

Infevers - RIPK1 (NM_003804.6) - cDNA + Protein - 2023-04-02

GGGAGTCCGC GGCGAGCGCA 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 CTCTTGAGG AGGCGAAGAT 197
 GlyProAsnC ysIleGluHi sAsnGluAla LeuLeuGluG luAlaLysMe 66

 GATGAACAGA CTGAGACACA GCCGGGTGGT GAAGCTCCTG GCGTCATCA 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 TTGGAATCA 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

 CAAACTGAAT 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 GACATTTCTT 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 TTGATTGTGT 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

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oGlnGluGlu AsnGluProS erLeuGlnSe rLysLeuGln AspGluAlaA 383

ACTACCATCT TTATGGCAGC CGCATGGACA GGCAGACGAA ACAGCAGCCC 1197
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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 AsnCysAlaA rgLysLeuGl yPheThrGln SerGlnIleA spGluIleAs 616
 CCATGACTAT GAGCGAGATG GACTGAAAGA AAAGGTTTAC CAGATGCTCC 1897

pHisAspTyr GluArgAspG lyLeuLysGl uLysValTyr GlnMetLeuG 633

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AlaGlnAlaL euHisGlnCy sSerArgIle AspLeuLeuS erSerLeuIl 666

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GCCTCACTTA GTGGATAACC CCAGAAAGTT GGCTGCCTCA GAGCATTTCAG *81

AATTCTGTCC TCACTGATAG GGGTTCTGTG TCTGCAGAAA TTTTGTTC *131

TGTACTTCAT AGCTGGAGAA TGGGGAAAGA AATCTGCAGC AAAGGGGTCT *181

CACTCTGTTG CCAGGCTGGT CTCAAACCTC TGGACTCAAG TGATCCTCCC *231

GCCTCGGCC TCCAAAGTGC TGGGATATCA GGCCTGAGC CACTGCGCCC *281

AGCCAACAAT CCGCTCTGAG GAAAGCGTAA GCAGGAAGAC CTCTTAATGG *331

CATAGCACCA ATAAAAAAT GACTCCTAGT TGTGTTTGA AAGGGAGAGA *381

AGAGATGTCT GAGGAAGGTC ATGTTCTTTC AGCTTATGGC ATTTCTAGA *431

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AAATTGTGTG CTCTCTTCTT CACGTAGGCT CCTGTAAAA ACAAAGTGCA *531

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CACTGTAGGC TCTAAGAACC ACGTGCAGTC TTCAGCCCAT TAAATTATCG *681

ATTATTTTTT AATGAATTGA ATTTATATTG AGTCTTCAAA TTAAGTGAAT *731

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GTTGTTGCAA GGAATTGGTA CTAACCGTGA CTACAACAAA AATTCTTGAT *831

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AGAACCTCAG GGCTGATACT GTTGAGTGGC TTCCTCGGTT TACTCTGTGT *981

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CTCGGCCTGG GTAATTCTGT 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
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CCAGGCTTTG CTGGAGGGGC CTGGGTGAGT TCTGTTTGCT CCTTGTACCA *1731
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AAAAATTTAT ACCACAA

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