



## TRNT1 (NM\_182916.3) - cDNA + Protein - 2024-05-19

AGCCCGGAAG TGC GCGTGGC GGC GGTGGCG GCTGCGGCAA CAGCGGGGCC -29

GATGTGTAGT TGGTGA CTCTCCAGAT GCTGAGGTGC CTGTATCATT 22

Me tLeuArgCys LeuTyrHisT 8

GGCACAGGCC AGTGCTGAAC CGTAGGTGGA GTAGGCTGTG CCTTCCGAAG 72

rpHisArgPr oValLeuAsn ArgArgTrpS erArgLeuCy sLeuProLys 24

CAGTATCTAT TCACAATGAA GTTGCACTCT CCCGAATTCC AGTCACTTTT 122 M30V

GlnTyrLeuP heThrMetLy sLeuGlnSer ProGluPheG lnSerLeuPh 41

CACAGAGGA CTGAAGAGTC TGACAGAATT ATTTGTCAAA GAGAATCAG 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

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 eThrAlaArg LeuHisGluGlu AsnPheGlu IleThrThr 124

CTACGGATTG ATGTCACCAC TGATGGAAGA CATGCTGAGG TAGAATTTAC 422 D128G  
 LeuArgIleAspValThrThrArgGlyArg HisAlaGluValAlaGluPheThr 141

AACTGACTGG CAGAAAGATG CGGAACGCAG AGATCTCACT ATAAATTCTA 472 A148V R150C T154L I155T M158V  
 rThrAspTrpGlnLysAspAlaGluArgArgAspLeuThrIleAsnSerMet 158

TGTTTTTAGG TTTTGATGGC ACTTTATTTG ACTACTTTAA TGGTTATGAA 522 L166S F167Tfs\*9 Y173F  
 etPheLeuGluPheAspGlyThrLeuPheAspTyrPheAsnGlyTyrGlu 174

GATTTAAAAA ATAAGAAAGT TAGATTTGTT GGACATGCTA AACAGAGAAT 572 p.Leu176X R190I  
 AspLeuLysAsnLysLysValArgPheValGlyHisAlaLysGlnArgIle 191

ACAAGAGGAT TATCTTAGAA TTTTAAGATA CTTCAGGTTT TATGGGAGAA 622 Q192\* R203K  
 eGlnGluAspTyrLeuArgIleLeuArgTyrPheArgPheTyrGlyArgIle 208

TTGTAGACAA ACCTGGTGAC CATGATCCTG AGACTTTGGA AGCAATTGCA 672 I223T  
 leValAspLysProGlyAspHisAspProGluThrLeuGluAlaIleAla 224

GAAAATGCAA AAGGCTTGGC TGGAATATCA GGAGAAAGGA TTTGGGTGGA 722  
 GluAsnAlaLysGlyLeuAlaGlyIleSerGlyGluArgIleTrpValGlu 241

ACTGAAAAAA ATTCTTGTTG GTAACCATGT AAATCATTTG ATTCACCTTA 772  
 uLeuLysLysIleLeuValGlyAsnHisValAsnHisLeuIleHisLeuIle 258

TCTATGATCT TGATGTGGCT CCTTATATAG GTTTACCTGC TAATGCAAGT 822

leTyrAspLe uAspValAla ProTyrIleG lyLeuProAl aAsnAlaSer 274

TTAGAAGAAT TTGACAAAGT CAGTAAAAAT GTTGATGGTT TTTCACCAAA 872 [E77X](#)

LeuGluGluP heAspLysVa lSerLysAsn ValAspGlyP heSerProLy 291

GCCAGTGA CT TTTGGCCT CATTATTCAA AGTACAAGAT GATGTCACAA 922

sProValThr LeuLeuAlaS erLeuPheLy sValGlnAsp AspValThrL 308

AATTGGATTT GAGGTIGAAG ATCGCAAAAG AGGAGAAAAA CCTTGGCTTA 972 [p.Leu313Ser](#) [A316V](#) [p.\(Glu318Argfs\\*11\)](#) [c.948-949delAAinsGG](#)

ysLeuAspLe uArgLeuLys IleAlaLysG luGluLysAs nLeuGlyLeu 324

TTTAIAGTTA 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 CTA CTACTGAAGT ACCAAGGAGA GCACTGTCTC 1122

laThrThrAr gValCysGlu LeuLeuLysT yrGlnGlyGl uHisCysLeu 374

CTAAAGGAAA TGCAGCAGTG GTCCATTCTCT CCATTCTCTG TAAGTGGCCA 1172 [W381\\*](#)

LeuLysGluM etGlnGlnTr pSerIlePro ProPheProV alSerGlyHi 391

TGACATCAGA AAAGTGGGCA TTTCTTCAGG AAAAGAAATT GGGGCTCTAT 1222 [G405R](#)

sAspIleArg LysValGlyI leSerSerGl yLysGluIle GlyAlaLeuL 408

TACAACAGTT GCGAGAACAG TGGAAAAAA GTGGTTACCA AATGGAAAAA 1272 [K416E](#) [S418fs](#) [c.1246del](#)

euGlnGlnLe uArgGluGln TrpLysLysS erGlyTyrGl nMetGluLys 424

GATGAAC TTC TGAGTTACAT AAAGAAGACC TAA AACTGAT 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  
G TTCAGGCTT TTA AAAAAAAA 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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