



TNFRSF11A (NM_003839.4) - cDNA + Protein - 2024-05-16

AGAGGCCGCT GAGGCCGCGG CGCCCGCCAG CCTGTCCCGC GCCATGCCCC 7

MetAlaP 3

CGCGCGCCCG GCGGCGCCGC CCGCTGTTCG CGCTGCTGCT GCTCTGCGCG 57 A5V

roArgAlaAr gArgArgArg ProLeuPheA lAlaLeuLeu uLeuCysAla 19

CTGCTCGCCC GGCTGCAGT GGCTTTGCAG ATCGCTCCTC CATGTACCAG 107 Q25L

LeuLeuAlaA rgLeuGlnVa lAlaLeuGln IleAlaProP roCysThrSe 36

TGAGAAGCAT TATGAGCATC TGGGACGGTG CTGTAACAAA TGTGAACCAG 157

rGluLysHis TyrGluHisL euGlyArgCy sCysAsnLys CysGluProG 53

GAAAGTACAT GTCTTCTAAA TGCACTACTA CCTCTGACAG TGTATGTCTG 207

lyLysTyrMe tSerSerLys CysThrThrT hrSerAspSe rValCysLeu 69

CCCTGTGGCC CGGATGAATA CTTGGATAGC TGAATGAAG AAGATAAATG 257

ProCysGlyP roAspGluTy rLeuAspSer TrpAsnGluG luAspLysCy 86

CTTGCTGCAT AAAGTTTGTG ATACAGGCAA GGCCCTGGTG GCCGTGGTCG 307

sLeuLeuHis LysValCysA spThrGlyLy sAlaLeuVal AlaValValA 103

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laGlyAsnSe rThrThrPro ArgArgCysA laCysThrAl aGlyTyrHis 119

TGGAGCCAGG ACTGCGAGTG CTGCCGC~~C~~GC AACACCGAGT GCGCGCCGGG 407 [R129C](#)

TrpSerGlnA spCysGluCy sCysArgArg AsnThrGluC ysAlaProGl 136

CCTGGG~~C~~GCC CAG~~C~~ACCCGT TGCAGCTCAA CAAGGACACA GTGTGCAAAC 457 [p.A139Wfs*19 and p.E132Dfs*19](#) [H141Y](#)

yLeuGlyAla GlnHisProL euGlnLeuAs nLysAspThr ValCysLysP 153

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roCysLeuAl aGlyTyrPhe SerAspAlaP heSerSerTh rAspLysCys 169

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ArgProTrpT hrAsnCysTh rPheLeuGly LysArgValG luHisHisGl 186

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yThrGluLys SerAspAlaV alCysSerSe rSerLeuPro AlaArgLysP 203

CACCAAATGA ACCCCATGTT TACTTGCCCC GTTTAATAAT TCTGCTTCTC 657

roProAsnGl uProHisVal TyrLeuProG lyLeuIleIl eLeuLeuLeu 219

TTCGCGTCTG TGGCCCTGGT GGCTGCCATC ATCTTTGGCG TTTGCTATAG 707

PheAlaSerV alAlaLeuVa lAlaAlaIle IlePheGlyV alCysTyrAr 236

GAAAAAAGGG ~~A~~AAGCACTCA CAGCTAATTT GTGGCACTGG ATCAATGAGG 757 [K240E](#)

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CTTGTGGCCG CCTAAGTGGG GATAAG~~G~~AGT CCTCAGGTGA CAGTTGTGTC 807 [E262*](#)

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AGTACACACA CGGCAAACCTT TGGTCAGCAG GGAGCATGTG AAGGTGTCTT 857
SerThrHisT hrAlaAsnPh eGlyGlnGln GlyAlaCysG luGlyValLe 286

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uLeuLeuThr LeuGluGluL ysThrPhePr oGluAspMet CysTyrProA 303

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CAAGGCGAAG ATGCCAGGAT GCTCTCATTG GTCAGCAAGA CCGAGATAGA 1007
GlnGlyGluA spAlaArgMe tLeuSerLeu ValSerLysT hrGluIleGl 336

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uGluAspSer PheArgGlnM etProThrGl uAspGluTyr MetAspArgP 353

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roSerGlnPr oThrAspGln LeuLeuPheL euThrGluPr oGlySerLys 369

TCCACACCTC CTTTCTCTGA ACCCCTGGAG GTGGGGGAGA ATGACAGTTT 1157 [V380V](#)
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AAGCCAGTGC TTCACGGGGA CACAGAGCAC AGTGGGTTC A GAAAGCTGCA 1207
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ACTGCACTGA GCCCCTGTGC AGGACTGATT GGA CTCCAT GTCCTCTGAA 1257 [M416Cfs*110](#)
snCysThrGl uProLeuCys ArgThrAspT rpThrProMe tSerSerGlu 419

AACTACTTGC AAAAAGAGGT GGACAGTGGC CATTGCCCCG ACTGGGCAGC 1307 [D427N](#)

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