



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

CTCTGTACAC TGTCCCTCTCA CAGAACAAAGA AGGTATCTGG TCTACAAGAA -218
CTCGAGGCCT CACTGAAACG GAAAGCAAAT ACAAAAGAAC TTTATTTTAA -168
AAACATGTCT TGGTCTCCCA AGAAGAGGGC AATTGGATTG CTCAGCCAGA -118
ATGAAGAGTA GTTTACAGA AAAAAGAGGA CAATATTGGG ATCACCTTG -68
ACCTTTCCAT TTGGAAATAA TATTTCTAT TGTGTTATAG AAAGGTGGGA -18
AGCTTCATC CAGAACAA**ATG** AATTCATAA AGGACAATAG CCGAGCCCTT 33
ATTCAAAGAA TGGGAATGAC TGTTATAAAG CAAATCACAG ATGACCTATT 83
TGTATGG**A**AT GTTCTGAATC GCGAAGAAGT AAACATCATT TGCTGCGAGA 133 **N31H**
AGGTGGAGCA GGATGCTGCT AGAGGGATCA TTCACATGAT TTTGAAAAG 183
GGTT**C**AGAGT CCTGTAACCT CTTT**C**TTAAA TCCCTTAAGG AGTGGAACTA 233 **E64Rfs*4 L70F**
TCCTCTATT CAGGACTTGA ATGGACAAAG TCTTTTCAT CAGACAT**CAG** 283 **E95***
AAGGAGACTT GGACGATTTG GCTCAGGATT TAAAGGACTT GTACCATAACC 333
CCATCTTTTC TGAACTTTA TCCCCTTGGT GAAGATA**TG** ACATTATTTT 383 **I124T**
TAAC**TGAAA** AGCA**C**TTCA CAGAACCTGT CCTGTGGAGG AAGGACCAAC 433 **S132Afs*21 T133I**
ACCATCACCG CGTGGAGCAG CTGACCCCTGA ATGGCCTCCT GCAG**G**CTCTT 483 **A160T**
CAGAGCCCC**T** GCATCATTGA AGGGGAAT**CT** **GG**CAAAGGCA AGT**CC**ACT**CT** 533 **C165R S171F G172S T177A T177S**
GCTGCAG**CGA** ATTGCCATGC TCTGGGGCTC CGGAAAGTGC AAGGCTCTGA 583 **R181X**
CCAAGTTCAA ATTGTCTTC TTCCTCC**GTC** TCAG**CA**GGC CCAGGGTGGA 633 **R204H R207K**
CTTTTGAAA CCCTCTGTGA TCAACTCCTG GATATACTG GCACAAT**CAG** 683
GAAGCAGACA TTCATGGCCA TGCTGCTGAA GCTGCGGCAG AGGGTTCTTT 733
TCCTTCTTGA TGGCTACAAT GAATTCAAGC **CCC**AGAACTG CCCAGAAAT**C** 783 **P255L**
GAAGCCCTGA TAAAGGAAAA CCACCGCTTC AAGAACATGG TCATCGTCAC 833

