



*NLRP7* (NM\_001127255.1) - cDNA + Protein - 2025-04-02

GAAACACAGG CTGGAAGCAA GACCTGACCT GAGGGAGTTC TTCAGCCTTA -27

ACCTAAGGTC TCATACTCGG AGCACTATGA CATCGCCCCA GCTAGAGTGG 24

MetT hrSerProGl nLeuGluTrp 8

ACTCTGCAGA CCCTTCTGGA GCAGCTGAAC GAGGATGAAT TAAAGAGTTT 74

ThrLeuGlnT hrLeuLeuGl uGlnLeuAsn GluAspGluL euLysSerPh 25

CAAATCCCTT TTATGGGCTT TTCCCCTCGA AGACGTGCTA CAGAAGACCC 124

eLysSerLeu LeuTrpAlaP heProLeuGl uAspValLeu GlnLysThrP 42

CATGGTCTGA GGTGGAAGAG GCTGATGGCA AGAAACTGGC AGAAATTCTG 174

roTrpSerGl uValGluGlu AlaAspGlyL ysLysLeuAl aGluIleLeu 58

GTCAACACCT CCTCAGAAAA TTGGATAAGG AATGCGACTG TGAACTATCTT 224 T61TfsX7 W66\* W66C N73N

ValAsnThrS erSerGluAs nTrpIleArg AsnAlaThrV alAsnIleLe 75

GGAAGAGATG AATCTCACGG AATTGTGTAA GATGGCAAAG GCTGAGATGA 274 C84Y

uGluGluMet AsnLeuThrG luLeuCysLy sMetAlaLys AlaGluMetM 92

TGGAGGACGG ACAGGTGCAA GAAATAGATA ATCCTGAGCT GGGAGATGCA 324 E99X

etGluAspGl yGlnValGln GluIleAspA snProGluLe uGlyAspAla 108

GAAGAAGACT CGGAGTTAGC AAAGCCAGGT GAAAAGGAAG GATGGAGAAA 374 [E113GfsX7](#) [K116X](#)

GluGluAspS erGluLeuAl aLysProGly GluLysGluG lyTrpArgAs 125

TTCAATGGAG AAACAGTCTT TGGTCTGGAA GAACACCTTT TGGCAAGGAG 424 [Q130Q](#) [L132Gfs\\*12](#) [Q140\\*](#)

nSerMetGlu LysGlnSerL euValTrpLy sAsnThrPhe TrpGlnGlyA 142

ACATTGACAA TTTCCATGAC GACGTCACCTC TGAGAAACCA ACGGTTTCATT 474 [D149G](#) [R156Q](#)

spIleAspAs nPheHisAsp AspValThrL euArgAsnGl nArgPheIle 158

CCATTCTTGA ATCCCAGAAC ACCCAGGAAG CTAACACCTT ACACGGTGGT 524

ProPheLeuA snProArgTh rProArgLys LeuThrProT yrThrValVa 175

GCTGCACGGC CCCGCAGGCG TGGGGAAAAC CACGCTGGCC AAAAAGTGT A 574 [V182M](#) [T185del](#) [M192L](#)

lLeuHisGly ProAlaGlyV alGlyLysTh rThrLeuAla LysLysCysM 192

TGCTGGACTG GACAGACTGC AACCTCAGCC CGACGCTCAG ATACGCGTTC 624 [W195X](#) [S201S](#)

etLeuAspTr pThrAspCys AsnLeuSerP roThrLeuAr gTyrAlaPhe 208

TACCCTCAGCT GCAAGGAGCT CAGCCGCATG GGCCCCTGCA GTTTTGCAGA 674 [L210F](#) [C221Lfs\\*13](#)

