



RIPK1 (NM_003804.6) - cDNA + Protein - 2024-12-06

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

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

TGTGTTTCCA CAGAACCCAG GGACTCATGA 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 GGCGTCATCA 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

CAAACCTGAAT AATGAAGAGC ACAATGAGCT GAGGGAAGTG GACGGCACCG 547 G181S

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 GACATTTCCCT GGCATTGAAG 847

uCysTrpGlu AlaAsnProG luAlaArgPr oThrPhePro GlyIleGluG 283

AAAAATTTAG GCCTTTTTAT TTAAGTCAAT TAGAAGAAAG TGTAGAAGAG 897 [Y289*](#)

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GACGTGAAGA GTTTAAAGAA AGAGTATTCA AACGAAAATG CAGTTGTGAA 947

AspValLysS erLeuLysLy sGluTyrSer AsnGluAsnA laValValLy 316

GAGAATGCAG TCTCTTCAAC TTGATTTGTGT 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

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CACCAGCCCT CAGGGCTCAC CAGCCAACCT CAAGTACTGT ATCAGAACAA 1397

HisGlnProS erGlyLeuTh rSerGlnPro GlnValLeuT yrGlnAsnAs 466

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AATTCGTGCC TCACTGATAG GGGTTCGTG TCTGCAGAAA TTTTGTTC *131

TGTACTTCAT AGCTGGAGAA TGGGGAAAGA AATCTGCAGC AAAGGGGTCT *181

CACTCTGTTG CCAGGCTGGT CTCAAACCTC TGGACTCAAG TGATCCTCCC *231

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TGCCCTGGAG AGGGAACAGG AAATGCTGAT CTCTACCCCT GGGTGAGACC *931
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