



NOD2 (NM_022162.3) - cDNA + Protein - 2025-04-02

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

GAGTCACC~~G~~G CCA~~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~~C~~GGTGAAAG 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~~ ~~A~~ATGACGATG ~~C~~GGACAC~~TGT~~ GCTGGTGGTG GGTGAGG~~CGG~~ 904 [H287Y](#) [N289S](#) [D291N](#) [A292V](#) [T294S](#) [V298V](#) [A301V](#)

oGlyHisLeu AsnAspAspA laAspThrVa lLeuValVal GlyGluAlaG 302

GCGTGGCAA 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~~ ~~C~~TCTTTGAGC 1054 [L348V](#) [L349F](#)

nLeuGlnCys MetAlaLysP roLeuSerVa lArgThrLeu LeuPheGluH 352

~~A~~CTGCTGTTG ~~G~~CCTG~~A~~TGTT GGTCAAGAAG ~~A~~C~~A~~TCTTCCA GTTACTCCTT 1104 [H352R](#) [W355X](#) [D357A](#) [I363F](#)

isCysCysTr pProAspVal GlyGlnGluA spIlePheGl nLeuLeuLeu 368

GAC~~CACCCTG~~ ~~A~~CCGTGTCCT GTTAACCTTT GATGGCTTTG ~~A~~CG~~A~~GTTCAA 1154 [H343Y](#) [R373C](#) [D382N](#) [D382E](#) [E383K](#) [E383G](#)

AspHisProA spArgValLe uLeuThrPhe AspGlyPheA spGluPheLy 385

G TTCAGGTT C ACGG~~A~~T~~C~~GTG AAC~~G~~CCACTG CTCCC~~C~~GACC 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

GCCCGCAAGG 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~~CCG~~G~~GGGT 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~~T~~ TG~~I~~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

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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 AGCCTTCTG 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

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TTCCACTCCA TCCCGCCAGC TGCACCGGGT GAGGCCAAGA GCCTGCATGC 2204 A725G P727L V733L

PheHisSerI leProProAl aAlaProGly GluAlaLysS erValHisAl 735

CATGCCCGGG TTCATCTGGC TCATCCGGAG CCTGTACGAG ATGCAGGAG 2254 I740I R744W

aMetProGly PheIleTrpL euIleArgSe rLeuTyrGlu MetGlnGluG 752

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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

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ACAACAAATT GACTGACGGC TGTGCACACT CCAATGGCTAA GCTCCTTGCA 2604 N852S N853S M863V A864T

snAsnLysLe uThrAspGly CysAlaHisS erMetAlaLy sLeuLeuAla 868

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CysArgGlnA snPheLeuAl aLeuArgLeu GlyAsnAsnT yrIleThrAl 885

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lnPheLeuGl yPheTrpGly AsnArgValG lyAspGluGl yAlaGlnAla 918

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AspGluGlyV alCysSerLe uAlaGluGly LeuLysLysA snSerSerLe 985

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uLysIleLeu LysLeuSerA snAsnCysIl eThrTyrLeu GlyAlaGluA 1002

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laLeuLeuGl nAlaLeuGlu ArgAsnAspT hrIleLeuGl uValTrpLeu 1018

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 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
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 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
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