RELA (NM_021975.4) - cDNA + Protein - 2025-04-03

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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
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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 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 TGTATTTCAC GGGACCAGGC TGGGAGGCCC GAGGCTCCTT 716
AspIleGluV alTyrPheTh rGlyProGly TrpGluAlaA rgGlySerPh 239

TTCGCAAGCT GATGTGCACC GACAAGTGGC CATTGTGTTC CGGACCCCTC 766   R246*
eSerGlnAla AspValHisA rgGlnValAl aIleValPhe ArgThrProP 256

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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 p.Y349*
aSerValPro LysProAlaP roGlnProTy rProPheThr SerSerLeuS 356

GCACCATCAA CTATGATGAG TTTCCCACCA TGGTGTTTCC TTCTGGGCAG 1116
erThrIleAs nTyrAspGlu PheProThrM etValPhePr oSerGlyGln 372

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IleSerGlnA laSerAlaLe uAlaProAla ProProGlnV alLeuProGl 389

GGCTCCAGCC CCTGCCCCTG CTCCAGCCAT GGTATCAGCT CTGGCCCAGG 1216
nAlaProAla ProAlaProA laProAlaMe tValSerAla LeuAlaGlnA 406

CCCCAGCCCC TGTCCCAGTC CTAGCCCCAG GCCCTCCTCA GGCTGTGGCC 1266 V410Sfs*4
laProAlaPr oValProVal LeuAlaProG lyProProGl nAlaValAla 422
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CCACCTGCCC CCAAGCCCAC CCAGGCTGGG GAAGGAACGC TGTCAGAGGC 1316 E438Rfs*9
ProProAlaP roLysProTh rGlnAlaGly GluGlyThrL euSerGluAl 439

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aLeuLeuGln LeuGlnPheA spAspGluAs pLeuGlyAla LeuLeuGlyA 456

ACAGCACAGA CCCAGCTGTG TTCACAGACC TGGCATCCGT CGACAACTCC 1416 T464Rfs*26 p.E473Rfs*18
snSerThrAs pProAlaVal PheThrAspL euAlaSerVa lAspAsnSer 472

GAGTTTCAGC AGCTGCTGAA CCAGGGCATA CCTGTGGCCC CCCACACAAC 1466 H487Tfs*7
GluPheGlnG lnLeuLeuAs nGlnGlyIle ProValAlaP roHisThrTh 489

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

GGGCCCAGAG GCCCCCCGAC CCAGCTCCTG CTCCACTGGG GGCCCCGGGG 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
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CAGCTCCCTT CTCTGTAGGG AACTCTGGGG TCCCCCATCC CCATCCTCCA *310

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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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