



## NOD2 (NM\_022162.3) - cDNA + Protein - 2024-12-04

ACTTACTTGT GGCCTGTCCC CTCGTGAATG TGTCTCATGT CCCAGTGGG -247  
GTTTTTCAGT GAGGGTCATG GTCTCCAGGA TGCACAAGGC TTTGTGCCAG -197  
AATTGCTTGG AATTGCCTAG TTCTGGAAGG CTGGTTGGCC AACTCTGGCC -147  
TCCGGCTTTT CCTTTGGGAA TTTCCCTTGA AGGTGGGGTT GGTAGACAGA -97  
TCCAGGCTCA CCAGTCCTGT GCCACTGGGC TTTTGGCGTT CTGCACAAGG -47 c.-53C>T  
CCTACCCGCA GATGCCATGC CTGCTCCCC AGCCTAATGG GCTTTGATGG 4  
MetG 2

GGGAAGAGGG TGGTTCAGCC TCTCACGATG AGGAGGAAAG AGCAAGTGTC 54  
lyGluGluG1 yGlySerAla SerHisAspG luGluGluAr gAlaSerVal 18

CTCCTCGGAC ATTCTCCGGG TTGTGAAATG TGCTCGCAGG AGGCTTTTCA 104  
LeuLeuGlyH isSerProG1 yCysGluMet CysSerGlnG luAlaPheG1 35

GGCACAGAGG AGCCAGCTGG TCGAGCTGCT GGTCTCAGGG TCCCTGGAAG 154 R38M E43Y  
nAlaGlnArg SerGlnLeuV alGluLeuLe uValSerGly SerLeuGluG 52

GCTTCGAGAG TGTCCGGAC TGGCTGCTGT CCTGGGAGGT CCTCTCCTGG 204  
lyPheGluSe rValLeuAsp TrpLeuLeuS erTrpGluVa lLeuSerTrp 68

GAGGACTACG AGGGCTTCCA CCTCCTGGGC CAGCCTCTCT CCCACTTGGC 254 L81Y  
GluAspTyrG luGlyPheHi sLeuLeuGly GlnProLeuS erHisLeuAl 85

CAGGCGCCTT CTGGAC~~A~~CCG TCTGGAATAA GGGTACTTGG GCCTGTCAGA 304 [T91A](#)  
aArgArgLeu LeuAspThrV alTrpAsnLy sGlyThrTrp AlaCysGlnL 102

AGCTCATCGC ~~G~~GCTGCCCAA GAAGCCCAGG ~~C~~GACAGCCA GTCCCCCAAG 354 [A105A](#) [D113N](#)  
ysLeuIleAl aAlaAlaGln GluAlaGlnA laAspSerGl nSerProLys 118

CT~~G~~CATGGCT GCTGGGACCC CCACTCGCTC CACCCAGCCC GAGACCTGCA 404 [L119L](#)  
LeuHisGlyC ysTrpAspPr oHisSerLeu HisProAlaA rgAspLeuGl 135

GAGTCACCGG ~~C~~CA~~G~~CCATTG TCAGGAGGCT CCACAGCCAT GTGGAGAACA 454 [R138Q](#) [A140T](#)  
nSerHisArg ProAlaIleV alArgArgLe uHisSerHis ValGluAsnM 152

TGCTG~~G~~ACCT ~~G~~GCA~~T~~GGGAG CGGGGTTTCG TCAGCCAGTA TGAATGTGAT 504 [D154N](#) [L155Q](#) [W157R](#)  
etLeuAspLe uAlaTrpGlu ArgGlyPheV alSerGlnTy rGluCysAsp 168

GAAATCAGGT TGCCGATCTT CACACCGT~~C~~C CAGAGGGCAA GAAGGCTGCT 554 [S178S](#)  
GluIleArgL euProIlePh eThrProSer GlnArgAlaA rgArgLeuLe 185

TGATCTTGCC ~~A~~CGGTGAAAG CGAATGGATT GGCTGCCTT~~C~~ CTTCTACAAC 604 [T189M](#) [T189T](#) [F198L](#)  
uAspLeuAla ThrValLysA laAsnGlyLe uAlaAlaPhe LeuLeuGlnH 202

ATGTTTCAGGA ATTA~~C~~CAGTC CCATTGGC~~C~~C TGCCTTTGGA AGCTGCCACA 654 [P207A](#) [A211A](#)  
isValGlnGl uLeuProVal ProLeuAlaL euProLeuGl uAlaAlaThr 218

