



NLRP3 (NM_001243133.2) - cDNA + Protein - 2024-05-03

GTTCTGAGG CTGGCATCTG GATGAGGAAA CTGAAGTTGA GGAATAGTGA -720

AGAGTTGTC CAATGTCATA GCCCCGTAAT CAACGGGACA AAAATTTCT -670

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AATACAATCC TGTTTATGGA TTTGTTGCA TATTTTCCC TCCATAGGGA -570

AACCTTCCTT CCATGGCTCA GGACACACTC CTGGATCGAG CCAACAGGAG -520

AACTTCTGG TAAGCATTG GCTAACCTTT TTTTTTTGA GATGGAGTCT -470

TGCTGTGTCG CCTAGGCTGG AGTGCAGTGG CGTGATCTG GCTCACTGCA -420

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GCTGGGATTA CAGGCCCG CCACACACC CGGCTCATT TTGTACTTTT -320

AGTAGAGACA CAGTTTGCC ATGTTGGCCA GGCTGGTCTT GAATT CCTCA -270

GCTCAGGTGA TCTGCCTGCC TTGGCCTCTC AAAGTGCTGG GATTACAGGC -220

GTGAGCCACT GTGCCGGCC TTGGCTAACT TTTCAAAATT AAAGATTTG -170

ACTTGTACA GTCATGTGAC ATTTTTTCT TTCTGTTGC TGAGTTTTG -120

ATAATTATA TCTCTCAAAG TGGAGACTTT AAAAAAGACT CATCCGTGTG -70

CCGTGTTCAC TGCCTGGTAT CTTAGTGTGG ACCGAAGCCT AAGGACCCTG -20 c.-40G>T

AAAACAGCTG CAGATGAAGA TGGCAAGCAC CCGCTGCAAG CTGGCCAGGT 31

M etAlaSerTh rArgCysLys LeuAlaArgT 11

ACCTGGAGGA CCTGGAGGAT GTGGACTTGA AGAAATTAA GATGCACTTA 81 D19H

yrLeuGluAs pLeuGluAsp ValAspLeuL ysLysPheLy sMetHisLeu 27

GAGGAACTATC CTCCCCAGAA GGGCTGCATC CCCCTCCCGA GGGGTCAGAC 131 D31V P38S

GluAspTyrP roProGlnLy sGlyCysIle ProLeuProA rgGlyGlnTh 44

AGAGAAGGCA GACCATGTGG ATCTAGCCAC GCTAATGATC GACTTCAATG 181 H49R

rGluLysAla AspHisValA spLeuAlaTh rLeuMetIle AspPheAsnG 61

GGGAGGAGAA GGCGTGGGCC ATGGCCGTGT GGATCTTCGC TGCGATCAAC 231 M68T A69A V70M A75V

lyGluGluLy sAlaTrpAla MetAlaValT rpIlePheAl aAlaIleAsn 77

AGGAGAGACC TTTATGAGAA AGCAAAAGA GATGAGCCGA AGTGGGGTTC 281 D88Y

ArgArgAspL euTyrGluLy sAlaLysArg AspGluProL ysTrpGlySe 94

AGATAATGCA CGTGTTTCGA ATCCCACTGT GATATGCCAG GAAGACAGCA 331 R98G R98H

rAspAsnAla ArgValSerA snProThrVa lIleCysGln GluAspSerI 111

TTGAAGAGGA GTGGAGGT TTACTGGAGT ACCTTCGAG AATCTCTATT 381 M116I S123L

leGluGluGl uTrpMetGly LeuLeuGluT yrLeuSerAr gIleSerIle 127

TGTAAATGA AGAAAGATTA CCGTAAGAAG TACAGAAAGT ACGTGAGAAG 431 K129R R135H Y141Y

CysLysMetL ysLysAspTy rArgLysLys TyrArgLysT yrValArgSe 144

CAGATTCCAG TGCATTGAAG ACAGGAATGC CCGTCTGGGT GAGAGTGTGA 481 C148Y E150E

rArgPheGln CysIleGluA spArgAsnAl aArgLeuGly GluSerVals 161

GCCTCAACAA ACGCTACACA CGACTGTC TCATCAAGGA GCACCGGAGC 531 R168Q R170S R170H I172T K173E R176W

erLeuAsnLy sArgTyrThr ArgLeuArgL euIleLysGl uHisArgSer 177

CAGCAGGAGA GGGAGCAGGA GCTTCTGGCC ATCGGCAAGA CCAAGACGTG 581 E182V T193K T195M

GlnGlnGluA rgGluGlnGl uLeuLeuAla IleGlyLysT hrLysThrCy 194

TGAGAGCCCC GTGAGTCCCA TTAAGATGGA GTTGCTGTT GACCCCGATG 631 S196N V198M P200T E204G D211N
sGluSerPro ValSerProI leLysMetG1 uLeuLeuPhe AspProAspA 211

