



RELA (NM_021975.4) - cDNA + Protein - 2026-05-25

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ATTTCGCCT CTGGCGAATG GCTCGTCTGT AGTGCACGCC GCGGGCCCAG -35
CTGCGACCCC GGCCCCGCC CCGGGACCCC GGCCATGGAC GAACTGTTCC 16 E3*
MetAsp GluLeuPheP 6

CCCTCATCTT CCCGGCAGAG CCAGCCCAGG CCTCTGGCCC CTATGTGGAG 66
roLeuIlePh eProAlaGlu ProAlaGlnA laSerGlyPr oTyrValGlu 22

ATCATTGAGC AGCCCAAGCA GCGGGGCATG CGCTTCCGCT ACAAGTGCGA 116
IleIleGluG lnProLysGl nArgGlyMet ArgPheArgT yrLysCysGl 39

GGGGCGCTCC GCGGGCAGCA TCCAGGCCA GAGGAGCACA GATACCACCA 166
uGlyArgSer AlaGlySerI leProGlyGl uArgSerThr AspThrThrL 56

AGACCCACCC CACCATCAAG ATCAATGGCT ACACAGGACC AGGGACAGTG 216
ysThrHisPr oThrIleLys IleAsnGlyT yrThrGlyPr oGlyThrVal 72

CGCATCTCCC TGGTCACCAA GGACCCTCCT CACCGGCCTC ACCCCCACGA 266
ArgIleSerL euValThrLy sAspProPro HisArgProH isProHisGl 89

GCTTGTAGGA AAGGACTGCC GGGATGGCTT CTATGAGGCT GAGCTCTGCC 316
uLeuValGly LysAspCysA rgAspGlyPh eTyrGluAla GluLeuCysP 106
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CGGACCGCTG CATCCACAGT TTCCAGAACC TGGGAATCCA GTGTGTGAAG 366

roAspArgCy sIleHisSer PheGlnAsnL euGlyIleGl nCysValLys 122

AAGCGGGACC TGGAGCAGGC TATCAGTCAG CGCATCCAGA CCAACAACAA 416

LysArgAspL euGluGlnAl aIleSerGln ArgIleGlnT hrAsnAsnAs 139

CCCCTTCCAA GTTCCATATAG AAGAGCAGCG TGGGGACTAC GACCTGAATG 466

nProPheGln ValProIleG luGluGlnAr gGlyAspTyr AspLeuAsnA 156

CTGTGCGGCT CTGCTTCCAG GTGACAGTGC GGGACCCATC AGGCAGGCCC 516

laValArgLe uCysPheGln ValThrValA rgAspProSe rGlyArgPro 172

CTCCGCTTGC CGCCTGTCCT TTCTCATCCC ATCTTTGACA ATCGTGCCCC 566

LeuArgLeuP roProValLe uSerHisPro IlePheAspA snArgAlaPr 189

CAACACTGCC GAGCTCAAGA TCTGCCGAGT GAACCGAAAC TCTGGCAGCT 616

oAsnThrAla GluLeuLysI leCysArgVa lAsnArgAsn SerGlySerC 206

GCCTCGGTGG GGATGAGATC TTCCTACTGT GTGACAAGGT GCAGAAAGAG 666

ysLeuGlyGl yAspGluIle PheLeuLeuC ysAspLysVa lGlnLysGlu 222

GACATTGAGG TGTATTTTAC GGGACCAGGC TGGGAGGCCC GAGGCTCCTT 716

AspIleGluV alTyrPheTh rGlyProGly TrpGluAlaA rgGlySerPh 239

TTCGCAAGCT GATGTGCACC GACAAGTGGC CAATTGTGTTT CGGACCCCTC 766 [R246*](#) [I250V](#)

eSerGlnAla AspValHisA rgGlnValAl aIleValPhe ArgThrProP 256

CCTACGCAGA CCCAGCCTG CAGGCTCCTG TCGTGTCTC CATGCAGCTG 816

roTyrAlaAs pProSerLeu GlnAlaProV alArgValSe rMetGlnLeu 272

CGGCGGCCTT CCGACCGGGA GCTCAGTGAG CCCATGGAAT TCCAGTACCT 866

ArgArgProS erAspArgGl uLeuSerGlu ProMetGluP heGlnTyrLe 289

GCCAGATACA GACGATCGTC ACCGGATTGA GGAGAAACGT AAAAGGACAT 916 [D291N](#) [R295H](#)

uProAspThr AspAspArgH isArgIleGl uGluLysArg LysArgThrT 306

ATGAGACCTT CAAGAGCATC ATGAAGAAGA GTCCTTTCAG CGGACCCACC 966 [P321A](#)

yrGluThrPh eLysSerIle MetLysLysS erProPheSe rGlyProThr 322

GACCCCCGGC CTCCACCTCG ACGCATTGCT GTGCCTTCCC GCAGCTCAGC 1016 [R329*](#) [R330H](#)

