TNFRSF1A (NM_001065.4) - cDNA + Protein - 2026-06-29

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ACTCTTCCCC TCCCACCTTC TCTCCCCTCC TCTCTGCTTT AATTTTCTCA -213
GAATTCTCTG GACTGAGGCT CCAGTTCTGG CCTTTGGGGT TCAAGATCAC -163
TGGGACCAGG CCGTGATCTC TATGCCCGAG TCTCAACCCT CAACTGTCAC -113
CCCAAGGCAC TTGGGACGTC CTGGACAGAC CGAGTCCCGG GAAGCCCCAG -63
CACTGCCGCT GCCACACTGC CCTGAGCCCA AATGGGGGAG TGAGAGGCCA -13
TAGCTGTCTG GCATGGGCCT CTCCACCGTG CCTGACCTGC TGCTGCCACT 38   c.15C>T c.36A>G
             MetGlyLe uSerThrVal ProAspLeuL euLeuProLe 13

GGTGCTCCTG GAGCTGTTGG TGGGAATATA CCCCTCAGGG GTTATTGGAC 88   c.59T>C c.81T>C
uValLeuLeu GluLeuLeuV alGlyIleTy rProSerGly ValIleGlyL 30

TGGTCCCTCA CCTAGGGGAC AGGGAGAAGA GAGATAGTGT GTGTCCCCAA 138  D12E C15Y
euValProHi sLeuGlyAsp ArgGluLysA rgAspSerVa lCysProGln 46

GGAAAATATA TCCACCCTCA AAATAATTCG ATTTGCTGTA CCAAGTGCCA 188  K19I Y20H Y20D Y20C H22Y H22R H22Q N25D S27S I28S C29R C29G  C29F C29Y C29S C29W
C30R C30S C30Y C30F C33G C33Y
GlyLysTyrI leHisProGl nAsnAsnSer IleCysCysT hrLysCysHi 63

CAAAGGAACC TACTTGTACA ATGACTGTCC AGGCCCGGGG CAGGATACGG 238  G36E T37I Y38C Y38S L39F D42DEL D42E C43R C43G C43Y C43S C43F P46L G47G Q48H T50M
T50K
sLysGlyThr TyrLeuTyrA snAspCysPr oGlyProGly GlnAspThrA 80
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ACTGCAGGGA GTGTGAGAGC GGCTCCTTCA CCGCTTCAGA AAACCACCTC 288  C52R C52G C52F C52Y C52S C52W R53G E54E C55R C55S C55Y S57_E64del E56D G58S G58V
S59P F60L(264C>G) F60V F60S F60L(267A>G) T61P T61I T61N N65I N65K H66Y H66L H66P L67P
spCysArgGl uCysGluSer GlySerPheT hrAlaSerGl uAsnHisLeu 96

AGACACTGCC TCAGCTGCTC CAAATGCCGA AAGGAAATGG GTCAGGTGGA 338  H69fs C70R C70S C70G C70Y C73R C73Y C73W S74C C105Y Q82K p.Q111R V83L V83M_
ArgHisCysL euSerCysSe rLysCysArg LysGluMetG lyGlnValGl 113

GATCTCTTCT TGCACAGTGG ACCGGGACAC CGTGTGTGGC TGCAGGAAGA 388  S86P S116del C88R C88G C88Y C88S T89A R92W R92P R92Q R121_D122insARHR D93H D93E T94T
V95M C96R C96Y C96F C96W C98R C98Y C98F
uIleSerSer CysThrValA spArgAspTh rValCysGly CysArgLysA 130

ACCAGTACCG GCATTATTGG AGTGAAAACC TTTTCCAGTG CTTCAATTGC 438  N101K Y103_R104DEL R104W R104Q H105P Y106C E109A F112I F112L F112C F112S C114R C114W
N116S
snGlnTyrAr gHisTyrTrp SerGluAsnL euPheGlnCy sPheAsnCys 146

AGCCTCTGCC TCAATGGGAC CGTGCACCTC TCCTGCCAGG AGAAACAGAA 488  T124T V125M H126T K132R
SerLeuCysL euAsnGlyTh rValHisLeu SerCysGlnG luLysGlnAs 163

CACCGTGTGC ACCTGCCATG CAGGTTTCTT TCTAAGAGAA AACGAGTGTG 538  V136M
nThrValCys ThrCysHisA laGlyPhePh eLeuArgGlu AsnGluCysV 180

TCTCCTGTAG TAACTGTAAG AAAAGCCTGG AGTGCACGAA GTTGTGCCTA 588  K157K L167_G175del
alSerCysSe rAsnCysLys LysSerLeuG luCysThrLy sLeuCysLeu 196