ATGAGCATTC TGAGCCTGTG CACACCCTGG TGTTCCAGGG GGCGGGCAGGG 681 H213R T219T A225V G227G
spGluHisSe rGluProVal HisThrValV alPheGlnG1 yAlaAlaGly 227

ATTGGGAAAA CAATCCTGGC CAGGAAGATG ATGTTGGACT GGGCGTCGGG 731 T231T L233L A242A
IleGlyLysT hrIleLeuAl aArgLysMet MetLeuAspT rpAlaSerG1 244

GACACTCTAC CAAGACAGGT TTGACTATCT GTTCTATATC CACTGTCGAG 781 p.L254M C259W R260W R260L R260P R260Q R260R
yThrLeuTyr GlnAspArgP heAspTyrLe uPheTyrIle HisCysArgG 261

AGGTGAGCCT TGTGACACAG AGGAGCCTGG GGGACCTGAT CATGAGCTGC 831 V262A V262G L264F L264V L264H L264R L264P T266P
luValSerLe uValThrGln ArgSerLeuG lyAspLeuIl eMetSerCys 277

TGCCCGACC CAAACCCACC CATCCACAAG ATCGTGAGAA AACCTCCAG 881 D280N I288M
CysProAspP roAsnProPr oIleHisLys IleValArgL ysProSerAr 294

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Q306K Q306E G307S G307V G307D p.G307 F309del G307A F309S F309Y G309 F311del D310D E311K
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luHisIleG1 yProLeuCys ThrAspTrpG lnLysAlaG1 uArgGlyAsp 327

ATTCTCCTGA GCAGCCTCAT CAGAAAGAAG CTGCTTCCCG AGGCCTCTCT 1031 S331N S331R S332N I334V P340P
IleLeuLeuS erSerLeuIl eArgLysLys LeuLeuProG luAlaSerLe 344

GCTCATCACCC ACGAGACCTG TGGCCCTGGA GAAACTGCAG CACTTGCTGG 1081 L344L T347I T348M T348T P350I V351M V351L V351LGT A352T A352S A352V L353P E354D K355T
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uLeuIleThr ThrArgProV alAlaLeuG1 uLysLeuGln HisLeuLeuA 361

ACCATCCTCG GCATGTGGAG ATCCTGGGTT TCTCCGAGG CAAAAGGAAA 1131 L369M A374D K375E
spHisProAr gHisValGlu IleLeuGlyP heSerGluAl aLysArgLys 377

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CAGAAAATCC TGTTTGAGGA GTCCGACCTC AGGAATCATG GACTGCAGAA 1481 I480F R488K

GlnLysIleL euPheGluGl uSerAspLeu ArgAsnHisG lyLeuGlnLy 494

GGC GGATGTG TCTGCTTCC TGAGGATGAA CCTGTTCAA AAGGAAGTGG 1531 A495V

sAlaAspVal SerAlaPheL euArgMetAs nLeuPheGln LysGluValA 511

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sGluGlyArg HisLeuAspM etValGlnCy sValLeuPro SerSerSerH 711

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luThrLeuG1 nHisProGly CysAsnIleA rgArgLeuTr pLeuGlyArg 777

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CysGlyLeuS erHisGluCy sCysPheAsp IleSerLeuV alLeuSerSe 794

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ValValPheG luProSerTr pStop

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ATCCATCCAG GCCAAGACCA CAGCTCTGTG ATCCTTCCGG TGGAGTGTG *126

GAGAAGAGAG CTTGCCGACG ATGCCTTCCT GTGCAGAGCT TGGGCATCTC *176

CCTTACGCCA GGGTGAGGAA GACACCAGGA CAATGACAGC ATCGGGTGT *226 c.*177delC

GTTGTCATCA CAGCGCCTCA GTTAGAGGAT GTTCCCTTG GTGACCTCAT *276 c.*230G>C

GTAATTAGCT CATTCAATAA AGCACTTCT TTATTTT

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