TyrLeuSerC ysLysGluLe uSerArgMet GlyProCysS erPheAlaGl 225

GCTGATCTCC AAAGACTGGC CTGAATTGCA GGATGACATT CCAAGCATCC 724 [W231X](#) [L234S](#)

uLeuIleSer LysAspTrpP roGluLeuGl nAspAspIle ProSerIleL 242

TAGCCAAGC ACAGAGAATC CTGTTCGTGG TCGATGGCCT TGATGAGCTG 774 [A243V](#) [F250C](#) [F250L](#)

euAlaGlnAl aGlnArgIle LeuPheValV alAspGlyLe uAspGluLeu 258

AAAGTCCCAC CTGGGGCGCT GATCCAGGAC ATCTGCGGGG ACTGGGAGAA 824

LysValProP roGlyAlaLe uIleGlnAsp IleCysGlyA spTrpGluLy 275

GAAGAAGCCG GTGCCCCGTCC TCCTGGGGAG TTTGCTGAAG AGGAAGATGT 874 [K277Q](#) [V279L](#)

sLysLysPro ValProValL euLeuGlySe rLeuLeuLys ArgLysMetL 292

TACCCAGGGC AGCCTTGCTG GTCACCACGC GGCCAGGGC ACTGAGGGAC 924 [A305A](#)

euProArgAl aAlaLeuLeu ValThrThrA rgProArgAl aLeuArgAsp 308

CTCCAGCCTCC TGGCGCAGCA GCCGATCTAC GTAAGGGTGG AGGGCTTCCT 974 [Q310R](#) [Q310Hfs\\*38](#) [L311H](#) [L311I](#) [Y318CfsX7](#) [Q314fs](#) [V319I](#)

LeuGlnLeuL euAlaGlnGl nProIleTyr ValArgValG luGlyPheLe 325

GGAGGAGGAC AGGAGGGCCT ATTTCCCTGAG ACACTTTGGA GACGAGGACC 1024 [R329K](#) [D339D](#) [E340K](#) [E340Qfs\\*11](#)

uGluGluAsp ArgArgAlaT yrPheLeuAr gHisPheGly AspGluAspG 342

AAGCCATGCG TGCCTTTGAG CTAATGAGGA GCAACGCGGC CCTGTTCCAG 1074 [F357L](#)

lnAlaMetAr gAlaPheGlu LeuMetArgS erAsnAlaAl aLeuPheGln 358

CTGGGCTCGG CCCCCGCGGT GTGCTGGATI GTGTGCACGA CTCTGAAGCT 1124 [I368I](#) [I368M](#)

LeuGlySerA laProAlaVa lCysTrpIle ValCysThrT hrLeuLysLe 375

GCAGATGGAG AAGGGGGAGG ACCCGGTCCC CACCTGCCTC ACCCGCACGG 1174 [K379K](#) [K379N](#) [G380R](#) [P383L](#) [R390Afs\\*26](#) [R390H](#) [T391A](#)

uGlnMetGlu LysGlyGluA spProValPr oThrCysLeu ThrArgThrG 392

GGCTGTTCCT GCGTTTCCTC TG CAGCCGGT TCCCGCAGGG CGCACAGCTG 1224 [F394F](#) [L398R](#) [C399Y](#)

lyLeuPheLe uArgPheLeu CysSerArgP heProGlnGl yAlaGlnLeu 408

CGGGGCGCGC TGCGGACGCT GAGCCTCCTG GCCGCGCAGG GCCTGTGGGC 1274 [L412P](#) [R413W](#) [R413Q](#)

ArgGlyAlaL euArgThrLe uSerLeuLeu AlaAlaGlnG lyLeuTrpAl 425

GCAGATGTCC GTGTTCCACC GAGAGGACTT GGAAAGGCTC GGGGTGCAGG 1324 M427T F430L F430F R432X D434D L435L  
aGlnMetSer ValPheHisA rgGluAspLe uGluArgLeu GlyValGlnG 442

AGTCCGACCT CCGTCTGTTC CTGGACGGAG ACATCCTCCG CCAGGACAGA 1374 L454L R458Sfs\*69  
luSerAspLe uArgLeuPhe LeuAspGlyA spIleLeuAr gGlnAspArg 458

GTCCTCAAAG GCTGCTACTC CTTTCATCCAC CTCAGCTTCC AGCAGTTTCT 1424 Y464\* Q472\*  
ValSerLysG lyCysTyrSe rPheIleHis LeuSerPheG lnGlnPheLe 475

CACTGCCCTG TTCTACGCC TGGAGAAGGA GGAGGGGGAG GACAGGGACG 1474 A481T E486GfsX42 G487E  
uThrAlaLeu PheTyrAlaL euGluLysGl uGluGlyGlu AspArgAspG 492