AspProArgP roProProAr gArgIleAla ValProSerA rgSerSerAl 339

TTCTGTCCCC AAGCCAGCAC CCCAGCCCTA TCCCTTTACG TCATCCCTGA 1066 [Q347*](#) [p.Y349*](#)

aSerValPro LysProAlaP roGlnProTy rProPheThr SerSerLeuS 356

GCACCATCAA CTATGATGAG TTTCCACCA TGGTGTTCCT TTCTGGGCAG 1116

erThrIleAs nTyrAspGlu PheProThrM etValPhePr oSerGlyGln 372

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IleSerGlnA laSerAlaLe uAlaProAla ProProGlnV alLeuProGl 389

GGCTCCAGCC CCTGCCCTG CTCCAGCCAT GGTATCAGCT CTGGCCCAGG 1216

nAlaProAla ProAlaProA laProAlaMe tValSerAla LeuAlaGlnA 406

CCCCAGCCCC TGTCCAGTC CTAGCCCCAG GCCCTCCTCA GGCTGTGGCC 1266 [V410Sfs*4](#)

laProAlaPr oValProVal LeuAlaProG lyProProGl nAlaValAla 422

CCACCTGCCC CCAAGCCCAC CCAGGCTGGG GAAGGA^ACGC TGTC^AGAGGC 1316 [p.Thr435fs](#) [E438Rfs*9](#)
 ProProAlaP roLysProTh rGlnAlaGly GluGlyThrL euSerGluAl 439

CCTGCTGCAG CTGCAGTTTG ATGATGAAGA CCTGGGGGCC TTGCTTGGCA 1366
 aLeuLeuGln LeuGlnPheA spAspGluAs pLeuGlyAla LeuLeuGlyA 456

ACAGCACAGA CCCAGCTGTG TTCA^CAGACC TGGCATCCGT CGACAACT^CC 1416 [T464Rfs*26](#) [p.\(Asp465ThrfsTer14\)](#) [p.E473Rfs*18](#)
 snSerThrAs pProAlaVal PheThrAspL euAlaSerVa lAspAsnSer 472

GAGTTTCAGC AGCTGCTGAA CCAGGGCATA CCTGTGGCCC CC^CCACACAAC 1466 [H487Tfs*7](#)
 GluPheGlnG lnLeuLeuAs nGlnGlyIle ProValAlaP roHisThrTh 489

TGAGCCCATG CTGATG^GAGT ACCCTGAGGC TATAACTCGC CTAGTGACAG 1516 [p.\(Glu495SerfsTer6\)](#)
 rGluProMet LeuMetGluT yrProGluAl aIleThrArg LeuValThrG 506

GGGCCCAGAG GCCCCCC^GAC CCAGCTCCTG CTCCACTGGG GGCCCCGGGG 1566 [D512N](#)
 lyAlaGlnAr gProProAsp ProAlaProA laProLeuGl yAlaProGly 522

CTCCCCAATG GCCTCCTTTC AGGAGATGAA GACTTCTCCT CCATTGCGGA 1616
 LeuProAsnG lyLeuLeuSe rGlyAspGlu AspPheSerS erIleAlaAs 539

CATGGACTTC TCAGCCCTGC TGAGTCAGAT CAGCTCC^{TAA} GGGGGTGACG *10
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CCTGCCCTCC CCAGAGCACT GGGTTGCAGG GGATTGAAGC CCTCCAAAAG *60
 CACTTACGGA TTCTGGTGGG GTGTGTTCCA ACTGCCCCCA ACTTTGTGGA *110
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CCTGTGCCA ACACCAGCGT TTGAGGGGCT GGCCTTCCTG CCCTACAGAG *510
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GTGGGGGAGA GCAGGCTGGC AGCTCTCCAG TCAGGAGGCA TAGTTTTTAC *710
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ATCTGTTGCC AAGCTGG

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