



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

AGCCCGGAAG TGCGCGTGGC GGCGGTGGCG GCTGCGGCAA CAGCGGGGCC -29
GATGTGTAGT TGGTGACTGC CTCTCCAGAT GCTGAGGTGC CTGTATCATT 22
GGCACAGGCC AGTGCTGAAC CGTAGGTGGA GTAGGCTGTG CCTTCCGAAG 72
CAGTATCTAT TCACAATGAA GTTGCAGTCT CCCGAATTCC AGTCACTTTT 122 M30V
CACAGAAGGA CTGAAGAGTC TGACAGAATT ATTTGTCAAA GAGAATCACG 172 c.126_128delAGA T49*
AATTAAGAAT AGCAGGAGGA GCAGTGAGGG ATTTATTAAA TGGAGTAAAG 222
CCTCAGGATA TAGATTTTGC CACCACTGCT ACCCCTACTC AAATGAAGGA 272 T82S P86S
GATGTTTCAG TCGGCTGGGA TTCGGATGAT AAACAACAGA GGAGAAAAGC 322 R99W p.I101T
ACGGAACAAT TACTGCCAGG CTTCATGAAG AAAATTTTGA GATTACTACA 372 p.(Thr110Ile) p.E121K E121D
CTACGGATTG ATGTCACCAC TGATGGAAGA CATGCTGAGG TAGAATTTAC 422 D128G p.A136G
AACTGACTGG CAGAAAGATG CGGAACGCAG AGATCTCACT ATAAATTCTA 472 A148V R150C T154L I155T M158V
TGTTTTTTAGG TTTTATGGC ACTTTATTTTG ACTACTTTAA TGGTATTGAA 522 p.(D163V) L166S F167Tfs*9 Y173F
GATTTAAAAA ATAAGAAAGT TAGATTTGTT GGACATGCTA AACAGAGAAT 572 p.Leu176X R190I
ACAAGAGGAT TATCTTAGAA TTTTAAGATA CTTCAGGTTT TATGGGAGAA 622 Q192* R203K
TTGTTAGACAA ACCTGGTGAC CATGTATCCTG AGACTTTTGGGA AGCAATTGCA 672 p.H215A I223T
GAAAATGCAA AAGCTTGGC TGGAATATCA GGAGAAAGGA TTTGGGTGGA 722
ACTGAAAAAA ATTCTTGTG GTAACCATGT AAATCATTTG ATTCACCTTA 772
TCTATGATCT TGATGTGGCT CCTTATATAG GTTTACCTGC TAATGCAAGT 822
TTTAGAACAAT TTGACAAAGT CAGTAAAAAT GTTGATGGTT TTTCACCAA 872 E77X
GCCAGTGACT CTTTTGGCCT CATTATTCAA AGTACAAGAT GATGTCACAA 922 p.D305V
AATTGGATTT GAGGTTGAAG ATCGCAAAAG AGGAGAAAA 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 p.E364D
CTAAAGGAAA TGCAGCAGTG GTCCATTCCCT CCATTTCCCTG TAAGTGGCCA 1172 W381* p.G390S
TGACATCAGA AAAGTGGGCA TTTCTTCAGG AAAAGAAATT GGGGCTCTAT 1222 G405R
TACAACAGTT GCGAGAACAG TGGAAAAAA GTGGTTACCA AATGGAAAA 1272 p.R412* K416E S418fs c.1246del
GATGAAC TTC TGAGTTACAT AAAGAAGACC TAAAACTGAT GGCTACTAAA *17
AAGCAGAGCA TTTCTGGTAA GACTAAATTT TCTCCCTCC CTCTTAATGA *67
GGTTTTAGAG ACTACACCAG AATAAAAGAC AGTTTAGGGG ACCTCTGTAG *117
AACAAACAAGG GTCATTATTT GTGAATTATA TATTTCAAGA ACTAAACAGA *167
GATCCACCTT TCTGGATCTG ATTTATATCA CTGAAATGTA CAGTTCCTTT *217
GGAATAGTTT CACCTGAGAA AACATAGTTG GCTATTATCT ATCTTAACCT *267
GTTTCAGGCTT 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
AGTGTTATTT TATTAATTAA AAGGATATGG CTATTATTAT ATATTCTCTA *817
AAGATTTGAG TCCTAAATGC TTTCATCAGG TAAATAAAAT GTATAATACA *867

AA

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