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

```
ACTTACTTGT GGCCTGTCCC CTCGTGAATG TGTCTCATGT CCCCAGTGGG -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 CTGCTCCCCC AGCCTAATGG GCTTTGATGG 4
                                                MetG 2

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

CTCCTCGGAC ATTCTCCGGG TTGTGAAATG TGCTCGCAGG AGGCTTTTCA 104
LeuLeuGlyH isSerProGl yCysGluMet CysSerGlnG luAlaPheGl 35

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

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

GAGGACTACG AGGGCTTCCA CCTCCTGGGC CAGCCTCTCT CCCACTTGGC 254  L81V
GluAspTyrG luGlyPheHi sLeuLeuGly GlnProLeuS erHisLeuAl 85
```

```
CAGGCGCCTT CTGGACACCG TCTGGAATAA GGGTACTTGG GCCTGTCAGA 304  T91A
aArgArgLeu LeuAspThrV alTrpAsnLy sGlyThrTrp AlaCysGlnL 102

AGCTCATCGC GGCTGCCCAA GAAGCCCAGG CCGACAGCCA GTCCCCCAAG 354  A105A D113N
ysLeuIleAl aAlaAlaGln GluAlaGlnA laAspSerGl nSerProLys 118

CTGCATGGCT GCTGGGACCC CCACTCGCTC CACCCAGCCC GAGACCTGCA 404  L119L
LeuHisGlyC ysTrpAspPr oHisSerLeu HisProAlaA rgAspLeuGl 135

GAGTCACCGG CCAGCCATTG TCAGGAGGCT CCACAGCCAT GTGGAGAACA 454  R138Q A140T
nSerHisArg ProAlaIleV alArgArgLe uHisSerHis ValGluAsnM 152

TGCTGGACCT GGCATGGGAG CGGGGTTTCG TCAGCCAGTA TGAATGTGAT 504  D154N L155Q W157R
etLeuAspLe uAlaTrpGlu ArgGlyPheV alSerGlnTy rGluCysAsp 168

GAAATCAGGT TGCCGATCTT CACACCGTCC CAGAGGGCAA GAAGGCTGCT 554  S178S
GluIleArgL euProIlePh eThrProSer GlnArgAlaA rgArgLeuLe 185

TGATCTTGCC ACGGTGAAAG CGAATGGATT GGCTGCCTTC CTTCTACAAC 604  T189M T189T F198L
uAspLeuAla ThrValLysA laAsnGlyLe uAlaAlaPhe LeuLeuGlnH 202

ATGTTCAGGA ATTACCAGTC CCATTGGCCC TGCCTTTGGA AGCTGCCACA 654  P207A A211A
isValGlnGl uLeuProVal ProLeuAlaL euProLeuGl uAlaAlaThr 218

TGCAAGAAGT ATATGGCCAA GCTGAGGACC ACGGTGTCTG CTCAGTCTCG 704  K225M Q233X R235C
CysLysLysT yrMetAlaLy sLeuArgThr ThrValSerA laGlnSerAr 235
```

