



CARD14 (NM_024110.4) - cDNA + Protein - 2026-06-18

GCTCTTCCTT CTGCCAGCT CCGTCCCACC CAGCAGCCCG CAGAGAAAGG -119
AGGCAGCTGG CACCACACTG GGCTTTGGAG ACACTGCGGG GACTGTGGAC -69
CCCACCCATG TGCACGGAGC TCCTGCAAAA GCAAACCTGA GAACCTTGGG -19
TCCTCCCAGC GCCCAGCCAT GGGGGAAC 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

GCCTGGTGGGA GAAGGACTCC CTCCGCAGGC AGGTGTTCGA GCTGACGGAC 1182 [p.Ser384Phe](#)
erLeuValGl uLysAspSer LeuArgArgG lnValPheGl uLeuThrAsp 394

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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GluProTrps erPheSerSe rCysLeuGlu ileProGluG lyAspProGl 511

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AGCCCGCAGG ATCCTGAGCC AGGTCACCAT GCTGGCGTTC CAGGGGGATG 1732

oAlaArgArg IleLeuSerG lnValThrMe tLeuAlaPhe GlnGlyAspA 578

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laLeuLeuGl uGlnIleSer ValIleGlyG lyAsnLeuTh rGlyIlePhe 594

ATCCACCGGG TCACCCCGGG CTCGGCGGCG GACCAGATGG CCTTGCGCCC 1832 [P600L](#) [S602L](#) [A603V](#) [p.\(Arg610Cys\)](#) [R610H](#)

IleHisArgV alThrProGl ySerAlaAla AspGlnMetA laLeuArgPr 611

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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

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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 [p.Val774Ile](#)
sProSerSer GlyGlyProG lnLysLeuVa lArgIleVal SerMetAspL 778

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ProSerArgM etGluGlySe rSerThrCys PheTrpAlaG luSerCysLe 811

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rgProValLe uLeuValPro ArgAlaValG lyLysIleLe uSerGluLys 844

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LeuCysLeuL euGlnGlyPh eLysLysCys LeuAlaGluT yrLeuSerGl 861

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euAspGlyLe uLeuSerCys ValArgGlnA laIleAlaAs pGluGlnLys 994

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LysValValT rpThrGluGl nSerProArg Stop

CGGGACTGTG GGGGCTTCTG TGTGCCTGTT AATGCAGTCC TGTTCTCAG *67 *18C>T *19G>A

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TGACCAAAAG CACAGAGGCA GCGGGTGGGG CGCCTGGGTG GTCCCAAGG *467
TCGCTGCCAC CTTGCCCCG GGCAGAGGCA GAAGCCCACA TATGCTGTGA *517
CGCTGGCCAC CTTTTCTCAG CTTCTGAGGC TCGATGCCT CAGGAACTCC *567
AGTTTACAGA GACCAGTGTG TTTACTTGTA AATAAAGCCT CTGCGTGGTG *617
GAGACGGTAC TTTCAGTGGG TCTGTGCCCC GTGGCCCCCTG TGCCTGTTCG *667
GTGGGGGTGT CCCAGAGAAG CCTGGCACCA GTACCCCCGT ACAAGGCCCA *717
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GTATCATCAT AAATGAGTTC AGAAAAAGAA CTTCTGTATA TTTACTAAA *967
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