



TRNT1 (NM_182916.3) - cDNA + Protein - 2024-12-22

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 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 CACCCTGCT ACCCCTACTC AAATGAAGGA 272 T82S P86S
ProGlnAspI leAspPheAl aThrThrAla ThrProThrG lnMetLysGl 91

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

ACGGAACAAT TACTGCCAGG CTTTCATGAAG AAAATTTTGA GATTACTACA 372 E121D
isGlyThrIle ThrAlaArg LeuHisGluG luAsnPheGlu IleThrThr 124

CTACGGATTG ATGTCACCAC TGATGGAAGA CATGCTGAGG TAGAATTTAC 422 D128G
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 L166S F167Tfs*9 Y173F
etPheLeuGlu yPheAspGly ThrLeuPheA spTyrPheAs nGlyTyrGlu 174

GATTTAAAAA ATAAGAAAGT TAGATTTGTT GGACATGCTA AACAGGAAT 572 p.Leu176X R190I
AspLeuLysA snLysLysVa lArgPheVal GlyHisAlaL ysGlnArgIle 191

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

TTGTAGACAA ACCTGGTGAC CATGATCCTG AGACTTTGGA AGCAATGTGCA 672 I223T
leValAspLy sProGlyAsp HisAspProG luThrLeuGlu uAlaIleAla 224

GAAAATGCAA AAGGCTTGGC TGGAATATCA GGAGAAAGGA TTTGGGTGGA 722
GluAsnAlaL ysGlyLeuAl aGlyIleSer GlyGluArgI leTrpValGlu 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

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LeuGluGluP heAspLysVa lSerLysAsn ValAspGlyP heSerProLy 291

GCCAGTGACT CTTTTGGCCT CATTATTCAA AGTACAAGAT GATGTCACAA 922

sProValThr LeuLeuAlaS erLeuPheLy sValGlnAsp AspValThrL 308

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ysLeuAspLe uArgLeuLys ileAlaLysG luGluLysAs nLeuGlyLeu 324

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PheIleValL ysAsnArgLy sAspLeuIle LysAlaThrA spSerSerAs 341

CCCATTGAAA CCCTATCAAG ACTTCATTAT AGATTCCTAGG GAACCTGATG 1072 D348V c.1054_1056+10del

pProLeuLys ProTyrGlnA spPheIleIl eAspSerArg GluProAspA 358

CAACTACTCG TGTATGTGAA CTACTGAAGT ACCAAGGAGA GCACTGTCTC 1122

laThrThrAr gValCysGlu LeuLeuLysT yrGlnGlyGl uHisCysLeu 374

CTAAAGGAAA TGCAGCAGTG GTCCATTCCCT CCATTTCCCTG TAAGTGGCCA 1172 W381*

LeuLysGluM etGlnGlnTr pSerIlePro ProPheProV alSerGlyHi 391

TGACATCAGA AAAGTGGGCA TTTCTTCAGG AAAAGAAATT GGGGCTCTAT 1222 G405R

sAspIleArg LysValGlyI leSerSerGl yLysGluIle GlyAlaLeuL 408

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euGlnGlnLe uArgGluGln TrpLysLysS erGlyTyrGl nMetGluLys 424

GATGAACTTC TGAGTTACAT AAAGAAGACC TAAACTGAT GGCTACTAAA *17

AspGluLeuL euSerTyrIl eLysLysThr Stop

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GGTTTTAGAG ACTACACCAG AATAAAAGAC AGTTTAGGGG ACCTCTGTAG *117

AACAACAAGG GTCCTATTTT GTGAATTATA TATTTCAAGA ACTAAACAGA *167

GATCCACCTT TCTGGATCTG ATTTATATCA CTGAAATGTA CAGTCTTTT *217

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G TTCAGGCTT TTAATAAAAA CTGTTTTTGC ATAGGGTAGT ACTAAGATCT *317

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TTGAAATAAC AGGGTTACCT TAACAATGAC TGTCTATGAT GTGTCAGTTC *417

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AGTAAGTTTG CATAAAATGT GAATACTAAA TGTGTCCCCA GTTGCTGGCA *517

TTCATATGTA CAGGATTTGT TCTAGCAAGC TATGCTTCAG TATGTGGTTG *567

ATATTTTTCT GTCACAATGA TTTCTTTATG CATGCAGAGC CTGGGGAAGT *617

CATGGGATTA ACTTGAGGGT CACTATTGAG CCTATTAATT AATTATTGTT *667

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AGTGTTATTT TATTAATTAA AAGGATATGG CTATTATTAT ATATTCTCTA *817

AAGATTTGAG TCCTAAATGC TTTCATCAGG TAAATAAAAT GTATAATACA *867

AA

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