



NLRC4 (NM_001199138.2) - cDNA + Protein - 2025-04-02

CTCTGTACAC TGCCTCTCA CAGAACAAGA AGGTATCTGG TCTACAAGAA -218

CTCGAGGCCT CACTGAAACG GAAAGCAAAT ACAAAGAAAC TTTATTTTAA -168

AAACATGTCT TGGTCTCCCA AGAAGAGGGC AATTGGATTG CTCAGCCAGA -118

ATGAAGAGTA GTTTTACAGA AAAAAGAGGA CAATATTGGG ATCACCTTTG -68

ACCTTTCCAT TTGGAAATAA TATTTTCTAT TGTGTTATAG AAAGGTGGGA -18

AGCTTTCATC CAGAACAATG AATTTTCATAA AGGACAATAG CCGAGCCCTT 33

Met AsnPheIleL ysAspAsnSe rArgAlaLeu 11

ATTCAAAGAA TGGGAATGAC TGTTATAAAG CAAATCACAG ATGACCTATT 83

IleGlnArgM etGlyMetTh rValIleLys GlnIleThrA spAspLeuPh 28

TGTATGGAAT GTTCTGAATC GCGAAGAAGT AAACATCATT TGCTGCGAGA 133 N31H

eValTrpAsn ValLeuAsnA rgGluGluVa lAsnIleIle CysCysGluL 45

AGGTGGAGCA GGATGCTGCT AGAGGGATCA TTCACATGAT TTTGAAAAAG 183

ysValGluGl nAspAlaAla ArgGlyIleI leHisMetIl eLeuLysLys 61

GGTTCAGAGT CCTGTAACCT CTTTCTTAAA TCCCTTAAGG AGTGGAACTA 233 E64Rfs*4 L70F

GlySerGluS erCysAsnLe uPheLeuLys SerLeuLysG luTrpAsnTy 78

TCCTCTATTT CAGGACTTGA ATGGACAAAG TCTTTTTTCAT CAGACATCAG 283 E95*

rProLeuPhe GlnAspLeuA snGlyGlnSe rLeuPheHis GlnThrSerG 95

AAGGAGACTT GGACGATTTG GCTCAGGATT TAAAGGACTT GTACCATAACC 333

luGlyAspLe uAspAspLeu AlaGlnAspL euLysAspLe uTyrHisThr 111

CCATCTTTTC TGAACTTTTA TCCCCTTGGT GAAGATAITG ACATTATTTT 383 [I124T](#)

ProSerPheL euAsnPheTy rProLeuGly GluAspIleA spIleIlePh 128

TAAC TTGAAA AGCA CTTTCA CAGAACCTGT CCTGTGGAGG AAGGACCAAC 433 [S132Afs*21](#) [T133I](#)

eAsnLeuLys SerThrPheT hrGluProVa lLeuTrpArg LysAspGlnH 145

ACCATCACCG CGTGGAGCAG CTGACCCTGA ATGGCCTCCT GCAGGCTCTT 483 [A160T](#)

isHisHisAr gValGluGln LeuThrLeuA snGlyLeuLe uGlnAlaLeu 161

CAGAGCCCCI GCATCATTGA AGGGGAATCT GCGCAAAGGCA AGTCCACTCT 533 [C165R](#) [S171F](#) [G172S](#) [T177A](#) [T177S](#)

GlnSerProC ysIleIleGl uGlyGluSer GlyLysGlyL ysSerThrLe 178

GCTGCAGCGA ATTGCCATGC TCTGGGGCTC CGGAAAGTGC AAGGCTCTGA 583 [R181X](#)

uLeuGlnArg IleAlaMetL euTrpGlySe rGlyLysCys LysAlaLeuT 195

CCAAGTTCAA ATTCGTCTTC TTCCTCCGTC TCAGCAGGGC CCAGGGTGGG 633 [R204H](#) [R207K](#)

hrLysPheLy sPheValPhe PheLeuArgL euSerArgAl aGlnGlyGly 211

CTTTTTGAAA CCCTCTGTGA TCAACTCCTG GATATACCTG GCACAATCAG 683

LeuPheGluT hrLeuCysAs pGlnLeuLeu AspIleProG lyThrIleAr 228

GAAGCAGACA TTCATGGCCA TGCTGCTGAA GCTGCGGCAG AGGGTTCTTT 733

gLysGlnThr PheMetAlaM etLeuLeuLy sLeuArgGln ArgValLeuP 245

TCCTTCTTGA TGGCTACAAT GAATTCAAGC CCAGAACTG CCCAGAAATC 783 P255L
heLeuLeuAs pGlyTyrAsn GluPheLysP roGlnAsnCy sProGluIle 261