GCCACGCCTG GGACATCGGG GACGTACAGA AGCTGCTTTC CGGAGAAGAA 1524 A494T I497I G498R G506\* E508DfsX27  
lyHisAlaTr pAspIleGly AspValGlnL ysLeuLeuSe rGlyGluGlu 508

AGACTCAAGA ACCCGACCT GATTCAAGTA GACACTTCT TATTCGGCCT 1574 K511R N512fs P513S P513L H520Tfs\*46 c.1548\_1566dup;1566\_1567insAF15169.2:g.106\_4191  
ArgLeuLysA snProAspLe uIleGlnVal GlyHisPheL euPheGlyLe 525

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TGTCACCGGA CATCAAACAG GAATTGCTGC AATGCAAAGC ACATCTTCAT 1674 M542Tfs  
etSerProAs pIleLysGln GluLeuLeuG lnCysLysAl aHisLeuHis 558

GCAAATAAGC CTTATCCGT GACCGACCTG AAGGAGGTCT TGGGCTGCCT 1724 E570X c.1719\_1720insT  
AlaAsnLysP roLeuSerVa lThrAspLeu LysGluValL euGlyCysLe 575

GTATGAGTCT CAGGAGGAGG AGCTGGCGAA GGTGGTGGTG GCCCCGTTCA 1774 L575L E580\* P590P

uTyrGluSer GlnGluGluG luLeuAlaLy sValValVal AlaProPheL 592

AGGAAATTTT TATTCACCTG ACAAATACTT CTGAAGTGAT GCATTGTTCC 1824 H613Rfs\*8 S608F

ysGluIleSe rIleHisLeu ThrAsnThrs erGluValMe tHisCysSer 608

TTCAGCCTGA AGCATTGTCA AGACTTGCAG AAACTCTCAC TGCAGGTAGC 1874 K619Nfs\*18 S621Tfs\*16

PheSerLeuL ysHisCysGl nAspLeuGln LysLeuSerL euGlnValAl 625

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aLysGlyVal PheLeuGluA snTyrMetAs pPheGluLeu AspIleGluP 642

TTGAAAGGTG CACTTACCTA ACCATTCCGA ACTGGGCTCG GCAGGATCTT 1974 P651S W653\* D657V

heGluArgCy sThrTyrLeu ThrIleProA snTrpAlaAr gGlnAspLeu 658

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rAsnLeuLys PheLeuGluV alLysGlnSe rPheLeuSer AspSerSerV 692

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alArgIleLe uCysAspHis ValThrArgS erThrCysHi sLeuGlnLys 708

