLeuPro PheGlyAlaG 475

GCCCACGGAG CTGCCTCGGG GTGCGTCTAG GGCTGCTTGA GGTCAAGTTG 1473
lyProArgSe rCysLeuGly ValArgLeuG lyLeuLeuGl uValLysLeu 491

ACACTGCTCC ACGTGCTGCA CAAGTTCGGG TTCCAAGCCT GCCCTGAGAC 1523
ThrLeuLeuH isValLeuHi sLysPheArg PheGlnAlaC ysProGluTh 508

CCAGGTACCG CTGCAGCTAG AATCCAAATC TGCCCTAGGT CCAAAAAATG 1573
rGlnValPro LeuGlnLeuG luSerLysSe rAlaLeuGly ProLysAsnG 525

GTGTCTATAT CAAGATCGTA TCCCGCTGAC ACAGAAGGCT GCCGGGTGGG *21
lyValTyrIl eLysIleVal SerArgStop

GGGAGGGCAC CCCCAAATC AAAGAAAACC CTAAGTGTGG ATGTTTCAGAA *71
TTTTTGAAAA ATGTCACTGA AGTGATTGAA AGAGTGCCTG GCATGCAAGG *121
ATAAGAGGTT CTTTACATAA CATTTCCTAA ATGCTTAATA AACGTTTGTT *171
GCACCTGGTT TTGACATTGC CAA

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