GAAGCCCTGA TAAAGGAAAA CCACCGCTTC AAGAACATGG TCATCGTCAC 833
GluAlaLeuI leLysGluAs nHisArgPhe LysAsnMetV alIleValTh 278

CACTACCACT GAGTGCCTGA GGCACATACG GCAGTTTGGT GCCCTGACTG 883 C283G I287T G291S
rThrThrThr GluCysLeuA rgHisIleAr gGlnPheGly AlaLeuThrA 295

CTGAGGTGGG GGATATGACA GAAGACAGCG CCCAGGCTCT CATCCGAGAA 933 R310*
laGluValGl yAspMetThr GluAspSerA laGlnAlaLe uIleArgGlu 311

GTGCTGATCA AGGAGCTTGC TGAAGGCTTG TTGCTCCAAA TTCAGAAATC 983
ValLeuIleL ysGluLeuAl aGluGlyLeu LeuLeuGlnI leGlnLysSe 328

CAGGTGCTTG AGGAATCTCA TGAAGACCCC TCTCTTTGTG GTCATCACTT 1033 T337S T337N L339P V341L V341A I343N
rArgCysLeu ArgAsnLeuM etLysThrPr oLeuPheVal ValIleThrC 345

GTGCAATCCA GATGGGTGAA AGTGAGTTCC ACTCTCACAC ACAAACAACG 1083
ysAlaIleGl nMetGlyGlu SerGluPheH isSerHisTh rGlnThrThr 361

CTGTTCCATA CCTTCTATGA TCTGTTGATA CAGAAAAACA AACACAAACA 1133 H376Y
LeuPheHist hrPheTyrAs pLeuLeuIle GlnLysAsnL ysHisLysHi 378

TAAAGGTGTG GCTGCAAGTG ACTTCATTCG GAGCCTGGAC CACTGTGGAG 1183 I387T H392del
sLysGlyVal AlaAlaSerA spPheIleAr gSerLeuAsp HisCysGlyA 395

ACCTAGCTCT GGAGGGTIG TTCTCCACA AGTTTGATT CGAACTGCAG 1233 V401A

spLeuAlaLe uGluGlyVal PheSerHisL ysPheAspPh eGluLeuGln 411

GATGTGTCCA GCGTGAATGA GGATGTCCTG CTGACAACCTG GGCTCCTCTG 1283

AspValSerS erValAsnGl uAspValLeu LeuThrThrG lyLeuLeuCy 428

TAAATATACA GCTCAAAGGT TCAAGCCAAA GTATAAATTC TTTCACAAGT 1333 [H443P](#) [H443Q](#) [S445P](#)

sLysTyrThr AlaGlnArgP heLysProLy sTyrLysPhe PheHisLysS 445

CATTCAGGA GTACACAGCA GGACGAAGAC TCAGCAGTTT ATTGACGTCT 1383

erPheGlnGl uTyrThrAla GlyArgArgL euSerSerLe uLeuThrSer 461

CATGAGCCAG AGGAGGTGAC CAAGGGGAAT GGTTACTTGC AGAAAATGGT 1433

HisGluProG luGluValTh rLysGlyAsn GlyTyrLeuG lnLysMetVa 478

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lSerIleSer AspIleThrS erThrTyrSe rSerLeuLeu ArgTyrThrC 495

GTGGGTCATC TGTGGAAGCC ACCAGGGCTG TTATGAAGCA CCTCGCAGCA 1533

ysGlySerSe rValGluAla ThrArgAlaV alMetLysHi sLeuAlaAla 511

GTGTATCAAC ACGGCTGCCT TCTCGGACTT TCCATCGCCA AGAGGCCTCT 1583

ValTyrGlnH isGlyCysLe uLeuGlyLeu SerIleAlaL ysArgProLe 528

CTGGAGACAG GAATCTTTGC AAAGTGTGAA AACACCACT GAGCAAGAAA 1633

uTrpArgGln GluSerLeuG lnSerValLy sAsnThrThr GluGlnGluI 545

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euPheAspPh ePheGluHis LeuProAsnC ysAlaSerAl aLeuAspPhe 611

