



TRNT1 (NM_182916.3) - cDNA - 2025-04-03

AGCCCGGAAG TGC GCGTGGC GCGGTGGCG GCTGCGGCAA CAGCGGGGCC -29
GATGTGTAGT TGGT GACTGC CTCTCCAGAT GCTGAGGTGC CTGTATCATT 22
GGCACAGGCC AGTGCTGAAC CGTAGGTGGA GTAGGCTGTG CCTTCCGAAG 72
CAGTATCTAT TCACAATGAA GTTGCAGTCT CCCGAATTCC AGTCACTTTT 122 M30V
CACAGAGGA CTGAAGAGTC TGACAGAATT ATTTGTCAAA GAGAATCACG 172 c.126_128delAGA T49*
AATTAAGAAT AGCAGGAGGA GCAGTGAGGG ATTTATTAAA TGGAGTAAAG 222
CCTCAGGATA TAGATTTTGC CACCACCTGCT ACCCCTACTC AAATGAAGGA 272 T82S P86S
GATGTTTCAG TCGGCTGGGA TTGGATGAT AAACAACAGA GGAGAAAAGC 322 R99W
ACGGAACAAT TACTGCCAGG CTTTCATGAAG AAAATTTTGA GATTACTACA 372 E121D
CTACGGATTG ATGTCACCAC TGATGGAAGA CATGCTGAGG TAGAATTTAC 422 D128G
AACTGACTGG CAGAAAGATG CGGAAACGAG AGATCTCACT ATAAATCTA 472 A148V R150C T154L I155T M158V
TGTTTTTAGG TTTTGATGGC ACTTTAATTTG ACTACTTTAA TGTTATGAA 522 L166S F167Tfs*9 Y173F
GATTTAAAA ATAAGAAAGT TAGATTTGTT GGACATGCTA AACAGAGAAT 572 p.Leu176X R190I
ACAAGAGGAT TATCTTAGAA TTTTAAGATA CTTCAAGTTT TATGGGAGAA 622 Q192* R203K
TTGTAGACAA ACCTGGTGAC CATGATCCTG AGACTTTGGA AGCAATGCA 672 I223T
GAAAATGCAA AAGGCTTGGC TGGAATATCA GGAGAAAGGA TTTGGGTGGA 722
ACTGAAAAA ATTC TTGTTG GTAACCATGT AAATCATTTG ATTCACCTTA 772
TCTATGATCT TGATGTGGCT CCTTATATAG GTTACCTGC TAATGCAAGT 822
TTAGAAGAAT TTGACAAAGT CAGTAAAAAT GTTGATGGTT TTCACCAA 872 E77X
GCCAGTGACT CTTTTGGCCT CATTATTCAA AGTACAAGAT GATGTCACAA 922
AATTGGATTT GAGGTGAAG ATCGCAAAG AGGAGAAAAA CCTTGGCTTA 972 p.Leu313Ser A316V p.(Glu318Argfs*11) c.948-949delAAinsGG
TTTATAGTTA AAAATAGGAA AGATTTAATT AAAGCAACAG ATAGTTCAGA 1022 I326T

CCCATTGAAA CCCTATCAAG ACTTCATTAT AGATTCTAGG GAACCTGATG 1072 D348V c.1054_1056+10del
CAACTACTCG TGTATGTGAA CTACTGAAGT ACCAAGGAGA GCACTGTCTC 1122
CTAAAGGAAA TGCAGCAGTG GTCCATTCCCT CCATTTCCCTG TAAGTGGCCA 1172 W381*
TGACATCAGA AAAGTGGGCA TTTCTTCAGG AAAAGAAATT GGGGCTCTAT 1222 G405R
TACAACAGTT GCGAGAACAG TGGAAAAAA GTGGTTACCA AATGGAAAAA 1272 K416E S418fs c.1246del
GATGAAC TTC TGAGTTACAT AAAGAAGACC TAAAACTGAT GGCTACTAAA *17
AAGCAGAGCA TTTCTGGTAA GACTAAATTT TCTCCCTCC CTCTTAATGA *67
GGTTTTAGAG ACTACACCAG AATAAAAGAC AGTTTAGGGG ACCTCTGTAG *117
AACAAACAAGG GTCCTATTTT GTGAATTATA TATTTCAAGA ACTAAACAGA *167
GATCCACCTT TCTGGATCTG ATTTATATCA CTGAAATGTA CAGTTCCTTT *217
GGAATAGTTT CACCTGAGAA AACATAGTTG GCTATTATCT ATCTTAACCT *267
GTTCAGGCTT 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
TTAATAAAAC AAACATTGGT ATTGGAAGAT AAATATGTTT ATGTGGTATC *717
TGACAATGTG TATTAGGTGT CATATACAAT GGTAATATGC CTGTCTTTAA *767
AGTGTATTTT TATTAATTA AAGGATATGG CTATTATTAT ATATTCTCTA *817
AAGATTTGAG TCCTAAATGC TTTTCATCAGG TAAATAAAAT GTATAATACA *867

AA

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