GTGGAGATTA AAAACGTCAC CCCTGACACC GCGTACCGGG ACTTCTGTCT 2174 V714I P716A P716S P716LfsX21 A719V R721W R721Q D722G

ValGluIleL ysAsnValTh rProAspThr AlaTyrArgA spPheCysLe 725

TGCTTTCATT GGGAAGAAGA CCCTCACGCA CCTGACCCTG GCAGGGCACA 2224 H735P

uAlaPheIle GlyLysLysT hrLeuThrHi sLeuThrLeu AlaGlyHisI 742

TCGAGTGGGA ACGCACGATG ATGCTGATGC TGTGTGACCT GCTCAGAAAT 2274 I742I E743\* L750Y

leGluTrpGl uArgThrMet MetLeuMetL euCysAspLe uLeuArgAsn 758

CATAAATGCA ACCTGCAGTA CCTGAGGTTG GGAGGTCACT GTGCCACCCC 2324 C761Y

HisLysCysA snLeuGlnTy rLeuArgLeu GlyGlyHisC ysAlaThrPr 775

GGAGCAGTGG GCTGAATTCCT TCTATGTCCT CAAAGCCAAC CAGTCCCTGA 2374 P775P E776Gfs\*14 W778X N788N

oGluGlnTrp AlaGluPheP heTyrValLe uLysAlaAsn GlnSerLeuL 792

AGCACCTGCG TCTCICAGCC AATGTGCTCC TGGATGAGGG TGCCATGTTG 2424 R795C A798fs

ysHisLeuAr gLeuSerAla AsnValLeuL euAspGluGl yAlaMetLeu 808

CTGTACAAGA CCATGACACG CCCAAAACAC TTCCTGCAGA TGTIGTCGTT 2474 R815H L820Cfs\*29 L823X

LeuTyrLysT hrMetThrAr gProLysHis PheLeuGlnM etLeuSerLe 825

GGAAAACTGTC CGTCTTACAG AAGCCAGTTG CAAGGACCTT GCTGCTGTCT 2524 c.2482\_2483delTG A833T

uGluAsnCys ArgLeuThrG luAlaSerCy sLysAspLeu AlaAlaValL 842

TGGTTGTCAG CAAGAAGCTG ACACACCTGT GCTTGCCCAA GAACCCCAT 2574 I858HfsX11 I858T

euValValSe rLysLysLeu ThrHisLeuC ysLeuAlaLy sAsnProIle 858

GGGGATACAG GGGTGAAGTT TCTGTGTGAG GGCTTGAGTT ACCCTGATTG 2624 Y872\*

GlyAspThrG lyValLysPh eLeuCysGlu GlyLeuSerT yrProAspCy 875

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sLysLeuGln ThrLeuValL euGlnGlnCy sSerIleThr LysLeuGlyC 892

GTAGATATCT CTCAGAGGCG CTCCAAGAAG CCTGCAGCCT CACAAACCTG 2724 Y894Y A902A N907N  
ysArgTyrLe uSerGluAla LeuGlnGluA laCysSerLe uThrAsnLeu 908

GACTTGAGTA TCAACCAGAT AGCTCGTGGG TTGTGGATTC TCTGTCAGGC 2774 N913S W920\* W920\*(2760)  
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ATTAGAGAAT CCAAACTGTGA ACCTAAAACA CCTACGCCTC TGGAGCTGCT 2824 A925A L926\* C931X  
aLeuGluAsn ProAsnCysA snLeuLysHi sLeuArgLeu TrpSerCysS 942

CCCTCATGCC TTTCTATTGT CAGCATCTTG GATCTGCTCT CCTCAGCAAT 2874  
erLeuMetPr oPheTyrCys GlnHisLeuG lySerAlaLe uLeuSerAsn 958

CAGAAGCTTG AAACTCTGGG CCTGGGCCAG AATCATTGT GGAAGAGTGG 2924 L964P  
GlnLysLeuG luThrLeuAs pLeuGlyGln AsnHisLeuT rpLysSerGl 975

CATAATTAAG CTCTTTGGGG TTCTAAGACA AAGAACTGGA TCCTTGAAGA 2974 G981Rfs  
yIleIleLys LeuPheGlyV alLeuArgGl nArgThrGly SerLeuLysI 992

TACTCAGGTT GAAGACCTAT GAAACTAATT TGGAAATCAA GAAGCTGTTG 3024  
leLeuArgLe uLysThrTyr GluThrAsnL euGluIleLy sLysLeuLeu 1008

GAGGAAGTGA AAGAAAAGAA TCCCAAGCTG ACTATTGATT GCAATGCTTC 3074 D1021V  
GluGluValL ysGluLysAs nProLysLeu ThrIleAspC ysAsnAlaSe 1025

CGGGGCAACG GCACCTCCGT GCTGTGACTT TTTTTGCTGA GCAGCCTGGG \*10 T1028A c.\*5C>T  
rGlyAlaThr AlaProProC ysCysAspPh ePheCysSto p

ATCGCTCTAC GAATTACACA GGAAGCGGGA TTCGGGTCTC TAAGATGTCT \*60 c.\*20C>T c.\*44G>A  
TATGAATGCA GGTCAGAGGG TCACATGTTA AACTAGAGT CTGTCGAGAG \*110  
GTAGGATTTG AACTGGTTT TCTCACTATT TTTGGGAGAT TCTGCACGAG \*160  
TCACGCACCC CCTTCACATG ACGCTATGTA CTTTCTCACA GGGATAATAA \*210 c.\*180G>C  
AGTTAGAGCA CTCTCGTTGC A

*NLRP7* (NM\_001127255.1) - cDNA + Protein - 2025-04-02

