



CARD14 (NM_024110.4) - cDNA + Protein - 2025-04-02

GCTCTTCCTT CTGCCAGCT CCGTCCCACC CAGCAGCCCG CAGAGAAAGG -119

AGGCAGCTGG CACCACACTG GGCTTTGGAG ACACTGCGGG GACTGTGGAC -69

CCCACCCCTGC TGCACGGAGC TCCTGCAAAA GCAAACCTGA GAACCTTGGG -19

TCCTCCAGC GCCCAGCCAT GGGGAACTG TGCCGCAGGG ACTCCGCACT 32

Me tGlyGluLeu CysArgArgA spSerAlaLe 11

CACGGCACTG GACGAGGAGA CACTGTGGGA GATGATGGAG AGCCACCGCC 82

uThrAlaLeu AspGluGluT hrLeuTrpGl uMetMetGlu SerHisArgH 28

ACAGGATCGT ACGCTGCATC TGCCCCAGCC GCCTCACCCC CTACCTGCGC 132

isArgIleVa lArgCysIle CysProSerA rgLeuThrPr oTyrLeuArg 44

CAGGCCAAGG TGCTGTGCCA GCTGGACGAG GAGGAGGTGC TGCACAGCCC 182 C50Y

GlnAlaLysV aLeuCysGl nLeuAspGlu GluGluValL euHisSerPr 61

CCGGCTCACC AACAGCGCCA TGCGGGCCGG GCACTTGCTG GATTTGCTGA 232 R62Q R69W R69Q

oArgLeuThr AsnSerAlaM etArgAlaGl yHisLeuLeu AspLeuLeuL 78

AGACTCGAGG GAAGAACGGG GCCATCGCCT TCCTGGAGAG CCTGAAGTTC 282 K78N K93Q

ysThrArgGl yLysAsnGly AlaIleAlaP heLeuGluSe rLeuLysPhe 94

CACAACCCTG ACGTCTACAC CCTGGTCACC GGGCTGCAGC CTGATGTTGA 332 V110A

HisAsnProA spValTyrTh rLeuValThr GlyLeuGlnP roAspValAs 111

[CTTCAGTAAC](#) [TTTAGCGGTC](#) [TCATGGAGAC](#) [ATCCAAGCTG](#) [ACCGAGTGCC](#) 382 [G117S](#) [M119V](#) [M119R](#) [M119T](#) [M119K](#) [T121I](#) [L124P](#) [C127S](#)

pPheSerAsn PheSerGlyL euMetGluTh rSerLysLeu ThrGluCysL 128

[TGGCTGGGGC](#) [CATCGGCAGC](#) [CTGCAAGGAGG](#) [AGCTGAACCA](#) [GGAAAAGGGG](#) 432 [Q136L](#) [E138del](#) [E138K](#) [E138A](#)

euAlaGlyAl aIleGlySer LeuGlnGluG luLeuAsnGl nGluLysGly 144

[CAGAAGGAGG](#) [TGCTGCTGCG](#) [GCGGTGCCAG](#) [CAGCTGCAAGG](#) [AGCACCTGGG](#) 482 [L149R](#) [L150R](#) [R151W](#) [R151Q](#) [C153S](#) [L156P](#) [Q157P](#)

GlnLysGluV aLeuLeuAr gArgCysGln GlnLeuGlnG luHisLeuGl 161

[CCTGGCCGAG](#) [ACCCGTGCCG](#) [AGGGCCTGCA](#) [CCAGCTGGAG](#) [GCTGACCACA](#) 532 [R166H](#) [D176H](#)

yLeuAlaGlu ThrArgAlaG luGlyLeuHi sGlnLeuGlu AlaAspHisS 178

[GCCGCATGAA](#) [GCGTGAGGTT](#) [AGCGCACACT](#) [TCCATGAGGT](#) [GCTGAGGCTG](#) 582 [R179H](#) [R182C](#)

erArgMetLy sArgGluVal SerAlaHisP heHisGluVa lLeuArgLeu 194

[AAGGACGAGA](#) [TGCTCAACCT](#) [CTCGCTGCAC](#) [TATAGCAATG](#) [CGCTGCAGGA](#) 632 [E197K](#) [S200N](#) [L209P](#)

LysAspGluM etLeuSerLe uSerLeuHis TyrSerAsnA laLeuGlnGl 211

[GAAGGAGCTG](#) [GCCGCCTCAC](#) [GCTGCCGCAG](#) [CCTGCAGGAG](#) [GAGCTGTATC](#) 682 [A216T](#) [R218C](#)

uLysGluLeu AlaAlaSerA rgCysArgSe rLeuGlnGlu GluLeuTyrL 228

[TACTGAAGCA](#) [GGAGCTGCAG](#) [CGAGCCAACA](#) [TGGTTTCCTC](#) [CTGTGAGCTG](#) 732

euLeuLysGl nGluLeuGln ArgAlaAsnM etValSerSe rCysGluLeu 244

[GAATTGCAAG](#) [AGCAGTCCCT](#) [GAGGACAGCC](#) [AGCGACCAGG](#) [AGTCCGGGGA](#) 782 [A254T](#)

