TBXAS1 (NM_001061.7) - cDNA + Protein - 2026-06-20

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ACTCCATGTG ATGTTTGCTT GGTTGCCTGT TCCCTTTTCT ACCTGCAGAG -78
CACGGTTCCC ATAAGGGCGG CGAGATCAGC CTCCTGTCTC ATCTGGAAGA -28
CCACCACTCT GGGGTCTCAG AGGAATGATG GAAGCCTTGG GGTTTCTAAA 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 GTAACTTTAC 323
GluProAspM etIleLysGl nValLeuVal GluAsnPheS erAsnPheTh 108
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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
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uIleArgAsn ValIleAlaL euArgAspGl nGlnAlaAla GluGluArgA 275

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

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MetGlyValG lnAspPheAs pIleValArg AspValPheS erSerThrGl 308

GTGCAAGCCG AACCCTTCCC 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 CATGGCCCCT 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
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eArgPheThr ArgGluAlaA laGlnAspCy sGluValLeu GlyGlnArgI 425

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

CCTGAGCACT GGCCAAGCCC GGAGACCTTC AACCCTGAAA GGTTCACGGC 1373 P448L
ProGluHisT rpProSerPr oGluThrPhe AsnProGluA rgPheThrAl 458

TGAGGCCCGG CAGCAGCACC GGCCCTTCAC GTACCTGCCC TTCGGGGCCG 1423 G473W
aGluAlaArg GlnGlnHisA rgProPheTh rTyrLeuPro PheGlyAlaG 475

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

ACACTGCTCC ACGTGCTGCA CAAGTTCCGG 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 CCCCAAATTC AAAGAAAACC CTAAGTGTGG ATGTTCAGAA *71
TTTTGGAAAA ATGTCACTGA AGTGATTGAA AGAGTGCCTG GCATGCAAGG *121
ATAAGAGGTT CTTTACATAA CATTTCCTAA ATGCTTAATA AACGTTTGTT *171
GCACTTGGTT TTGACATTGC CAA
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