



TRNT1 (NM_182916.3) - cDNA + Protein - 2026-05-25

AGCCCGGAAG TGC GCGTGGC GCGGTGGCG GCTGCGGCAA CAGCGGGGCC -29
GATGTGTAGT TGGT GACTGC 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 M30Y
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 CACCCTGCT ACCCCTACTC AAATGAAGGA 272 T82S P86S
ProGlnAspI leAspPheAl aThrThrAla ThrProThrG lnMetLysGl 91

GATGTTTCAG TCGGCTGGGA TTGGGATGAT AAACAACAGA GGAGAAAAGC 322 R99W p.I101T
uMetPheGln SerAlaGlyI leArgMetIl eAsnAsnArg GlyGluLysH 108

ACGGAACAAT TACTGCCAGG CTTTCATGAAG AAAATTTTGA GATTACTACA 372 [p.\(Thr110Ile\)](#) [p.E121K](#) [E121D](#)
 isGlyThrI1 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

GATTIAAAAA ATAAGAAAGT TAGATTTGTT GGACATGCTA AACAGAGAAT 572 [p.Leu176X](#) [R190I](#)
 AspLeuLysA snLysLysVa lArgPheVal GlyHisAlaL ysGlnArgI1 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

ACTGAAAAA ATTCTTGTTG GTAACCATGT AAATCATTG ATTCACCTTA 772
 uLeuLysLys IleLeuValG lyAsnHisVa lAsnHisLeu IleHisLeuI 258

TCTATGATCT TGATGTGGCT CCTTATATAG GTTTACCTGC TAATGCAAGT 822

leTyrAspLe uAspValAla ProTyrIleG lyLeuProAl aAsnAlaSer 274

TTAGAA~~G~~AAT TTGACAAAGT CAGTAAAAAT GTTGATGGTT TTTCACCAAA 872 ~~E77X~~

LeuGluGluP heAspLysVa lSerLysAsn ValAspGlyP heSerProLy 291

GCCAGTGA~~C~~CT CTTTTGGCCT CATTATTCAA AGTACAAGAT ~~G~~ATGTCACAA 922 ~~p.D305V~~

sProValThr LeuLeuAlaS erLeuPheLy sValGlnAsp AspValThrL 308

AATTGGATTT GAGGT~~T~~GAAG ATCG~~C~~AAAAG AGGAGAAAAA CCTTGGCTTA 972 ~~p.Leu313Ser A316V p.(Glu318Argfs*11) c.948-949delAAinsGG~~

ysLeuAspLe uArgLeuLys ileAlaLysG luGluLysAs nLeuGlyLeu 324

TTTA~~T~~AGTTA AAAATAGGAA AGATTTAATT AAAGCAACAG ATAGTTCAGA 1022 ~~I326T~~

PheIleValL ysAsnArgLy sAspLeuIle LysAlaThrA spSerSerAs 341

CCCATTGAAA CCCTATCAAG ~~A~~CTTCATTAT ~~A~~GATTCCTAGG GAACCTGATG 1072 ~~D348V c.1054 1056+10del~~

pProLeuLys ProTyrGlnA spPheIleIl eAspSerArg GluProAspA 358

CAACTACTCG TGTATGTGA~~A~~ C~~T~~ACTGAAGT ACCAAGGAGA GCACTGTCTC 1122 ~~p.E364D~~

laThrThrAr gValCysGlu LeuLeuLysT yrGlnGlyGl uHisCysLeu 374

CTAAAGGAAA TGCAGCAGT~~G~~ GTCCATTCCT CCATTCCTG TAAGT~~G~~GCCA 1172 ~~W381* p.G390S~~

LeuLysGluM etGlnGlnTr pSerIlePro ProPheProV alSerGlyHi 391

TGACATCAGA AAAGTGGGCA TTTCTTCAGG AAAAGAAATT ~~G~~GGGCTCTAT 1222 ~~G405R~~

sAspIleArg LysValGlyI leSerSerGl yLysGluIle GlyAlaLeuL 408

TACAACAGTT ~~G~~C~~G~~GAGAACAG TGG~~A~~AAAAAA GTGGTTACCA AATGGAAAAA 1272 ~~p.R412* K416E S418fs c.1246del~~

euGlnGlnLe uArgGluGln TrpLysLysS erGlyTyrGl nMetGluLys 424

GATGAACTTC TGAGTTACAT AAAGAAGACC TAAACTGAT GGCTACTAAA *17

AspGluLeuL euSerTyrIl eLysLysThr Stop

AAGCAGAGCA TTTCTGGTAA GACTAAATTT TCTCCCCTCC CTCTTAATGA *67
GGTTTTAGAG ACTACACCAG AATAAAAGAC AGTTTAGGGG ACCTCTGTAG *117
ACAACAAGG GTCCTATTTT GTGAATTATA TATTTCAAGA ACTAAACAGA *167
GATCCACCTT TCTGGATCTG ATTTATATCA CTGAAATGTA CAGTTCTTTT *217
GGAATAGTTT CACCTGAGAA AACATAGTTG GCTATTATCT ATCTTAACCT *267
G TTCAGGCTT TTAATAAAAA 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
TTAATAAAC AACATTGGT ATTGGAAGAT AAATATGTTT ATGTGGTATC *717
TGACAATGTG TATTAGGTGT CATATACAAT GGTAATATGC CTGTCTTTAA *767
AGTGTTATTT TATTAATTAA AAGGATATGG CTATTATTAT ATATTCTCTA *817
AAGATTTGAG TCCTAAATGC TTTTCATCAGG TAAATAAAAT GTATAATACA *867

AA

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