GluLeuGlnG luGlnSerLe uArgThrAla SerAspGlnG luSerGlyAs 261

TGAGGAGCTG AACCGCCTGA AGGAGGAGAA TGAGAAACTG CGCTCGCTGA 832 [R266C](#)
pGluGluLeu AsnArgLeuL ysGluGluAs nGluLysLeu ArgSerLeuT 278

CTTTCAGCCT GCGGGAGAAG GACATTCTGG AGCAGAGCCT GGACGAGGCG 882
hrPheSerLe uAlaGluLys AspIleLeuG luGlnSerLe uAspGluAla 294

CGGGGGAGCC GACAGGAGCT GGTGGAGCGC ATCCACTCGC TCGGGGAGCG 932 [R298*Stop](#) [R304C](#) [R311W](#)
ArgGlySerA rgGlnGluLe uValGluArg IleHisSerL euArgGluAr 311

GGCCGTGGCT GCCGAGAGGC AGCGAGAGCA GTACTGGGAA GAGAAGGAAC 982 [R319Q](#)
gAlaValAla AlaGluArgG lnArgGluGl nTyrTrpGlu GluLysGluG 328

AGACCCTGCT GCAGTTCAG AAGAGTAAGA TGGCCTGCCA ACTCTACAGG 1032 [M338V](#)
lnThrLeuLe uGlnPheGln LysSerLysM etAlaCysGl nLeuTyrArg 344

GAGAAGGTGA ATGCGCTGCA GGCCCAGGTG TCGGAGCTGC AGAAGGAGCG 1082 [L350P](#) [V354M](#)
GluLysValA snAlaLeuGl nAlaGlnVal CysGluLeuG lnLysGluAr 361

AGACCAGGCG TACTCCGCGA GGGACAGTGC TCAGAGGGAG ATTTCCCAGA 1132 [A364V](#)
gAspGlnAla TyrSerAlaA rgAspSerAl aGlnArgGlu IleSerGlnS 378

GCCTGGTGGG GAAGGACTCC CTCCGCAGGC AGGTGTTCGA GCTGACGGAC 1182
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CAGGTCTGCG AGCTGCGCAC ACAGCTTCGC CAGCTGCAGG CAGAGCCTCC 1232
GlnValCysG luLeuArgTh rGlnLeuArg GlnLeuGlnA laGluProPr 411

GGGTGTGCTC AAGCAGGAAG CCAGGACCAG GGAGCCCTGT CCACGGGAGA 1282 T420A E422K

oGlyValLeu LysGlnGluA laArgThrAr gGluProCys ProArgGluL 428

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ysGlnArgLe uValArgMet HisAlaIleC ysProArgAs pAspSerAsp 444

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CysSerLeuV alSerSerTh rGluSerGln LeuLeuSerA spLeuSerAl 461

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aThrSerSer ArgGluLeuV alAspSerPh eArgSerSer SerProAlaP 478

CCCCAGCCA GCAGTCCCTG TACAAGCGGG TGGCCGAGGA CTTCGGGGAA 1482 P479R

roProSerGl nGlnSerLeu TyrLysArgV alAlaGluAs pPheGlyGlu 494

GAACCCTGGT CTTTCAGCAG CTGCCCTGGAG ATCCCGGAGG GAGACCCGGG 1532 c.1488del P506L A512Sfs*6

GluProTrps erPheSerSe rCysLeuGlu ileProGluG lyAspProGl 511

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CCTGGAAGGC TTGATGTCTC GGAGAGCGGC GTCCCTCATGC GGCGGAGGCC 1682 R547S V555I

ProGlyArgL euAspValSe rGluSerGly ValLeuMetA rgArgArgPr 561

AGCCCGCAGG ATCCTGAGCC AGGTCACCAT GCTGGCGTTC CAGGGGGATG 1732

oAlaArgArg IleLeuSerG lnValThrMe tLeuAlaPhe GlnGlyAspA 578

CATTGCTGGA GCAGATCAGC GTCATCGGCG GGAACCTCAC GGGCATCTTC 1782 [T591M](#)

laLeuLeuGl uGlnIleSer ValIleGlyG lyAsnLeuTh rGlyIlePhe 594

ATCCACCGGG TCACCCCGGG CTCGGCGGCG GACCAGATGG CCTTGCGCCC 1832 [P600L](#) [S602L](#) [A603V](#) [R610H](#)