CACTACCACT GAGTGCCCTGA GGCACATACG GCAGTTGGT GCCCTGACTG 883 C283G I287T G291S
CTGAGGTGGG GGATATGACA GAAGACAGCG CCCAGGCTCT CATCCGAGAA 933 R310*
GTGCTGATCA AGGAGCTTGC TGAAGGCTTG TTGCTCCAAA TTCAGAAATC 983
CAGGTGCTTG AGGAATCTCA TGAAGACCCC TCTCTTTGTG GTCATCACTT 1033 T337S T337N L339P V341L V341A I343N
GTGCAATCCA GATGGGTGAA AGTGAGTTCC ACTCTCACAC ACAAACAACG 1083
CTGTTCCATA CCTTCTATGA TCTGTTGATA CAGAAAAACA AACACAAAACA 1133 H376Y
TAAAGGTGTG GCTGCAAGTG ACTTCATCG GAGCCTGGAC CACTGTGGAG 1183 I387T H392del
ACCTAGCTCT GGAGGGTGTG TTCTCCCACA AGTTGATTT CGAACTGCAG 1233 V401A
GATGTGTCCA GCGTGAATGA GGATGTCCTG CTGACAACTG GGCTCCTCTG 1283
TAAATATACA GCTCAAAGGT TCAAGCCAAA GTATAAATTC ACAAGT 1333 H443P H443Q S445P
CATTCCAGGA GTACACAGCA GGACGAAGAC TCAGCAGTTT ATTGACGTCT 1383
CATGAGCCAG AGGAGGTGAC CAAGGGGAAT GGTTACTTGC AGAAAATGGT 1433
TTCCATTCG GACATTACAT CCACTTATAG CAGCCTGCTC CGGTACACCT 1483
GTGGGTCATC TGTGGAAGCC ACCAGGGCTG TTATGAAGCA CCTCGCAGCA 1533
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TTCTGAAAGC CATAAACATC AATTCCTTTTG TAGAGTGTGG CATCCATTTA 1683
TATCAAGAGA GTACATCCAA ATCAGCCCTG AGCCAAGAAT TTGAAGCTTT 1733
CTTTCAAGGT AAAAGCTTAT ATATCAACTC AGGGAACATC CCCGATTACT 1783
TATTGACTT CTTTGAACAT TTGCCAATT GTGCAAGTGC CCTGGACTTC 1833
ATTAAACTGG ACTTTATGG GGGAGCTATG GCTTCATGGG AAAAGGCTGC 1883
AGAAGACACA GGTGGAATCC ACATGGAAAGA GGCCCCAGAA ACCTACATTC 1933
CCAGCAGGGC TGTATCTTG TTCTCAACT GGAAGCAGGA ATTCAGGACT 1983 W655S W655C Q657L
CTGGAGGTCA CACTCCGGGA TTTCAGCAAG TTGAATAAGC AAGATATCAG 2033
ATATCTGGGG AAAATATTCA GCTCTGCCAC AAGCCTCAGG CTGCAAATAA 2083 L680M
AGAGATGTGC TGGTGTGGCT GGAAGCCTCA GTTGGTCCT CAGCACCTGT 2133
AAGAACATTT ATTCTCTCAT GGTGGAAGCC AGTCCCCTCA CCATAGAAGA 2183
TGAGAGGCAC ATCACATCTG TAACAAACCT GAAAACCTTG AGTATTCATG 2233

ACCTACAGAA TCAACGGCTG **CCGGGTCGTC** TGACTGACAG CTTGGGTAAC 2283 **P752L delexon5**
TTGAAGAACC TTACAAAGCT CATAATGGAT AACATAAAGA **TGAATGAAGA** 2333 **M775I**
AGATGCTATA AAACTAGCTG AAGGCCTGAA AAACCTGAAG AAGATGTGTT 2383 **G786V**
TATTCATTG GACCCACTTG TCTGACATTG GAGAGGGAAT GGATTACATA 2433 **L801V**
GTCAAGTCTC TGTCAAGTGA ACCCTGTGAC CTTGAAGAAA TTCAATTAGT 2483
CTCCTGCTGC TTGTC TGCAA ATGCAGTGAA AATCCTAGCT CAGAATCTC 2533
ACAATTGGT CAAACTGAGC ATTCTTGATT TATCAGAAAA TTACCTGGAA 2583
AAAGATGGAA ATGAAGCTCT TCATGAACGT ATCGACAGGA TGAACGTGCT 2633
AGAACCAGCTC ACCGCACTGA TGCTGCCCTG **GGGCTGTGAC** GTGCAAGGCA 2683 **Q880E C890R**
GCCTGAGCAG CCTGTTGAAA CATTGGAGG AGGTCCCACA ACTCGTCAAG 2733
CTTGGTTGA AAAACTGGAG ACTCACAGAT ACAGAGATTA GAATTTAGG 2783
TGCATTTTT GGAAAGAACCTCTGAAAA CTTCCAGCAG TTGAATTGG 2833 **A929S**
CGGGAAATCG TGTGAGCAGT GATGGATGGC TTGCCTTCAT GGGTGTATTT 2883
GAGAATCTTA AGCAATTAGT GTTTTTGAC TTTAGTACTA AAGAATTCT 2933
ACCTGATCCA GCATTAGTCA GAAAACCTAG CCAAGTGTAA TCCAAGTTAA 2983
CTTTCTGCA AGAAGCTAGG CTTGTTGGGT GGCAATTGA TGATGATGAT 3033
CTCAGTGTAA TTACAGGTGC TTTAAACTA GTAACTGCTT **AAATAAAGTG** *8
TACTCGAAC CA

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