



NOD2 (NM_022162.3) - cDNA - 2025-08-21

ACTTACTTGT GGCTGTCCC CTCGTGAATG TGTCTCATGT CCCCAGTGGG -247
GTTTTTCAGT GAGGGTCATG GTCTCCAGGA TGCACAAGGC TTTGTGCCAG -197
AATTGCTTGG AATTGCCAG TTCTGGAAGG CTGGTTGGCC AACTCTGGCC -147
TCCGGCTTTT CCTTTGGAA TTCCCTTGA AGGTGGGGTT GGTAGACAGA -97
TCCAGGCTCA CCAGTCCTGT GCCACTGGC TTTTGGCGTT CTGCACAAGG -47 c.-53C>T
CCTACCCGCA GATGCCATGC CTGCTCCCCC AGCCTAATGG GCTTGATGG 4
GGGAAGAGGG TGGTCAGCC TCTCACGATG AGGAGGAAAG AGCAAGTGTc 54
CTCCTCGGAC ATTCTCCGGG TTGTGAAATG TGCTCGCAGG AGGCTTTCA 104
GGCACAGAG AGCCAGCTGG TCGAGCTGCT GGTCTCAGGG TCCCTGGAAG 154 R38M E43Y
GCTTCGAGAG TGTCTGGAC TGGCTGCTGT CCTGGGAGGT CCTCTCCTGG 204
GAGGACTACCG AGGGCTTCCA CCTCCTGGC CAGCCTCTT CCCACTTGGC 254 L81V
CAGGCGCCTT CTGGACACCG TCTGGAATAA GGGTACTTGG GCCTGTcAGA 304 T91A
AGCTCATCGC GGCTGCCAA GAAGCCCAGG CCGACAGCCA GTCCCCAAG 354 A105A D113N
CTGCATGGCT GCTGGGACCC CCACTCGCTC CACCCAGCCC GAGACCTGCA 404 L119L
GAGTCACCGG CCAGCATTG TCAGGAGGCT CCACAGCCAT GTGGAGAAC 454 R138Q A140T
TGCTGGACCT GGCATGGGAG CGGGGTTTCG TCAGCCAGTA TGAATGTGAT 504 D154N L155Q W157R
GAAATCAGGT TGCCGATCTT CACACCGTCC CAGAGGGCAA GAAGGCTGCT 554 S178S
TGATCTTGCC ACGGTGAAAG CGAATGGATT GGCTGCCTTC CTTCTACAAAC 604 T189M T189T F198L
ATGTTCAGGA ATTACCAGTC CCATTGGCCC TGCCTTGGA AGCTGCCACA 654 P207A A211A
TGCAAGAAGT ATATGCCA GCTGAGGACC ACGGTGTCTG CTCAGTCTCG 704 K225M Q233X R235C
CTTCCTCAGT ACCTATGATG GAGCAGAGAC GCTCTGCCTG GAGGACATAT 754 T245M L248R
ACACAGAGAA TGTCTGGAG GTCTGGCAG ATGTGGCAT GGCTGGCC 804 P268S/SNP5

