



RIPK1 (NM_003804.6) - cDNA + Protein - 2024-11-25

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 CAGAAGCCAG GACTCATGA 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 GACG~~GCACCG~~ 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*](#)

luLysPheAr gProPheTyr LeuSerGlnL euGluGluSe rValGluGlu 299

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

ArgGlnAsnV alAlaTyrAs nArgGluGlu GluArgArgA rgArgValSe 416

CCATGACCCT TTTGCACAGC AAAGACCTTA CGAGAATTTT CAGAATACAG 1297 Y426*

rHisAspPro PheAlaGlnG lnArgProTy rGluAsnPhe GlnAsnThrG 433

AGGGAAAAGG CACTGCTTAT TCCAGTGCAG CCAGTCATGG TAATGCAGTG 1347

luGlyLysGl yThrAlaTyr SerSerAlaA laSerHisGl yAsnAlaVal 449

CACCAGCCCT CAGGGCTCAC CAGCCAACCT CAAGTACTGT ATCAGAACAA 1397

HisGlnProS erGlyLeuTh rSerGlnPro GlnValLeuT yrGlnAsnAs 466

TGGATTATAT AGCTCACATG GCTTTGGAAC AAGACCACTG GATCCAGGAA 1447

nGlyLeuTyr SerSerHisG lyPheGlyTh rArgProLeu AspProGlyT 483

CAGCAGGTCC CAGAGTTTGG TACAGGCCAA TTCCAAGTCA TATGCCTAGT 1497

hrAlaGlyPr oArgValTrp TyrArgProI leProSerHi sMetProSer 499

CTGCATAATA TCCCAGTGCC TGAGACCAAC TATCTAGGAA ATACACCCAC 1547

LeuHisAsnI leProValPr oGluThrAsn TyrLeuGlyA snThrProTh 516

CATGCCATTC AGCTCCTTGC CACCAACAGA TGAATCTATA AAATATACCA 1597

rMetProPhe SerSerLeuP roProThrAs pGluSerIle LysTyrThrI 533

TATACAATAG TACTGGCATT CAGATTGGAG CCTACAATTA TATGGAGATT 1647

leTyrAsnSe rThrGlyIle GlnIleGlyA laTyrAsnTy rMetGluIle 549

GGTGGGACGA GTTCATCACT ACTAGACAGC ACAAATACGA ACTTCAAAGA 1697

GlyGlyThrS erSerSerLe uLeuAspSer ThrAsnThrA snPheLysGl 566

AGAGCCAGCT GCTAAGTACC AAGCTATCTT TGATAATACC ACTAGTCTGA 1747

uGluProAla AlaLysTyrG lnAlaIlePh eAspAsnThr ThrSerLeuT 583

CGGATAAACA CCTGGACCCA ATCAGGGAAA ATCTGGGAAA GCACTGGAAA 1797

hrAspLysHi sLeuAspPro IleArgGluA snLeuGlyLy sHisTrpLys 599

AACTGTGCCG GTAAACTGGG CTTACACACAG TCTCAGATTG ATGAAATGA 1847 C601Y I615T

AsnCysAlaA rgLysLeuGl yPheThrGln SerGlnIleA spGluIleAs 616

CCATGACTAT GAGCGAGATG GACTGAAAGA AAAGGTTTAC CAGATGCTCC 1897

pHisAspTyr GluArgAspG lyLeuLysGl uLysValTyr GlnMetLeuG 633

AAAAGTGGGT GATGAGGGAA GGCATAAAGG GAGCCA_CGGT GGGGAAGCTG 1947 T645M

lnLysTrpVa lMetArgGlu GlyIleLysG lyAlaThrVa lGlyLysLeu 649

GCCCAGGCGC TCCACCAGTG TTCCAGGATC GACCTTCTGA GCAGCTTGAT 1997

AlaGlnAlaL euHisGlnCy sSerArgIle AspLeuLeuS erSerLeuIl 666