CCCCAGATTG AGAATGTTAA GGGCACTGAG GACTCAGGCA CCACAGTGCT 638  I170N I170T V173D V173G G175C
ProGlnIleG luAsnValLy sGlyThrGlu AspSerGlyT hrThrValLe 213

GTTGCCCCTG GTCATTTTCT TTGGTCTTTG CCTTTTATCC CTCCTCTTCA 688  S197C S197S
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uLeuProLeu ValIlePheP heGlyLeuCy sLeuLeuSer LeuLeuPheI 230

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leGlyLeuMe tTyrArgTyr GlnArgTrpL ysSerLysLe uTyrSerIle 246

GTTTGTGGGA AATCGACACC TGAAAAAGAG GGGGAGCTTG AAGGAACTAC 788
ValCysGlyL ysSerThrPr oGluLysGlu GlyGluLeuG luGlyThrTh 263

TACTAAGCCC CTGGCCCCAA ACCCAAGCTT CAGTCCCACT CCAGGCTTCA 838
rThrLysPro LeuAlaProA snProSerPh eSerProThr ProGlyPheT 280

CCCCCACCCT GGGCTTCAGT CCCGTGCCCA GTTCCACCTT CACCTCCAGC 888  S261I  F264 T2269del
hrProThrLe uGlyPheSer ProValProS erSerThrPh eThrSerSer 296

TCCACCTATA CCCCCGGTGA CTGTCCCAAC TTTGCGGCTC CCCGCAGAGA 938  P272H  R283K
SerThrTyrT hrProGlyAs pCysProAsn PheAlaAlaP roArgArgGl 313

GGTGGCACCA CCCTATCAGG GGGCTGACCC CATCCTTGCG ACAGCCCTCG 988  A330T
uValAlaPro ProTyrGlnG lyAlaAspPr oIleLeuAla ThrAlaLeuA 330

CCTCCGACCC CATCCCCAAC CCCCTTCAGA AGTGGGAGGA CAGCGCCCAC 1038
laSerAspPr oIleProAsn ProLeuGlnL ysTrpGluAs pSerAlaHis 346

AAGCCACAGA GCCTAGACAC TGATGACCCC GCGACGCTGT ACGCCGTGGT 1088 S321I  L330L  Y331X
LysProGlnS erLeuAspTh rAspAspPro AlaThrLeuT yrAlaValVa 363

GGAGAACGTG CCCCCGTTGC GCTGGAAGGA ATTCGTGCGG CGCCTAGGGC 1138 R341R
lGluAsnVal ProProLeuA rgTrpLysGl uPheValArg ArgLeuGlyL 380
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TGAGCGACCA CGAGATCGAT CGGCTGGAGC TGCAGAACGG GCGCTGCCTG 1188 R365H
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CGCGAGGCGC AATACAGCAT GCTGGCGACC TGGAGGCGGC GCACGCCGCG 1238
ArgGluAlaG lnTyrSerMe tLeuAlaThr TrpArgArgA rgThrProAr 413

GCGCGAGGCC ACGCTGGAGC TGCTGGGACG CGTGCTCCGC GACATGGACC 1288 R426L D398E
gArgGluAla ThrLeuGluL euLeuGlyAr gValLeuArg AspMetAspL 430

TGCTGGGCTG CCTGGAGGAC ATCGAGGAGG CGCTTTGCGG CCCCGCCGCC 1338 L412I
euLeuGlyCy sLeuGluAsp IleGluGluA laLeuCysGl yProAlaAla 446

CTCCCGCCCG CGCCCAGTCT TCTCAGATGA GGCTGCGCCC CTGCGGGCAG *20  P419L
LeuProProA laProSerLe uLeuArgSto p

CTCTAAGGAC CGTCCTGCGA GATCGCCTTC CAACCCCACT TTTTTCTGGA *70  c.*64T>C
AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG CTAGCAGCCG CCTACTTGGT *120
GCTAACCCCT CGATGTACAT AGCTTTTCTC AGCTGCCTGC GCGCCGCCGA *170
CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT *220
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTTG *270
GGTGTCCTCA CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC *320
CTTTTTCACA GTGCATAAGC AGTTTTTTTT GTTTTTGTTT TGTTTTGTTT *370
TGTTTTTAAA TCAATCATGT TACACTAATA GAAACTTGGC ACTCCTGTGC *420
CCTCTGCCTG GACAAGCACA TAGCAAGCTG AACTGTCCTA AGGCAGGGGC *470
GAGCACGGAA CAATGGGGCC TTCAGCTGGA GCTGTGGACT TTTGTACATA *520
CACTAAAATT CTGAAGTTAA A
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