



*TNFRSF11A* (NM\_003839.4) - cDNA + Protein - 2026-05-25

AGAGGCCGCT GAGGCCGCGG CGCCCGCCAG CCTGTCCCGC GCCATGCCCC 7

MetAlaP 3

CGCGCGCCG GCGGCGCCG CCGCTGTTCG CGCTGCTGCT GCTCTGCGCG 57 A5V

roArgAlaAr gArgArgArg ProLeuPheA laLeuLeuLe uLeuCysAla 19

CTGCTCGCCC GGCTGCAGGT 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 TGCAC TACTA CCTCTGACAG TGTATGTCTG 207

lyLysTyrMe tSerSerLys CysThrThrT hrSerAspSe rValCysLeu 69

CCCTGTGGCC CGGATGAATA CTTGGATAGC TGGAATGAAG AAGATAAATG 257

ProCysGlyP roAspGluTy rLeuAspSer TrpAsnGluG luAspLysCy 86

CTTGCTGCAT AAAGTTTGTG ATACAGGCAA GGCCCTGGTG GCCGTGGTTCG 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

CTTGCCTTGC AGGCTACTTC TCTGATGCCT TTCCTCCAC GGACAAATGC 507

roCysLeuAl aGlyTyrPhe SerAspAlaP heSerSerTh rAspLysCys 169

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ArgProTrpT hrAsnCysTh rPheLeuGly LysArgValG luHisHisGl 186

GACAGAGAAA TCCGATGCGG TTTGCAGTTC TTCTCTGCCA GCTAGAAAAC 607

yThrGluLys SerAspAlaV alCysSerSe rSerLeuPro AlaArgLysP 203

CACCAAATGA ACCCCATGTT TACTTGCCCG GTTTAATAAT TCTGCTTCTC 657

roProAsnGl uProHisVal TyrLeuProG lyLeuIleIl eLeuLeuLeu 219

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PheAlaSerV alAlaLeuVa lAlaAlaIle IlePheGlyV alCysTyrAr 236

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

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

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SerThrHisT hrAlaAsnPh eGlyGlnGln GlyAlaCysG luGlyValLe 286

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uLeuLeuThr LeuGluGluL ysThrPhePr oGluAspMet CysTyrProA 303

ATCAAGGTGG TGTCTGTCAG GGCACATGTG TAGGAGGTGG TCCCTACGCA 957 [G316D](#)  
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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

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SerThrProP roPheSerGl uProLeuGlu ValGlyGluA snAspSerLe 386

AAGCCAGTGC TTCACGGGGA CACAGAGCAC AGTGGGTTC A GAAAGCTGCA 1207  
uSerGlnCys PheThrGlyT hrGlnSerTh rValGlySer GluSerCysA 403

ACTGCACTGA GCCCCTGTGC AGGACTGATT GGACTCCCAT GTCCTCTGAA 1257 [M416Cfs\\*110](#)  
snCysThrGl uProLeuCys ArgThrAspT rpThrProMe tSerSerGlu 419

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ProAlaSerG lyAsnValTh rGlyAsnSer AsnSerThrP heIleSerSe 536

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CTGAGTAGTA GTCCATTGTA TGGATGTACT GCGGTTTATT CACCAACATA \*6206  
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