TTACGTCAGC CAGAACTAAC CCTGGATGGG CTACGGCAGC TGAAGTGGAC *31

eTyrValSer GlnAsnStop

GCCTCACTTA GTGGATAACC CCAGAAAGTT GGCTGCCTCA GAGCATTGAG *81

AATTCGTGCC TCACTGATAG GGGTTCGTG TCTGCAGAAA TTTTGTTTCC *131

TGTACTTCAT AGCTGGAGAA TGGGGAAAGA AATCTGCAGC AAAGGGGTCT *181

CACTCTGTTG CCAGGCTGGT CTCAAACCTC TGGACTCAAG TGATCCTCCC *231

GCCTCGGCC TCCAAAGTGC TGGGATATCA GGCAGTGCAG CACTGCGCCC *281

AGCCAACAAT CCGCTCTGAG GAAAGCGTAA GCAGGAAGAC CTCTTAATGG *331

CATAGCACCA ATAAAAAAT GACTCCTAGT TGTGTTTGGG AAGGGAGAGA *381

AGAGATGTCT GAGGAAGGTC ATGTTCTTTC AGCTTATGGC ATTCCTAGA *431

GTTTTGTTGA AGCAAGAAGA AAAACTCAGA GAATATAAAA TCAACTTTTA *481
AAATTGTGTG CTCTCTTCTT CACGTAGGCT CCTGTAAAAA ACAAAGTGCA *531
GTCAGATTCT AAGCCCTGTT CAGAGACTTC GTGGATCACA GCTGCAGCTC *581
ACCGCCACAT CACAGGATCC GTTAACGTTA ATACCCAATA CTCTGTCAGC *631
CACTGTAGGC TCTAAGAACC ACGTGCAGTC TTCAGCCCAT TAAATTATCG *681
ATTATTTTTT AATGAATTGA ATTTATATTG AGTCTTCAAA TTAAGTGAAT *731
GGATTTAAAG GGGTACCAAG GAGGGGGAA ACATCAGAAT TTCCCAGGCA *781
GTTGTTGCAA GGAATTGGTA CTAACCGTGA CTACAACAAA AATCTTGAT *831
TGACTTTTAA AGTTATTTCC TGGCATCTG GTACCTTAC CCAGCCTGAG *881
TGCCCTGGAG AGGGAACAGG AAATGCTGAT CTCTACCCCT GGGTGAGACC *931
AGAACCCTCAG GGCTGATACT GTTGAGTGGC TTCCTCGGTT TACTCTGTGT *981
ACTGTGAAAG TATTTTCATA TTTTTTCTGT GTGCCAGAGT GAAAAAGGAC *1031
AGCTTCTGAG TGTGGTAATT GTGCCTCTAG CACCCAGCCT TTCAAAGCCC *1081
ACCTGAAACC TGGGGTGGGA TGAAAGAACT AGAATAGAAG ACTGAAGCTG *1131
GGTAGGCCGC TCAGTGTCCA CTGGCATTTT GCTAAACCGA CAAGGAAGGC *1181
TGTGTGCTTA GCTCTCCCCA GAGGGAGGGC GAGAAGGGTG TGGTGATGGT *1231
CAATCTGGCT GTCGGAACAG ATTCTGGTGT CTTGGGCTGA TAACAGTGTT *1281
GTTGATTCTG ATTGTGAATC CCCTCAACTC TAGCAGACAC ATACACACCC *1331
CTGAAATGGG GCTGCAGAGC AGGCTGTCTC AGCCTTGCCA CTGTCGGCAT *1381
CTCGGCCTGG GTAATCTGT TGTGGGGACT GTCCTGTTCC TTGTAGGATG *1431
TTTAGTAGCA TCCCTGCCCC CACCTACTAG ATGCCAGGGG CACTGTTCTC *1481
CCCAGCCCCC CGCCCCAGTT GTGACAATAG TCTCTAAACA TTGTCAAATG *1531
GTCCAAGGAA AGGGGAAAAT TGCCCCGGTT GAGAAGAGCA CTGCTGTAAA *1581
GTAATGAGCC TCGGCTCTCC TGTCTGCACC TGTCCGGTTA CTACTTGGCC *1631
ACCACGCAGC CTTGGCTCCT ACAGCCCAA AGGGAGAATG GAGGGAGGCT *1681
CCAGGCTTTG CTGGAGGGC CTGGGTGAGT TCTGTTTGCT CCTTGTACCA *1731
CCATCCAAAT GGTGTTATCA AATCTCTTAG ATTCCAAAGA GGTGAATAA *1781
TTAATGTTCA AAGGCAAGAG GGCAAGGCAT TTTTAAACAC TTTTAAAAAT *1831

AAAAATTAT ACCACAA

RIPK1 (NM_003804.6) - cDNA + Protein - 2024-11-25