CCGCAGAAGA GCCCAGCCAC CCTGGGCCTG GAGGAGCTCT TCAGCACCCC 854
TGGCCACCTC AAATGACGATG CGGACACTGT GCTGGTGGTG GGTGAGGCCG 904 H287Y N289S D291N A292V T294S V298V A301V
GCAGTGGCAA GAGCACGCTC CTGCAGCGC TGCACTTGCT GTGGGCTGCA 954 R311W
GGGCAAGACT TCCAGGAATT TCTCTTGTC TTCCCCATTCA GCTGC~~CGGCA~~ 1004 R334W R334Q
GCTGCAGTGC ATGGCAAAC CACTCTGT GCGGACT~~CTA~~ CTCTTGAGC 1054 L348V L349F
ACTGCTGTTG GCCTGA~~TGTT~~ GGTCAAGAAG ACATCTCCA GTTACTCCTT 1104 H352R W355X D357A I363F
GACCACCCCTG ACC~~G~~TGTCCT GTTAACCTT GATGGCTTG ACGA~~G~~TTCAA 1154 H343Y R373C D382N D382E E383K E383G
GTTCA~~G~~TT AC~~G~~GA~~T~~CGTG AACGCCACTG CTCCCCGACC GACCCCACCT 1204 D390V R391C R393H P397L
CTGTCCAGAC CCTGCTCTTC AACCTCTGC AGGGCA~~AC~~CT GCTGAAGAA~~T~~ 1254 N414S
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GAAGTACATC CGCACCGAGT TCAACCTCAA GGGCTTCTCT GAACAGGGCA 1354 E441K
TCGAGCTGTA CCTGAGGAAG CGC~~C~~CATCATG AG~~CCC~~GGGT GGCGGAC~~CG~~C 1404 L456L R459R/SNP6 P463A G464W R468C
~~C~~TCATCCGCC TGCTCCAAGA G~~A~~CCTCAGCC CTGCACGGTT TGTG~~C~~CACCT 1454 L469F R471C T476P H480R G481D c.1447T>C C483W
GCC~~T~~GCTCTTC TCATGGATGG TGTCAAATG CC~~A~~CCAGGA~~A~~ CTGTTG~~T~~GC 1504 W490L W490S C495Y H496L E498 L500delinsV E498D L501P
AGGAGGGGG GT~~CC~~CAAAG ACCACTACAG ATATGTACCT GCTGATTCTG 1554 E503E S506Pfs*11 P507S T510I D512H D512Y D512V M513T M513R
CAGCATTTC TGCTGCATGC CACCC~~CC~~CA GACTCAGCTT CCCAAGGTCT 1604 H520Y P527P
GGGACCCAGT CTTCT~~TC~~GGG GCCGCCTCCC CACCC~~T~~CCTG CAC~~T~~GGGCA 1654 R541fs R541W R541P L550V
GA~~T~~GGCTCT GTGGGCC~~T~~G GGCATGTGCT GCTACGTGTT CTCAGCCCAG 1704 558DELLG Y563H
CAGCTCCAGG CAGCACAGGT CAGCCCTGAT GACATTCTC TTGGCTTCT 1754
GGTGC~~G~~TGCC AAAGGTGTCG TGCCAGGGAG TAC~~G~~CGCCC CT~~G~~AATTCC 1804 R587C R587R/SNP7 T596T E600K E600A
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GCTGATGTGC CACCAGCTT GCTCAGACAC CTCTCAATT GTGGCAGGCC 1904
AGGCAACTCA CCAATGGCCA GGCTCCTGCC CACGATGTGC ATCCAGGCC 1954
CGGAGGGAAA GGACAGCAGC GTGGCAGCTT TGCTGCAGAA GGCC~~G~~AGCCG 2004 E667K P668L
CACAA~~C~~CTTC AGATCA~~C~~AGC AGC~~C~~TT~~C~~CTG GCAGGGCTGT T~~G~~TCC~~CG~~GA 2054 N670K T674I F677L L682F R684W R684O
GCACTGGGGC CTGCTGGCTG AGTGCCAGAC ATCTGAGAAG GCCCTG~~T~~CC 2104 R702W/SNP8
GGC~~G~~CCAGGC CTGTGCCCGC TGGTGTCTGG CC~~CG~~CAGCCT CCGCAAGCAC 2154 R703C R713C R713H R716C
T~~T~~CCACTCCA TCCC~~G~~CCAGC TGCAC~~G~~GGGT GAGGCCAAGA GCGTGCATGC 2204 A725G P727L V733L