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IleLysLeuA spPheTyrGl yGlyAlaMet AlaSerTrpG luLysAlaAl 628

AGAAGACACA GGTGGAATCC ACATGGAAGA GGCCCCAGAA ACCTACATTC 1933

aGluAspThr GlyGlyIleH isMetGluGl uAlaProGlu ThrTyrIleP 645

CCAGCAGGGC TGTATCTTTG TTCTTCAACT GGAAGCAGGA ATTCAGGACT 1983 [W655S](#) [W655C](#) [Q657L](#)

roSerArgAl aValSerLeu PhePheAsnT rpLysGlnGl uPheArgThr 661

CTGGAGGTCA CACTCCGGGA TTTCAGCAAG TTGAATAAGC AAGATATCAG 2033

LeuGluValT hrLeuArgAs pPheSerLys LeuAsnLysG lnAspIleAr 678

ATATCTGGGG AAAATATTCA GCTCTGCCAC AAGCCTCAGG CTGCAAATAA 2083 [L680M](#)

gTyrLeuGly LysIlePheS erSerAlaTh rSerLeuArg LeuGlnIleL 695

AGAGATGTGC TGGTGTGGCT GGAAGCCTCA GTTTGGTCCT CAGCACCTGT 2133

ysArgCysAl aGlyValAla GlySerLeuS erLeuValLe uSerThrCys 711

AAGAACATTT ATTCTCTCAT GGTGGAAGCC AGTCCCCTCA CCATAGAAGA 2183

LysAsnIleT yrSerLeuMe tValGluAla SerProLeuT hrIleGluAs 728

TGAGAGGCAC ATCACATCTG TAACAAACCT GAAAACCTTG AGTATTCATG 2233

pGluArgHis IleThrSerV alThrAsnLe uLysThrLeu SerIleHisA 745

ACCTACAGAA TCAACGGCTG CCGGGTGGTC TGA CTGACAG CTTGGGTAAC 2283 [P752L](#) [delexon5](#)

spLeuGlnAs nGlnArgLeu ProGlyGlyL euThrAspSe rLeuGlyAsn 761

TTGAAGAACC TTACAAAGCT CATAATGGAT AACATAAAGA TGAATGAAGA 2333 [M775I](#)

LeuLysAsnL euThrLysLe uIleMetAsp AsnIleLysM etAsnGluGl 778

AGATGCTATA AAAC TAGCTG AAGGCCTGAA AAACCTGAAG AAGATGTGTT 2383 [G786V](#)

uAspAlaIle LysLeuAlaG luGlyLeuLy sAsnLeuLys LysMetCysL 795

TATTTTATTT GACCCACTTG TCTGACATTG GAGAGGGAAT GGATTACATA 2433 [L801V](#)

euPheHisLe uThrHisLeu SerAspIleG lyGluGlyMe tAspTyrIle 811

GTCAAGTCTC TGTC AAGTGA ACCCTGTGAC CTTGAAGAAA TTCAATTAGT 2483

ValLysSerL euSerSerGl uProCysAsp LeuGluGluI leGlnLeuVa 828

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LysAspGlyA snGluAlaLe uHisGluLeu IleAspArgM etAsnValLe 878

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uGluGlnLeu ThrAlaLeuM etLeuProTr pGlyCysAsp ValGlnGlyS 895

GCCTGAGCAG CCTGTTGAAA CATTGGAGG AGGTCCCACA ACTCGTCAAG 2733

erLeuSerSe rLeuLeuLys HisLeuGluG luValProGl nLeuValLys 911

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LeuGlyLeuL ysAsnTrpAr gLeuThrAsp ThrGluIleA rgIleLeuGl 928

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yAlaPhePhe GlyLysAsnP roLeuLysAs nPheGlnGln LeuAsnLeuA 945

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laGlyAsnAr gValSerSer AspGlyTrpL euAlaPheMe tGlyValPhe 961

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CTTTTCTGCA AGAAGCTAGG CTTGTTGGGT GGCAATTTGA TGATGATGAT 3033

hrPheLeuGl nGluAlaArg LeuValGlyT rpGlnPheAs pAspAspAsp 1011

CTCAGTGTTA TTACAGGTGC TTTTAAACTA GTAACCTGCTT AAATAAAGTG *8

LeuSerValI leThrGlyAl aPheLysLeu ValThrAlaS top

TACTCGAAGC CA

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