TGCAAGAAGT ATATGGCCA~~A~~ GCTGAGGACC ACGGTGTCTG CT~~C~~AGTCT~~C~~G 704 [K225M](#) [Q233X](#) [R235C](#)  
CysLysLysT yrMetAlaLy sLeuArgThr ThrValSerA laGlnSerAr 235

CTTCCTCAGT ACCTATGATG GAGCAGAGAC GCTCTGCCIG GAGGACATAT 754 [T245M](#) [L248R](#)

gPheLeuSer ThrTyrAspG lyAlaGluTh rLeuCysLeu GluAspIleT 252

ACACAGAGAA TGTCTGGAG GTCTGGGCAG ATGTGGGCAT GGCTGGA~~CCC~~ 804 [P268S/SNP5](#)

yrThrGluAs nValLeuGlu ValTrpAlaA spValGlyMe tAlaGlyPro 268

CCGCAGAAGA GCCCAGCCAC CCTGGGCCTG GAGGAGCTCT TCAGCACCCC 854

ProGlnLysS erProAlaTh rLeuGlyLeu GluGluLeuP heSerThrPr 285

TGGC~~CACCTC~~ [AATGACGATG](#) [CGGACACTGT](#) GCTGGTGGTG GGTGAGG~~CGG~~ 904 [H287Y](#) [N289S](#) [D291N](#) [A292V](#) [T294S](#) [V298V](#) [A301V](#)

oGlyHisLeu AsnAspAspA laAspThrVa lLeuValVal GlyGluAlaG 302

GCA~~GTGGCAA~~ GAGCACGCTC CTGCAG~~CGGC~~ TGCAC~~TTGCT~~ GTGGGCTGCA 954 [R311W](#)

lySerGlyLy sSerThrLeu LeuGlnArgL euHisLeuLe uTrpAlaAla 318

GGGCAAGACT TCCAGGAATT TCTCTTTGTC TTCCCATTC A GCTGC~~CGGCA~~ 1004 [R334W](#) [R334Q](#)

GlyGlnAspP heGlnGluPh eLeuPheVal PheProPheS erCysArgGl 335

GCTGCAGTGC ATGGCCAAAC CACTCTCTGT GCGGACT~~CTA~~ ~~CTCTTTGAGC~~ 1054 [L348V](#) [L349F](#)

nLeuGlnCys MetAlaLysP roLeuSerVa lArgThrLeu LeuPheGluH 352

~~ACTGCTGTTG~~ [GCCTGATGTT](#) GGTCAAGAAG ~~ACATCTTCCA~~ GTTACTCCTT 1104 [H352R](#) [W355X](#) [D357A](#) [I363F](#)

isCysCysTr pProAspVal GlyGlnGluA spIlePheGl nLeuLeuLeu 368

GAC~~CACCCTG~~ [ACC~~GTGTCCT~~](#) GTTAACCTTT GATGGCTTTG [ACGA~~GTTCAA~~](#) 1154 [H343Y](#) [R373C](#) [D382N](#) [D382E](#) [E383K](#) [E383G](#)

AspHisProA spArgValLe uLeuThrPhe AspGlyPheA spGluPheLy 385

G~~TTCAGGTTTC~~ [ACGA~~TCTGTG~~](#) AAC~~GCCACTG~~ CTCCC~~CGACC~~ GACCCACCT 1204 [D390V](#) [R391C](#) [R393H](#) [P397L](#)

sPheArgPhe ThrAspArgG luArgHisCy sSerProThr AspProThrS 402

CTGTCCAGAC CCTGCTCTTC AACCTTCTGC AGGGCA~~A~~CCT GCTGAAGAAT 1254 [N414S](#)

erValGlnTh rLeuLeuPhe AsnLeuLeuG lnGlyAsnLe uLeuLysAsn 418

GCCCCAAGG TGGTGACCAG CCGT~~C~~CGGCC GCTGTGT~~C~~GG ~~C~~GTTCCCTCAG 1304 [R426H](#) [P427S](#) [P427P](#) [S431L](#) [A432V](#)

AlaArgLysV alValThrSe rArgProAla AlaValSerA laPheLeuAr 435

GAAGTACATC CGCACCGAGT TCAACCTCAA GGGCTTCTCT GAACAGGGCA 1354 [E441K](#)

gLysTyrIle ArgThrGluP heAsnLeuLy sGlyPheSer GluGlnGlyI 452

TCGAGCTGTA C~~C~~TGAGGAAG CG~~C~~CATCATG AG~~C~~CCGGGGT GGCGGAC~~C~~GC 1404 [L456L](#) [R459R/SNP6](#) [P463A](#) [G464W](#) [R468C](#)

leGluLeuTy rLeuArgLys ArgHisHisG luProGlyVa lAlaAspArg 468

~~C~~TCATC~~C~~GCC TGCTCCAAGA G~~A~~CCTCAGCC CTGC~~A~~CGGT TG~~T~~G~~C~~CACCT 1454 [L469F](#) [R471C](#) [T476P](#) [H480R](#) [G481D](#) [c.1447T>C](#) [C483W](#)