IleHisArgV alThrProGl ySerAlaAla AspGlnMetA laLeuArgPr 611

GGGCACCCAG ATTGTGATGG TTGATTACGA AGCCTCAGAG CCCTTGTTCA 1882

oGlyThrGln IleValMetV alAspTyrGl uAlaSerGlu ProLeuPheL 628

AGGCAGTCCT GGAGGACACG ACCCTGGAGG AGGCCGTGGG GCTTCTCAGG 1932 [A639G](#)

ysAlaValLe uGluAspThr ThrLeuGluG luAlaValGl yLeuLeuArg 644

AGGGTGGACG GCTTCTGCTG CCTGTCTGTG AAGGTCAACA CGGACGGTTA 1982 [G648S](#)

ArgValAspG lyPheCysCy sLeuSerVal LysValAsnT hrAspGlyTy 661

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rLysArgLeu LeuGlnAspL euGluAlaLy sValAlaThr SerGlyAspS 678

CATTCTACAT CCGGGTCAAC CTGGCCATGG AGGGCAGGGC CAAAGGGGAG 2082 [R682W](#)

erPheTyrIl eArgValAsn LeuAlaMetG luGlyArgAl aLysGlyGlu 694

CTGCAGGTGC ATTGCAACGA GGTCTGCAC GTCACCGACA CCATGTTCCA 2132

LeuGlnValH isCysAsnGl uValLeuHis ValThrAspT hrMetPheGl 711

GGGCTGCGGC TGCTGGCATG CCCACCGCGT GAACTCTTAC ACCATGAAGG 2182 [Y724*Stop](#)

nGlyCysGly CysTrpHisA laHisArgVa lAsnSerTyr ThrMetLysA 728

ATACTGCCGC GCACGGCACC ATCCCCAACT ACTCCAGGGC TCAGCAGCAG 2232
spThrAlaAl aHisGlyThr IleProAsnT yrSerArgAl aGlnGlnGln 744

CTCATAGCCC TCATCCAGGA CATGACTCAG CAGTGCACCG TGACCCGCAA 2282
LeuIleAlaL euIleGlnAs pMetThrGln GlnCysThrV alThrArgLy 761

GCCATCTTCT GGGGGACCAC AGAAGCTGGT CCGCATCGTC AGTATGGACA 2332
sProSerSer GlyGlyProG lnLysLeuVa lArgIleVal SerMetAspL 778

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ysAlaLysAl aSerProLeu ArgLeuSerP heAspArgGl yGlnLeuAsp 794

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ProSerArgM etGluGlySe rSerThrCys PheTrpAlaG luSerCysLe 811

CACCCTGGTG CCCTATACCC TGGTGCGGCC CCATCGACCC GCCCGGCCCC 2482 [R820W](#) [R826W](#)
uThrLeuVal ProTyrThrL euValArgPr oHisArgPro AlaArgProA 828

GGCCTGTGCT CCTCGTGCCC AGGGCGGTTG GGAAGATCCT GAGCGAGAAA 2532
rgProValLe uLeuValPro ArgAlaValG lyLysIleLe uSerGluLys 844

CTGTGCCCTCC TCCAAGGGTT TAAGAAGTGC CTGGCAGAGT ACTTGAGCCA 2582 [L847F](#)
LeuCysLeuL euGlnGlyPh eLysLysCys LeuAlaGluT yrLeuSerGl 861

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nGluGluTyr GluAlaTrpS erGlnArgGl yAspIleIle GlnGluGlyG 878

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ATGGAAAAGA ACACCCATGC CCTCCTGGAC GTCCAGCTGG ACAGTGTCTG 2732
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snGluLysMe tAlaLysLys LeuLysLysG lyLeuGlnAr gLeuGlyThr 944

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AAGGTGGTGT GGACGGAGCA GAGCCCCCGA TGATGCACCG TGCCCCCTCC *17
LysValValT rpThrGluGl nSerProArg Stop

CGGGACTGTG GGGGCTTCTG TGTGCCTGTT AATGCAGTCC TGTTCTCAG *67 *18C>T *19G>A
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TCGCTGCCAC CTTGCCCCG GGCAGAGGCA GAAGCCCACA TATGCTGTGA *517
CGCTGGCCAC CTTTTCTCAG CTTCTGAGGC TGCATGCCT CAGGAACTCC *567
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GAGACGGTAC TTTCAGTGGG TCTGTGCCCC GTGGCCCCCTG TGCCTGTTCG *667
GTGGGGGTGT CCCAGAGAAG CCTGGCACCA GTACCCCCGT ACAAGGCCCA *717
GCGGACTCTG CCTTCCCTG ACCTGGCTTT GCACCCAGC CCTTCTGGG *767
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TTTTGACAGC AGTGCCAAG AATCAGGAAG CTGTTCTAGA ATTCAGGTTG *917
GTATCATCAT AAATGAGTTC AGAAAAAGAA CTTCTGTATA TTTACTAAA *967
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