



RELA (NM_021975.4) - cDNA + Protein - 2024-05-17

ATTTCCGCCT CTGGCGAATG GCTCGTCTGT AGTGCACGCC GCGGGCCCAG -35

CTGCGACCCC GGCCCCGCCC CCGGGACCCC GGCCATGGAC GAACTGTTCC 16

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 TCCCAGGCGA 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

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 GTTCCTATAG AAGAGCAGCG TGGGGACTAC GACCTGAATG 466

nProPheGln ValProIleG luGluGlnAr gGlyAspTyr AspLeuAsnA 156

CTGTGCGGCT CTGCTTCCAG GTGACAGTGC GGGACCCATC AGGCAGGCCC 516

laValArgLe uCysPheGln ValThrValA rgAspProSe rGlyArgPro 172

CTCCGCCTGC 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 CATTGTGTTC CGGACCCCTC 766 [R246*](#)

eSerGlnAla AspValHisA rgGlnValAl aIleValPhe ArgThrProP 256

CCTACGCAGA CCCCAGCCTG 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

uProAspThr AspAspArgH isArgIleGl uGluLysArg LysArgThrT 306

ATGAGACCTT CAAGAGCATC ATGAAGAAGA GTCCTTTCAG CGGACCCACC 966

yrGluThrPh eLysSerIle MetLysLysS erProPheSe rGlyProThr 322

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

AspProArgP roProProAr gArgIleAla ValProSerA rgSerSerAl 339

TTCTGTCCCC AAGCCAGCAC CCCAGCCCTA TCCCTTTACG TCATCCCTGA 1066

aSerValPro LysProAlaP roGlnProTy rProPheThr SerSerLeuS 356

GCACCATCAA CTATGATGAG TTTCCACCA TGGTGTTTCC TTCTGGGCAG 1116

erThrIleAs nTyrAspGlu PheProThrM etValPhePr oSerGlyGln 372

ATCAGCCAGG CCTCGGCCTT GGCCCCGGCC CCTCCCAG TCCTGCCCCA 1166 [Q385*](#) [Q389*](#)

IleSerGlnA laSerAlaLe uAlaProAla ProProGlnV alLeuProGl 389

GGCTCCAGCC CTGCCCCTG CTCCAGCCAT GGTATCAGCT CTGGCCCAGG 1216

nAlaProAla ProAlaProA laProAlaMe tValSerAla LeuAlaGlnA 406

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

laProAlaPr oValProVal LeuAlaProG lyProProGl nAlaValAla 422

CCACCTGCCC CCAAGCCCAC CCAGGCTGGG GAAGGAACGC TGTCAGAGGC 1316 [E438Rfs*9](#)
 ProProAlaP roLysProTh rGlnAlaGly GluGlyThrL euSerGluAl 439

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

ACAGCACAGA CCCAGCTGTG TTCAAGACC TGGCATCCGT CGACAACTCC 1416 [T464Rfs*26](#)
 snSerThrAs pProAlaVal PheThrAspL euAlaSerVa lAspAsnSer 472

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

TGAGCCCATG CTGATGGAGT ACCCTGAGGC TATAACTCGC CTAGTGACAG 1516
 rGluProMet LeuMetGluT yrProGluAl aIleThrArg LeuValThrG 506

GGGCCCAGAG GCCCCCGAC CCAGCTCCTG CTCCACTGGG GGGCCCGGGG 1566
 lyAlaGlnAr gProProAsp ProAlaProA laProLeuGl yAlaProGly 522

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

CATGGACTTC TCAGCCCTGC TGAGTCAGAT CAGCTCCTAA GGGGGTGACG *10
 pMetAspPhe SerAlaLeuL euSerGlnIl eSerSerSto p

CCTGCCCTCC CCAGAGCACT GGGTTGCAGG GGATTGAAGC CCTCCAAAAG *60
 CACTTACGGA TTCTGGTGGG GTGTGTTCCA ACTGCCCCCA ACTTTGTGGA *110
 TGTCTTCCTT GGAGGGGGGA GCCATATTTT ATTCTTTTAT TGTCAGTATC *160

TGTATCTCTC TCTCTTTTTG GAGGTGCTTA AGCAGAAGCA TTAAC TTCTC *210
TGGAAGGGG GGAGCTGGG AACTCAAAC TTTCCCCTG TCCTGATGGT *260
CAGCTCCCTT CTCTGTAGG AACTCTGGG TCCCCATCC CCATCCTCCA *310
GCTTCTGGTA CTCTCCTAGA GACAGAAGCA GGCTGGAGGT AAGGCCTTTG *360
AGCCCACAAA GCCTTATCAA GTGTCTTCCA TCATGGATTC ATTACAGCTT *410
AATCAAAATA ACGCCCCAGA TACCAGCCCC TGTATGGCAC TGGCATTGTC *460
CCTGTGCCTA ACACCAGCGT TTGAGGGGCT GGCCTTCCTG CCCTACAGAG *510
GTCTCTGCCG GCTCTTTCCT TGCTCAACCA TGGCTGAAGG AAACCAGTGC *560
AACAGCACTG GCTCTCTCCA GGATCCAGAA GGGGTTTGGT CTGGGACTTC *610
CTTGCTCTCC CTCTTCTCAA GTGCCTTAAT AGTAGGGTAA GTTGTTAAGA *660
GTGGGGGAGA GCAGGCTGGC AGCTCTCCAG TCAGGAGGCA TAGTTTTTAC *710
TGAACAATCA AAGCACTTGG ACTCTTGCTC TTTCTACTCT GAACTAATAA *760
ATCTGTTGCC AAGCTGG

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