LeuIleArgL euLeuGlnGl uThrSerAla LeuHisGlyL euCysHisLe 485

GCCTGTCTTC TCAT~~G~~GATGG TGTCCAAAT~~G~~ CC~~A~~CCAGG~~AA~~ CTGTTGCT~~T~~GC 1504 [W490L](#) [W490S](#) [C495Y](#) [H496L](#) [E498](#) [L500delinsV](#) [E498D](#) [L501P](#)

uProValPhe SerTrpMetV alSerLysCy sHisGlnGlu LeuLeuLeuG 502

AGGAGGGGGG G~~T~~CC~~C~~CAAAG ACCA~~C~~TACAG ~~A~~TATGTACCT GCTGATTCTG 1554 [E503E](#) [S506Pfs\\*11](#) [P507S](#) [T510I](#) [D512H](#) [D512Y](#) [D512V](#) [M513T](#) [M513R](#)

lnGluGlyGl ySerProLys ThrThrThrA spMetTyrLe uLeuIleLeu 518

CAG~~C~~ATTTTC TGCTGCATGC CACCCC~~C~~CCA GACTCAGCTT CCCAAGGTCT 1604 [H520Y](#) [P527P](#)

GlnHisPheL euLeuHisAl aThrProPro AspSerAlaS erGlnGlyLe 535

GGGACCCAGT CTTCT~~T~~CGGG GCCGCCTCCC CACCCTCCTG CAC~~C~~TGGGCA 1654 [R541fs](#) [R541W](#) [R541P](#) [L550V](#)

uGlyProSer LeuLeuArgG lyArgLeuPr oThrLeuLeu HisLeuGlyA 552

GACTGGCTCT GTGGGGCCTG GGCATGTGCT GCTACGTGTT CTCAGCCCAG 1704 [558DELLG](#) [Y563H](#)

rgLeuAlaLe uTrpGlyLeu GlyMetCysC ysTyrValPh eSerAlaGln 568

CAGCTCCAGG CAGCACAGGT CAGCCCTGAT GACATTTCTC TTGGCTTCCT 1754

GlnLeuGlnA laAlaGlnVa lSerProAsp AspIleSerL euGlyPheLe 585

GGTGCGTGCC AAAGGTGTCTG TGCCAGGGAG TACGGCGCCC CTGGAATTCC 1804 [R587C](#) [R587R/SNP7](#) [T596T](#) [E600K](#) [E600A](#)

uValArgAla LysGlyValV alProGlySe rThrAlaPro LeuGluPheL 602

TTCACATCAC TTTCCAGTGC TTCTTTGCCG CGTTCTACCT GGCCTCAGT 1854 [H603R](#) [T605P](#) [T605N](#) [A611A](#) [A612T](#) [A612V](#)

euHisIleTh rPheGlnCys PhePheAlaA laPheTyrLe uAlaLeuSer 618

GCTGATGTGC CACCAGCTTT GCTCAGACAC CTCTTCAATT GTGGCAGGCC 1904

AlaAspValP roProAlaLe uLeuArgHis LeuPheAsnC ysGlyArgPr 635

AGGCAACTCA CCAATGGCCA GGCTCCTGCC CACGATGTGC ATCCAGGCCT 1954

oGlyAsnSer ProMetAlaA rgLeuLeuPr oThrMetCys ileGlnAlaS 652

CGGAGGGAAA GGACAGCAGC GTGGCAGCTT TGCTGCAGAA GGCCGAGCCG 2004 [E667K](#) [P668L](#)

erGluGlyLy sAspSerSer ValAlaAlaL euLeuGlnLy sAlaGluPro 668

CACAACTTTC AGATCACAGC AGCCTTCTTG GCAGGGCTGT TGTCCCGGGA 2054 [N670K](#) [T674I](#) [F677L](#) [L682F](#) [R684W](#) [R684Q](#)