CTTCCTCAGT ACCTATGATG GAGCAGAGAC GCTCTGCCTG GAGGACATAT 754 T245M L248R

gPheLeuSer ThrTyrAspG lyAlaGluTh rLeuCysLeu GluAspIleT 252

ACACAGAGAA TGTCCTGGAG GTCTGGGCAG ATGTGGGCAT GGCTGGACCC 804 P268S/SNP5

yrThrGluAs nValLeuGlu ValTrpAlaA spValGlyMe tAlaGlyPro 268

CCGCAGAAGA GCCCAGCCAC CCTGGGCCTG GAGGAGCTCT TCAGCACCCC 854

ProGlnLysS erProAlaTh rLeuGlyLeu GluGluLeuP heSerThrPr 285

TGGCCACCTC AATGACGATG CGGACACTGT GCTGGTGGTG GGTGAGGCGG 904 H287Y N289S D291N A292V T294S V298V A301V

oGlyHisLeu AsnAspAspA laAspThrVa lLeuValVal GlyGluAlaG 302

GCAGTGGCAA GAGCACGCTC CTGCAGCGGC TGCACTTGCT GTGGGCTGCA 954 R311W

lySerGlyLy sSerThrLeu LeuGlnArgL euHisLeuLe uTrpAlaAla 318

GGGCAAGACT TCCAGGAATT TCTCTTTGTC TTCCCATTCA GCTGCCGGCA 1004 R334W R334Q

GlyGlnAspP heGlnGluPh eLeuPheVal PheProPheS erCysArgGl 335

GCTGCAGTGC ATGGCCAAAC CACTCTCTGT GCGGACTCTA 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

GACCACCCTG ACCGTGTCCT GTTAACCTTT GATGGCTTTG ACGAGTTCAA 1154 H343Y R373C D382N D382E E383K E383G

AspHisProA spArgValLe uLeuThrPhe AspGlyPheA spGluPheLy 385

GTTCAGGTTC ACGGATCGTG AACGCCACTG CTCCCCGACC GACCCCACCT 1204 D390V R391C R393H P397L

```
sPheArgPhe ThrAspArgG luArgHisCy sSerProThr AspProThrS 402

CTGTCCAGAC CCTGCTCTTC AACCTTCTGC AGGGCAACCT GCTGAAGAAT 1254 N414S
erValGlnTh rLeuLeuPhe AsnLeuLeuG lnGlyAsnLe uLeuLysAsn 418

GCCCGCAAGG TGGTGACCAG CCGTCCGGCC GCTGTGTCGG CGTTCCTCAG 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 CCTGAGGAAG CGCCATCATG AGCCCGGGGT GGCGGACCGC 1404 L456L R459R/SNP6 P463A G464W R468C
leGluLeuTy rLeuArgLys ArgHisHisG luProGlyVa lAlaAspArg 468

CTCATCCGCC TGCTCCAAGA GACCTCAGCC CTGCACGGTT TGTGCCACCT 1454 L469F R471C T476P H480R G481D c.1447T>C C483W
LeuIleArgL euLeuGlnGl uThrSerAla LeuHisGlyL euCysHisLe 485

GCCTGTCTTC TCATGGATGG TGTCCAAATG CCACCAGGAA CTGTTGCTGC 1504 W490L W490S C495Y H496L E498 L500delinsV E498D L501P
uProValPhe SerTrpMetV alSerLysCy sHisGlnGlu LeuLeuLeuG 502

AGGAGGGGGG GTCCCCAAAG ACCACTACAG ATATGTACCT GCTGATTCTG 1554 E503E S506Pfs*11 P507S T510I D512H D512Y D512V M513T M513R
lnGluGlyGl ySerProLys ThrThrThrA spMetTyrLe uLeuIleLeu 518

CAGCATTTTC TGCTGCATGC CACCCCCCCA GACTCAGCTT CCCAAGGTCT 1604 H520Y P527P
GlnHisPheL euLeuHisAl aThrProPro AspSerAlaS erGlnGlyLe 535

GGGACCCAGT CTTCTTCGGG GCCGCCTCCC CACCCTCCTG CACCTGGGCA 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 AAAGGTGTCG TGCCAGGGAG TACGGCGCCC CTGGAATTCC 1804 R587C R587R/SNP7 T596T E600K E600A

uValArgAla LysGlyValV alProGlySe rThrAlaPro LeuGluPheL 602

TTCACATCAC TTTCCAGTGC TTCTTTGCCG CGTTCTACCT GGCACTCAGT 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

CACAACCTTC AGATCACAGC AGCCTTCCTG 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 CTGTGCCCGC TGGTGTCTGG CCCGCAGCCT CCGCAAGCAC 2154 R703C R713C R713H R716C

rgArgGlnAl aCysAlaArg TrpCysLeuA laArgSerLe uArgLysHis 718

TTCCACTCCA TCCCGCCAGC TGCACCGGGT GAGGCCAAGA GCGTGCATGC 2204 A725G P727L V733L