CATGCCCGGG TTCAT**C**TGGC TCAT**C**GGAG CCTGTACGAG ATGCAGGAGG 2254 I740I R744W
AGCGGCTGG**C** TCGGAAGG**CT** GCA**CGT**GGCC TGAATGTTGG GCACCTCAAG 2304 A755V A758V R760C
TTGACATTTT GCAGTGTGGG CCCC**ACTGAG** TGTGCTGCC TGGCCTTGT 2354 E778K
GCTGCAGCAC CTC**CGGCGGC** CCC**GT**GGCC GCAGCTGGAC TACA**ACTCTG** 2404 R790W R791W R791Q V793M
TGGGTGACAT TGGCGTGGAG CAGCTGCTGC CTTGCC**TTGG** T**G**TCTGCAAG 2454 V802V Q809K V816I
GCTCTGTATT TGCGCGATAA CAATATCTCA GACCGAGGCA TCTGCAAG**CT** 2504 D824N N825K
CA**T**GAA**TGT** GCTCTTC**ACT** GCGAGCAATT GCAGAA**GTTA** G**C**TCTATT**CA** 2554 I836T C842Y E843K A849V
ACA**A**CAAATT GACTGACGGC TGTGCACACT CC**ATG**GCTAA GCTCCTTG**CA** 2604 N852S N853S M863V A864T
TGCAGGCAGA ACTT**CTTGGC** ATTGAGGCTG GGGAATAACT ACAT**CACTGC** 2654 F873E A885T A885P
CGCGGGAGCC CAAGTGCTGG CCGAGGGGCT CCGAGGCAAC ACCTCCTTG**U** 2704 A886T R896X Q902K
AGTTCC**TGGGGC** AACAGAGTGG GT**G**C**GAGGG** GGCC**CAGG****CC** 2754 W907R G908R/SNP12 G908C D913D E914K A918D
CTGGCTGAAG CCTTGG**GTGA** TCACCAGAGC TTGAGGTGGC TCAGCCTG**GT** 2804 G924D V935M
GGGGAA**CAAC** ATTGGCAGTG TGGGTGCCA AGCCTTG**CA** CTGATGCTGG 2854 I939V I939I
CAAAGAAC**GT** CATGCTAGAA GAA**CTTGCC** TGGAGGAGAA CC**ATCTCCAG** 2904 V955I H966R
GAT**G**AAGGT**G** TATGTTCT**CT** CCGAGAAGGA CTGAAGAAAA ATTCAAG**TTT** 2954 E970G V972I L975V L975L G978E
GAAAATCCTG AAGTTGTCCA ATA**ACTGCAT** CACCTACCTA GGGGCAGAAG 3004 c.2998G>A
CCCTCCTG**CA** GGCC**CTT**GAA AGGAATGACA CCATCCTGG**A** GTCTGG**CTC** 3054 1007FS/SNP13
CGAGGGAA**ACA** CTTTCTCT**CT** AGAGGAGGTT GACAAGCT**CG** GCTGCAGGG**A** 3104 R1019X R1019G R1019L
CACCAGACTC TTGCTT**TGAA** GTCTCC**GGGA** GGATGTT**CGT** CTCAGTTTGT *31 c.*9G>A
TTGTGAGCAG GCTGTGAGTT TGGGCC**CCAG** AGGCTGGGTG ACATGTGTTG *81
GCAGCCTCTT CAAAATGAGC CCTGTCCTGC CTAAGGCTGA ACTTGT**TTTC** *131
TGGGAACACC ATAGGT**CACC** TTTATTCTGG CAGAGGAGGG AGCATCAG**GTG** *181
CCCTCCAGGA TAGACTTT**TC** CCAAGCCTAC TTTGCCATT GACTTCTTCC *231
CAAGATTCAA TCCCAGGATG TACAAGGACA GCCCCTCCTC CATA**GTATGG** *281
GACTGGCCTC TGCTGATCCT CCCAGGCTTC CGTGTGGTC AGTGGGGCCC *331
ATGGATGTGC TTGTTAACTG AGTGC**CTTTT** GGTGGAGAGG CCC**GGCCTCT** *381 c.3498G>A
CACAAAAGAC CCCTTAC**ACAC** TGCTCTGATG AAGAGGAGTA CACAGAACAC *431
ATAATT**CAGG** AAGCAGCTTT CCCC**CATGTCT** CGACTCATCC ATCCAGGG**CA** *481

TTCCCCGTCT CTGGTTCCTC CCCTCCTCCT GGACTCCTGC ACACGCTCCT *531
TCCTCTGAGG CTGAAATTCA GAATATTAGT GACCTCAGCT TTGATATTC *581
ACTTACAGCA CCCCCAACCC TGGCACCCAG GGTGGGAAGG GCTACACCTT *631
AGCCTGCCCT CCTTTCCGGT GTTTAAGACA TTTTGGAAG GGGACACGTG *681
ACAGCCGTTT GTTCCCCAAG ACATTCTAGG TTTGCAAGAA AAATATGACC *731
ACACTCCAGC TGGGATCACA TGTGGACTTT TATTTCAGT GAAATCAGTT *781
ACTCTTCAGT TAAGCCTTG GAAACAGCTC GACTTTAAAA AGCTCCAAAT *831
GCAGCTTTAA AAAATAATC TGGGCCAGAA TTTCAAACGG CCTCACTAGG *881 *873C>T
CTTCTGGTTG ATGCCTGTGA ACTGAACTCT GACAACAGAC TTCTGAAATA *931
GACCCACAAG AGGCAGTTCC ATTCATTG TGCCAGAATG CTTTAGGATG *981
TACAGTTATG GATTGAAAGT TTACAGGAAA AAAAATTAGG CCGTTCCTC *1031 c.3505C>T *1030T>C
AAAGCAAATG TCTTCCTGGA TTATTCAAAA TGATGTATGT TGAAGCCTTT *1081
GTAAATTGTC AGATGCTGTG CAAATGTTAT TATTTAAC ATTATGATGT *1131
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