



***RIPK1* (NM_003804.6) - cDNA + Protein - 2024-05-17**

GGGAGTCCGC GGCAGCGCA GCAGCAGGGC CCGGTCCTGC GCCTCGGGAG -104
TCGGCGTCCA GGCTCGGAGC GCGACACGGA GACTAGGTGG CAGGGTACAG -54
CTCTGCCGGG GGGGGAAAAA GTGGTACCAT TTTGGGCGTT CTTGAGCTTC -4
AGA**ATG**CAAC CAGACATGTC CTTGAATGTC ATTAAGATGA AATCCAGTGA 47
MetGlnP roAspMetSe rLeuAsnVal IleLysMetL ysSerSerAs 16

CTTCCTGGAG AGTGCAGAAC TGGACAGCGG AGGCTTTGGG AAGGTGTCTC 97
pPheLeuGlu SerAlaGluL euAspSerGl yGlyPheGly LysValSerL 33

TGTGTTTCCA CAGAACCCAG GGAATCATGA TCATGAAAAC AGTGTACAAG 147
euCysPheHi sArgThrGln GlyLeuMetI leMetLysTh rValTyrLys 49

GGGCCCAACT GCATTGAGCA CAACGAGGCC CTCTTGGAGG AGGCGAAGAT 197
GlyProAsnC ysIleGluHi sAsnGluAla LeuLeuGluG luAlaLysMe 66

GATGAACAGA CTGAGACACA GCCGGGTGGT GAAGCTCCTG GGCATCATCA 247
tMetAsnArg LeuArgHisS erArgValVa lLysLeuLeu GlyValIleI 83

TAGAGGAAGG GAAGTACTCC CTGGTGATGG AGTACATGGA GAAGGGCAAC 297
leGluGluGl yLysTyrSer LeuValMetG luTyrMetGl uLysGlyAsn 99

CTGATGCACG TGCTGAAAGC CGAGATGAGT ACTCCGCTTT CTGTAAAAGG 347

LeuMetHisV alLeuLysAl aGluMetSer ThrProLeuS erValLysGl 116

AAGGATAATT TTGGAAATCA TTGAAGGAAT GTGCTACTTA CATGGAAAAG 397

yArgIleIle LeuGluIleI leGluGlyMe tCysTyrLeu HisGlyLysG 133

GCGTGATACA CAAGGACCTG AAGCCTGAAA ATATCCTTGT TGATAATGAC 447

lyValIleHi sLysAspLeu LysProGluA snIleLeuVa lAspAsnAsp 149

TTCCACATTA AGATCGCAGA CCTCGGCCTT GCCTCCTTTA AGATGTGGAG 497

PheHisIleL ysIleAlaAs pLeuGlyLeu AlaSerPheL ysMetTrpSe 166

CAAACGAAT AATGAAGAGC ACAATGAGCT GAGGGAAGTG GACGGCACCG 547

rLysLeuAsn AsnGluGluH isAsnGluLe uArgGluVal AspGlyThrA 183

CTAAGAAGAA TGGCGGCACC CTCTACTACA TGGCGCCCGA GCACCTGAAT 597

laLysLysAs nGlyGlyThr LeuTyrTyrM etAlaProGl uHisLeuAsn 199

GACGTCAACG CAAAGCCCAC AGAGAAGTCG GATGTGTACA GCTTTGCTGT 647 [Y212*](#)

AspValAsnA laLysProTh rGluLysSer AspValTyrS erPheAlaVa 216

AGTACTCTGG GCGATATTTG CAAATAAGGA GCCATATGAA AATGCTATCT 697 [c.688_688+20del](#)

lValLeuTrp AlaIlePheA laAsnLysGl uProTyrGlu AsnAlaIleC 233

GTGAGCAGCA GTTGATAATG TGCATAAAAT CTGGGAACAG GCCAGATGTG 747

ysGluGlnGl nLeuIleMet CysIleLysS erGlyAsnAr gProAspVal 249

GATGACATCA CTGAGTACTG CCCAAGAGAA ATTATCAGTC TCATGAAGCT 797

AspAspIleT hrGluTyrCy sProArgGlu IleIleSerL euMetLysLe 266

CTGCTGGGAA GCGAATCCGG AAGCTCGGCC GACATTCCT GGCATTGAAG 847

uCysTrpGlu AlaAsnProG luAlaArgPr oThrPhePro GlyIleGluG 283

AAAAATTTAG GCCTTTTTAI TTAAGTCAAT TAGAAGAAAAG TGTAGAAGAG 897 [Y289*](#)

