TRNT1 (NM_182916.3) - cDNA + Protein - 2026-03-03

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AGCCCGGAAG TGCGCGTGGC GGCGGTGGCG GCTGCGGCAA CAGCGGGGCC -29
GATGTGTAGT TGGTGACTGC CTCTCCAGAT GCTGAGGTGC CTGTATCATT 22
                              Me tLeuArgCys LeuTyrHisT 8

GGCACAGGCC AGTGCTGAAC CGTAGGTGGA GTAGGCTGTG CCTTCCGAAG 72
rpHisArgPr oValLeuAsn ArgArgTrpS erArgLeuCy sLeuProLys 24

CAGTATCTAT TCACAATGAA GTTGCAGTCT CCCGAATTCC AGTCACTTTT 122   M30V
GlnTyrLeuP heThrMetLy sLeuGlnSer ProGluPheG lnSerLeuPh 41

CACAGAAGGA CTGAAGAGTC TGACAGAATT ATTTGTCAAA GAGAATCACG 172   c.126_128delAGA  T49*
eThrGluGly LeuLysSerL euThrGluLe uPheValLys GluAsnHisG 58

AATTAAGAAT AGCAGGAGGA GCAGTGAGGG ATTTATTAAA TGGAGTAAAG 222
luLeuArgIl eAlaGlyGly AlaValArgA spLeuLeuAs nGlyValLys 74

CCTCAGGATA TAGATTTTGC CACCACTGCT ACCCCTACTC AAATGAAGGA 272   T82S  P86S
ProGlnAspI leAspPheAl aThrThrAla ThrProThrG lnMetLysGl 91

GATGTTTCAG TCGGCTGGGA TTCGGATGAT AAACAACAGA GGAGAAAAGC 322   R99W  p.I101T
uMetPheGln SerAlaGlyI leArgMetIl eAsnAsnArg GlyGluLysH 108
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ACGGAACAAT TACTGCCAGG CTTCATGAAG AAAATTTTGA GATTACTACA 372  p.(Thr110Ile) p.E121K E121D
isGlyThrIl eThrAlaArg LeuHisGluG luAsnPheGl uIleThrThr 124

CTACGGATTG ATGTCACCAC TGATGGAAGA CATGCTGAGG TAGAATTTAC 422  D128G p.A136G
LeuArgIleA spValThrTh rAspGlyArg HisAlaGluV alGluPheTh 141

AACTGACTGG CAGAAAGATG CGGAACGCAG AGATCTCACT ATAAATTCTA 472  A148V R150C T154L I155T M158V
rThrAspTrp GlnLysAspA laGluArgAr gAspLeuThr IleAsnSerM 158

TGTTTTTAGG TTTTGATGGC ACTTTATTTG ACTACTTTAA TGGTTATGAA 522  p.(D163V) L166S F167Tfs*9 Y173F
etPheLeuGl yPheAspGly ThrLeuPheA spTyrPheAs nGlyTyrGlu 174

GATTTAAAAA ATAAGAAAGT TAGATTTGTT GGACATGCTA AACAGAGAAT 572  p.Leu176X R190I
AspLeuLysA snLysLysVa lArgPheVal GlyHisAlaL ysGlnArgIl 191

ACAAGAGGAT TATCTTAGAA TTTTAAGATA CTTCAGGTTT TATGGGAGAA 622  Q192* R203K
eGlnGluAsp TyrLeuArgI leLeuArgTy rPheArgPhe TyrGlyArgI 208

TTGTAGACAA ACCTGGTGAC CATGATCCTG AGACTTTGGA AGCAATTGCA 672  p.H215A I223T
leValAspLy sProGlyAsp HisAspProG luThrLeuGl uAlaIleAla 224

GAAAATGCAA AAGGCTTGGC TGGAATATCA GGAGAAAGGA TTTGGGTGGA 722
GluAsnAlaL ysGlyLeuAl aGlyIleSer GlyGluArgI leTrpValGl 241

ACTGAAAAAA ATTCTTGTTG GTAACCATGT AAATCATTTG ATTCACCTTA 772
uLeuLysLys IleLeuValG lyAsnHisVa lAsnHisLeu IleHisLeuI 258

TCTATGATCT TGATGTGGCT CCTTATATAG GTTTACCTGC TAATGCAAGT 822
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leTyrAspLe uAspValAla ProTyrIleG lyLeuProAl aAsnAlaSer 274