HisAsnLeuG lnIleThrAl aAlaPheLeu AlaGlyLeuL euSerArgGl 685

GCACTGGGGC CTGCTGGCTG AGTGCCAGAC ATCTGAGAAG GCCCTGCTCC 2104 [R702W/SNP8](#)

uHisTrpGly LeuLeuAlaG luCysGlnTh rSerGluLys AlaLeuLeuA 702

GGCGCCAGGC CTGTGCCCCG TGGTGTCTGG CCGCAGCCT CCGCAAGCAC 2154 R703C R713C R713H R716C

rgArgGlnAl aCysAlaArg TrpCysLeuA laArgSerLe uArgLysHis 718

TTCCACTCCA TCCC GCCAGC TGCACCGGGT GAGGCCAAGA GC GTGCATGC 2204 A725G P727L V733L

PheHisSerI leProProAl aAlaProGly GluAlaLysS erValHisAl 735

CATGCCCGGG TTCATCTGGC TCATCCGGAG CCTGTACGAG ATGCAGGAG 2254 I740I R744W

aMetProGly PheIleTrpL euIleArgSe rLeuTyrGlu MetGlnGluG 752

AGCGGCTGGC TCGGAAGGCT GCACTGGCC TGAATGTTGG GCACCTCAAG 2304 A755V A758V R760C

luArgLeuAl aArgLysAla AlaArgGlyL euAsnValGl yHisLeuLys 768

TTGACATTTT GCAGTGTGGG CCCCACTGAG TGTGCTGCCC TGGCCTTTGT 2354 E778K

LeuThrPheC ysSerValGl yProThrGlu CysAlaAlaL euAlaPheVa 785

GCTGCAGCAC CTCGGCGGC CCGTGGCCCT GCAGCTGGAC TACAACCTCTG 2404 R790W R791W R791Q V793M

lLeuGlnHis LeuArgArgP roValAlaLe uGlnLeuAsp TyrAsnSerV 802

TGGGTGACAT TGGCGTGGAG CAGCTGCTGC CTTGCCTTGG TGTCTGCAAG 2454 V802V Q809K V816I

alGlyAspI1 eGlyValGlu GlnLeuLeuP roCysLeuGl yValCysLys 818

GCTCTGTATT TGCGCATAA CAATATCTCA GACCGAGGCA TCTGCAAGCT 2504 D824N N825K

AlaLeuTyrL euArgAspAs nAsnIleSer AspArgGlyI leCysLysLe 835

CAITGAATGT GCTCTTCACT GCGAGCAATT GCAGAAGTTA GCTCTATTCA 2554 I836T C842Y E843K A849V

uIleGluCys AlaLeuHisC ysGluGlnLe uGlnLysLeu AlaLeuPheA 852

ACAACAAATT GACTGACGGC TGTGCACACT CCAATGGCTAA GCTCCTTGCA 2604 N852S N853S M863V A864T

snAsnLysLe uThrAspGly CysAlaHisS erMetAlaLy sLeuLeuAla 868

TGCAGGCAGA ACTTCTTGGC ATTGAGGCTG GGGAACTAACT ACATCACTGC 2654 F873F A885T A885P

CysArgGlnA snPheLeuAl aLeuArgLeu GlyAsnAsnT yrIleThrAl 885

CGCGGGAGCC CAAGTGCTGG CCGAGGGGCT CCGAGGCAAC ACCTCCTTGC 2704 A886T R896X Q902K

aAlaGlyAla GlnValLeuA laGluGlyLe uArgGlyAsn ThrSerLeuG 902

AGTTCCCTGGG ATTCITGGGCG AACAGAGTGG GTGACGAGGG GGCCCAGGCC 2754 W907R G908R/SNP12 G908C D913D E914K A918D

lnPheLeuGl yPheTrpGly AsnArgValG lyAspGluGl yAlaGlnAla 918

CTGGCTGAAG CCTTGGGTGA TCACCAGAGC TTGAGGTGGC TCAGCCTGCT 2804 G924D V935M

LeuAlaGluA laLeuGlyAs pHisGlnSer LeuArgTrpL euSerLeuVa 935

GGGGAACAAC ATITGGCAGTG TGGGTGCCCA AGCCTTGGCA CTGATGCTGG 2854 I939V I939I

lGlyAsnAsn ileGlySerV alGlyAlaGl nAlaLeuAla LeuMetLeuA 952

CAAAGAACGT CATGCTAGAA GAACTCTGCC TGGAGGAGAA CCACTCTCCAG 2904 V955I H966R

