



TNFRSF1A (NM_001065.4) - cDNA + Protein - 2026-05-15

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 AAATAATTCTG 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 TACTTGATACA 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

ACTGCAGGGA GTGTGAGAGC GGCTCCTTCA CCGCTTCAGA AAACCACTC 288 C52R C52G C52F C52Y C52S C52W R53G E54E C55R C55S C55Y S57_E64del E56D G58S G58Y
S59P F60L(264C>G) F60Y F60S F60L(267A>G) T61P T61I T61N N65I N65K H66Y H66L H66P L67P
 spCysArgG1 uCysGluSer GlySerPheT hrAlaSerG1 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 lyGlnValG1 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 AGAACAGAA 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 GGCACTGAG GACTCAGGCA CCACAGTGCT 638 I170N I170T V173D V173G G175C
 ProGlnIleG luAsnValLy sGlyThrGlu AspSerGlyT hrThrValLe 213

GTTGCCCTG GTCATTTTCT TTGGTCTTTG CCTTTTATCC CTCCTTTC 688 S197C S197S

uLeuProLeu ValIlePheP heGlyLeuCy sLeuLeuSer LeuLeuPheI 230

TTGGTTTAAT GTATCGCTAC CAACGGTGGG AGTCCAAGCT CTACTCCATT 738

leGlyLeuMe tTyrArgTyr GlnArgTrpL ysSerLysLe uTyrSerIle 246

GTTTGTGGGA AATCGACACC TGAAAAAGAG GGGGAGCTTG AAGGAACTAC 788

ValCysGlyL ysSerThrPr oGluLysGlu GlyGluLeuG luGlyThrTh 263

TACTAAGCCC CTGGCCCCAA ACCCAAGCTT CAGTCCCACCT CCAGGCTTCA 838

rThrLysPro LeuAlaProA snProSerPh eSerProThr ProGlyPheT 280

CCCCACCCT GGGCTTCAGT CCCGTGCCCA GTTCCACCT CACCTCCAGC 888 [S261I](#) [F264](#) [T2269del](#)

hrProThrLe uGlyPheSer ProValProS erSerThrPh eThrSerSer 296

TCCACCTATA CCCCGGTGA 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 ATTCTGTGCGG CGCCTAGGGC 1138 [R341R](#)

lGluAsnVal ProProLeuA rgTrpLysGl uPheValArg ArgLeuGlyL 380

TGAGCGACCA CGAGATCGAT CGGCTGGAGC TGCAGAACGG GCGCTGCCTG 1188 [R365H](#)
euSerAspHi sGluIleAsp ArgLeuGluL euGlnAsnGl yArgCysLeu 396

CGCGAGGCGC AATACAGCAT GCTGGCGACC TGGAGGCGGC GCACGCCGCG 1238
ArgGluAlaG lnTyrSerMe tLeuAlaThr TrpArgArgA rgThrProAr 413

CGCGGAGGCC ACGCTGGAGC TGCTGGGACG CGTGCTCCGC GACATGGACC 1288 [R426L](#) [D398E](#)
gArgGluAla ThrLeuGluL euLeuGlyAr gValLeuArg AspMetAspL 430

TGCTGGGCTG CCTGGAGGAC ATCGAGGAGG CGCTTTGCGG CCCC GCCGCC 1338 [L412I](#)
euLeuGlyCy sLeuGluAsp IleGluGluA laLeuCysGl yProAlaAla 446

CTCCCGCCCG CGCCAGTCT TCTCAGATGA GGCTGCGCCC CTGCGGGCAG *20 [P419L](#)
LeuProProA laProSerLe uLeuArgSto p

CTCTAAGGAC CGTCCTGCGA GATCGCCTTC CAACCCCACT TTTTCTGGA *70 [c.*64T>C](#)
AAGGAGGGGT CCTGCAGGGG CAAGCAGGAG CTAGCAGCCG CCTACTTGGT *120
GCTAACCCTT CGATGTACAT AGCTTTTCTC AGCTGCCTGC GCGCCGCCGA *170
CAGTCAGCGC TGTGCGCGCG GAGAGAGGTG CGCCGTGGGC TCAAGAGCCT *220
GAGTGGGTGG TTTGCGAGGA TGAGGGACGC TATGCCTCAT GCCCGTTTGG *270
GGTGTCCCTCA CCAGCAAGGC TGCTCGGGGG CCCCTGGTTC GTCCCTGAGC *320
CTTTTTTACA 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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