luLysPheAr gProPheTyr LeuSerGlnL euGluGluSe rValGluGlu 299

GACGTGAAGA GTTTAAAGAA AGAGTATTCA AACGAAAATG CAGTTGTGAA 947

AspValLysS erLeuLysLy sGluTyrSer AsnGluAsnA laValValLy 316

GAGAATGCAG TCTCTTCAAC TTGATIGTGT GGCAGTACCT TCAAGCCGGT 997 [M318fs](#) [L321R](#) [D324H](#) [D324N](#) [D324Y](#) [D324V](#) [D324G](#) [C325R](#)

sArgMetGln SerLeuGlnL euAspCysVa lAlaValPro SerSerArgS 333

[CAAATTCAGC](#) CACAGAACAG CCTGGTTCAC TGCACAGTTC CCAGGGACTT 1047 [S333*](#)

erAsnSerAl aThrGluGln ProGlySerL euHisSerSe rGlnGlyLeu 349

GGGATGGGTC CTGTGGAGGA GTCCTGGTTT GCTCCTTCCC TGGAGCACCC 1097

GlyMetGlyP roValGluGl uSerTrpPhe AlaProSerL euGluHisPr 366

ACAAGAAGAG AATGAGCCCA GCCTGCAGAG TAAACTCCAA GACGAAGCCA 1147 [K377E](#)

oGlnGluGlu AsnGluProS erLeuGlnSe rLysLeuGln AspGluAlaA 383

ACTACCATCT TTATGGCAGC CGCATGGACA GGCAGACGAA ACAGCAGCCC 1197 [R390G](#)

snTyrHisLe uTyrGlySer ArgMetAspA rgGlnThrLy sGlnGlnPro 399

AGACAGAATG TGGCTTACAA CAGAGAGGAG GAAAGGAGAC GCAGGGTCTC 1247

ArgGlnAsnV alAlaTyrAs nArgGluGlu GluArgArgA rgArgValSe 416

CCATGACCCT TTTGCACAGC AAAGACCTTA CGAGAATTTT CAGAATACAG 1297 Y426*

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CACCAGCCCT CAGGGCTCAC CAGCCAACCT CAAGTACTGT ATCAGAACAA 1397

HisGlnProS erGlyLeuTh rSerGlnPro GlnValLeuT yrGlnAsnAs 466

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uGluProAla AlaLysTyrG lnAlaIlePh eAspAsnThr ThrSerLeuT 583

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hrAspLysHi sLeuAspPro IleArgGluA snLeuGlyLy sHisTrpLys 599

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pHisAspTyr GluArgAspG lyLeuLysGl uLysValTyr GlnMetLeuG 633

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GCCCAGGCGC TCCACCACTG TTCCAGGATC GACCTTCTGA GCAGCTTGAT 1997

AlaGlnAlaL euHisGlnCy sSerArgIle AspLeuLeuS erSerLeuIl 666

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eTyrValSer GlnAsnStop

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AATTCTGTCC TCACTGATAG GGGTTCTGTG TCTGCAGAAA TTTTGTTTCC *131

TGTACTTCAT AGCTGGAGAA TGGGGAAAGA AATCTGCAGC AAAGGGGTCT *181

CACTCTGTTG CCAGGCTGGT CTCAAACCTC TGGACTCAAG TGATCCTCCC *231

GCCTCGGCCT TCCAAAGTGC TGGGATATCA GGCACGTAGC CACTGCGCCC *281

AGCCAACAAT CCGCTCTGAG GAAAGCGTAA GCAGGAAGAC CTCTTAATGG *331

CATAGCACCA ATAAAAAAT GACTCCTAGT TGTGTTTGGA AAGGGAGAGA *381

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AAATTGTGTG CTCTCTTCTT CACGTAGGCT CCTGTAAAAA ACAAAGTGCA *531
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GTTGTTGCAA GGAATTGGTA CTAACCGTGA CTACAACAAA AATTCTTGAT *831
TGACTTTTAA AGTTATTTCC TGGCATTCTG GTACCTTCAC CCAGCCTGAG *881
TGCCCTGGAG AGGGAACAGG AAATGCTGAT CTCTACCCCT GGGTGAGACC *931
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ACTGTGAAAG TATTTTCATA TTTTTTCTGT GTGCCAGAGT GAAAAAGGAC *1031
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TTAATGTTCA AAGGCAAGAG GGCAAGGCAT TTTTAAACAC TTTTAAAAAT *1831

AAAAATTTAT ACCACAA

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