laLysAsnVa lMetLeuGlu GluLeuCysL euGluGluAs nHisLeuGln 968

GATGAAGGTG TATGTTCTCT CGCAGAAGGA CTGAAGAAAA ATTCAAGTTT 2954 E970G V972I L975V L975L G978E

AspGluGlyV alCysSerLe uAlaGluGly LeuLysLysA snSerSerLe 985

GAAAATCCTG AAGTTGTCCA ATAACCTGCAT CACCTACCTA GGGGCAGAAG 3004 c.2998G>A

uLysIleLeu LysLeuSerA snAsnCysIl eThrTyrLeu GlyAlaGluA 1002

CCCTCCTGCA GGCCCTTGAA AGGAATGACA CCATCCTGGA AGTCTGGCTC 3054 1007FS/SNP13

laLeuLeuGl nAlaLeuGlu ArgAsnAspT hrIleLeuGl uValTrpLeu 1018

CGAGGGAACA CTTTCTCTCT AGAGGAGGTT GACAAGCTCG GCTGCAGGGA 3104 R1019X R1019G R1019L  
 ArgGlyAsnT hrPheSerLe uGluGluVal AspLysLeuG lyCysArgAs 1035

CACCAGACTC TTGCTTTGAA GTCTCCGGGA GGATGTTTCGT CTCAGTTTGT \*31 c.\*9G>A  
 pThrArgLeu LeuLeuStop

TTGTGAGCAG GCTGTGAGTT TGGGCCCCAG AGGCTGGGTG ACATGTGTTG \*81  
 GCAGCCTCTT CAAAATGAGC CCTGTCCGTC CTAAGGCTGA ACTTGTTTTT \*131  
 TGGGAACACC ATAGGTCACC TTTATTCTGG CAGAGGAGGG AGCATCAGTG \*181  
 CCCTCCAGGA TAGACTTTTC CCAAGCCTAC TTTTGCCATT GACTTCTTCC \*231  
 CAAGATTCAA TCCCAGGATG TACAAGGACA GCCCCTCCTC CATAGTATGG \*281  
 GACTGGCCTC TGCTGATCCT CCCAGGCTTC CGTGTGGGTG AGTGGGGCCC \*331  
 ATGGATGTGC TTGTTAACTG AGTGCCTTTT GGTGGAGAGG CCCGGCCTCT \*381 c.3498G>A  
 CACAAAAGAC CCCTTACCAC TGCTCTGATG AAGAGGAGTA CACAGAACAC \*431  
 ATAATTCAGG AAGCAGCTTT CCCCATGTCT CGACTCATCC ATCCAGGCCA \*481  
 TTCCCCGTCT CTGGTTCCTC CCCTCCTCCT GGACTCCTGC ACACGCTCCT \*531  
 TCCTCTGAGG CTGAAATTCA GAATATTAGT GACCTCAGCT TTGATATTTT \*581  
 ACTTACAGCA CCCCCAACC TGGCACCCAG GGTGGGAAGG GCTACACCTT \*631  
 AGCCTGCCCT CTTTCCGGT GTTTAAGACA TTTTGGGAAG GGGACACGTG \*681  
 ACAGCCGTTT GTTCCCCAAG ACATTCCTAG TTTGCAAGAA AAATATGACC \*731  
 ACACTCCAGC TGGGATCACA TGTGGACTTT TATTTCAGT GAAATCAGTT \*781  
 ACTCTTCAGT TAAGCCTTTG GAAACAGCTC GACTTTAAAA AGCTCCAAAT \*831  
 GCAGCTTTAA AAAATTAATC TGGGCCAGAA TTTCAAACGG CCTCACTAGG \*881 \*873C>T  
 CTTCTGGTTG ATGCCTGTGA ACTGAACTCT GACAACAGAC TTCTGAAATA \*931  
 GACCCACAAG AGGCAGTTCC ATTTCAATTTG TGCCAGAATG CTTTAGGATG \*981  
TACAGTTATG GATTGAAAGT TTACAGGAAA AAAAATTAGG CCGTTCCTTC \*1031 c.3505C>T \*1030T>C  
 AAAGCAAATG TCTTCCTGGA TTATTCAAAA TGATGTATGT TGAAGCCTTT \*1081



GTAAATTGTC AGATGCTGTG CAAATGTTAT TATTTTAAAC ATTATGATGT \*1131  
GTGAAACTG GTTAATATTT ATAGGTCACT TTGTTTTACT GTCTTAAGTT \*1181  
TATACTCTTA TAGACAACAT GGCCGTGAAC TTTATGCTGT AAATAATCAG \*1231 c.4323A>G  
AGGGGAATAA ACTGTTGAGT CAAAA

NOD2 (NM\_022162.3) - cDNA + Protein - 2024-12-04