PheHisSerI leProProAl aAlaProGly GluAlaLysS erValHisAl 735

CATGCCCGGG TTCATCTGGC TCATCCGGAG CCTGTACGAG ATGCAGGAGG 2254 I740I R744W

aMetProGly PheIleTrpL euIleArgSe rLeuTyrGlu MetGlnGluG 752

AGCGGCTGGC TCGGAAGGCT GCACGTGGCC 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 CTCCGGCGGC CCGTGGCCCT GCAGCTGGAC TACAACTCTG 2404 R790W R791W R791Q V793M

lLeuGlnHis LeuArgArgP roValAlaLe uGlnLeuAsp TyrAsnSerV 802

TGGGTGACAT TGGCGTGGAG CAGCTGCTGC CTTGCCTTGG TGTCTGCAAG 2454 V802V Q809K V816I

alGlyAspIl eGlyValGlu GlnLeuLeuP roCysLeuGl yValCysLys 818

GCTCTGTATT TGCGCGATAA CAATATCTCA GACCGAGGCA TCTGCAAGCT 2504 D824N N825K

AlaLeuTyrL euArgAspAs nAsnIleSer AspArgGlyI leCysLysLe 835

CATTGAATGT GCTCTTCACT GCGAGCAATT GCAGAAGTTA GCTCTATTCA 2554 I836T C842Y E843K A849V

uIleGluCys AlaLeuHisC ysGluGlnLe uGlnLysLeu AlaLeuPheA 852

ACAACAAATT GACTGACGGC TGTGCACACT CCATGGCTAA GCTCCTTGCA 2604 N852S N853S M863V A864T

snAsnLysLe uThrAspGly CysAlaHisS erMetAlaLy sLeuLeuAla 868

TGCAGGCAGA ACTTCTTGGC ATTGAGGCTG GGGAATAACT 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

AGTTCCTGGG ATTCTGGGGC AACAGAGTGG GTGACGAGGG GGCCCAGGCC 2754 W907R G908R/SNP12 G908C D913D E914K A918D

lnPheLeuGl yPheTrpGly AsnArgValG lyAspGluGl yAlaGlnAla 918

CTGGCTGAAG CCTTGGGTGA TCACCAGAGC TTGAGGTGGC TCAGCCTGGT 2804 G924D V935M

LeuAlaGluA laLeuGlyAs pHisGlnSer LeuArgTrpL euSerLeuVa 935

GGGGAACAAC ATTGGCAGTG TGGGTGCCCA AGCCTTGGCA CTGATGCTGG 2854 I939V I939I

lGlyAsnAsn IleGlySerV alGlyAlaGl nAlaLeuAla LeuMetLeuA 952

CAAAGAACGT CATGCTAGAA GAACTCTGCC TGGAGGAGAA CCATCTCCAG 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 ATAACTGCAT 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 GGATGTTCGT CTCAGTTTGT *31  c.*9G>A
pThrArgLeu LeuLeuStop

TTGTGAGCAG GCTGTGAGTT TGGGCCCCAG AGGCTGGGTG ACATGTGTTG *81
GCAGCCTCTT CAAAATGAGC CCTGTCCTGC CTAAGGCTGA ACTTGTTTTC *131
TGGGAACACC ATAGGTCACC TTTATTCTGG CAGAGGAGGG AGCATCAGTG *181
CCCTCCAGGA TAGACTTTTC CCAAGCCTAC TTTTGCCATT GACTTCTTCC *231
CAAGATTCAA TCCCAGGATG TACAAGGACA GCCCCTCCTC CATAGTATGG *281
GACTGGCCTC TGCTGATCCT CCCAGGCTTC CGTGTGGGTC 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 TTGATATTTC *581
ACTTACAGCA CCCCCAACCC TGGCACCCAG GGTGGGAAGG GCTACACCTT *631
AGCCTGCCCT CCTTTCCGGT GTTTAAGACA TTTTTGGAAG GGGACACGTG *681
ACAGCCGTTT GTTCCCCAAG ACATTCTAGG TTTGCAAGAA AAATATGACC *731
ACACTCCAGC TGGGATCACA TGTGGACTTT TATTTCCAGT GAAATCAGTT *781
ACTCTTCAGT TAAGCCTTTG GAAACAGCTC GACTTTAAAA AGCTCCAAAT *831
GCAGCTTTAA AAAATTAATC TGGGCCAGAA TTTCAAACGG CCTCACTAGG *881 *873C>T
CTTCTGGTTG ATGCCTGTGA ACTGAACTCT GACAACAGAC TTCTGAAATA *931
GACCCACAAG AGGCAGTTCC ATTTCATTTG 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

GTGAAAACTG GTTAATATTT ATAGGTCACT TTGTTTTACT GTCTTAAGTT *1181

TATACTCTTA TAGACAACAT GGCCGTGAAC TTTATGCTGT AAATAATCAG *1231 c.4323A>G

AGGGGAATAA ACTGTTGAGT CAAAA

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