TTAGAAGAAT TTGACAAAGT CAGTAAAAAT GTTGATGGTT TTTCACCAAA 872  E77X
LeuGluGluP heAspLysVa lSerLysAsn ValAspGlyP heSerProLy 291

GCCAGTGACT CTTTTGGCCT CATTATTCAA AGTACAAGAT GATGTCACAA 922  p.D305V
sProValThr LeuLeuAlaS erLeuPheLy sValGlnAsp AspValThrL 308

AATTGGATTT GAGGTTGAAG ATCGCAAAAG AGGAGAAAAA CCTTGGCTTA 972  p.Leu313Ser A316V p.(Glu318Argfs*11) c.948–949delAAinsGG
ysLeuAspLe uArgLeuLys IleAlaLysG luGluLysAs nLeuGlyLeu 324

TTTATAGTTA AAAATAGGAA AGATTTAATT AAAGCAACAG ATAGTTCAGA 1022 I326T
PheIleValL ysAsnArgLy sAspLeuIle LysAlaThrA spSerSerAs 341

CCCATTGAAA CCCTATCAAG ACTTCATTAT AGATTCTAGG GAACCTGATG 1072 D348V c.1054_1056+10del
pProLeuLys ProTyrGlnA spPheIleIl eAspSerArg GluProAspA 358

CAACTACTCG TGTATGTGAA CTACTGAAGT ACCAAGGAGA GCACTGTCTC 1122 p.E364D
laThrThrAr gValCysGlu LeuLeuLysT yrGlnGlyGl uHisCysLeu 374

CTAAAGGAAA TGCAGCAGTG GTCCATTCCT CCATTTCCTG TAAGTGGCCA 1172 W381* p.G390S
LeuLysGluM etGlnGlnTr pSerIlePro ProPheProV alSerGlyHi 391

TGACATCAGA AAAGTGGGCA TTTCTTCAGG AAAAGAAATT GGGGCTCTAT 1222 G405R
sAspIleArg LysValGlyI leSerSerGl yLysGluIle GlyAlaLeuL 408

TACAACAGTT GCGAGAACAG TGGAAAAAAA GTGGTTACCA AATGGAAAAA 1272 p.R412* K416E S418fs c.1246del
euGlnGlnLe uArgGluGln TrpLysLysS erGlyTyrGl nMetGluLys 424
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GATGAACTTC TGAGTTACAT AAAGAAGACC TAAAACTGAT GGCTACTAAA *17
AspGluLeuL euSerTyrIl eLysLysThr Stop

AAGCAGAGCA TTTCTGGTAA GACTAAATTT TCTCCCCTCC CTCTTAATGA *67
GGTTTTAGAG ACTACACCAG AATAAAAGAC AGTTTAGGGG ACCTCTGTAG *117
AACAACAAGG GTCTTATTTT GTGAATTATA TATTTCAAGA ACTAAACAGA *167
GATCCACCTT TCTGGATCTG ATTTATATCA CTGAAATGTA CAGTTCTTTT *217
GGAATAGTTT CACCTGAGAA AACATAGTTG GCTATTATCT ATCTTAACCT *267
GTTCAGGCTT TTAAAAAAAA CTGTTTTTGC ATAGGGTAGT ACTAAGATCT *317
TAAAAAGTGG TAACTGTCTT GAAGAAAAAA CGTTTATTGT TTGTTTGCAA *367
TTGAAATAAC AGGGTTACCT TAACAATGAC TGTCTATGAT GTGTCAGTTC *417
TTATCTGAAT TCCAAAATAA ACCTGTGCTT AAAAAAGAAA TAATTGACCA *467
AGTAAGTTTG CATAAAATGT GAATACTAAA TGTGTCCCCA GTTGCTGGCA *517
TTCATATGTA CAGGATTTGT TCTAGCAAGC TATGCTTCAG TATGTGGTTG *567
ATATTTTTCT GTCACAATGA TTTCTTTATG CATGCAGAGC CTGGGGAAGT *617
CATGGGATTA ACTTGAGGGT CACTATTGAG CCTATTAATT AATTATTGTT *667
TTAATAAAAC AAACATTGGT ATTGGAAGAT AAATATGTTT ATGTGGTATC *717
TGACAATGTG TATTAGGTGT CATATACAAT GGTAATATGC CTGTCTTTAA *767
AGTGTTATTT TATTAATTAA AAGGATATGG CTATTATTAT ATATTCTCTA *817
AAGATTTGAG TCCTAAATGC TTTCATCAGG TAAATAAAAT GTATAATACA *867
AA
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