RBCK1 (NM_031229.4) - cDNA - 2026-02-23

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ACTTTCACTT TCTCTTCCGC CGAAGCCGCT CCCCTTGCGA AGAACTGGGG -410    c.ex1_ex4del

CCTCCCGGGA GGAGAGAGGG CTTTGCCTTG AAACCCGGGA CGCCAGGGGC -360

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CTCCTGCGCC CAGTGCGGAC CTGTCTCGGC GCCCGCTGCC CTCTCACCGC -210

CCCACGCAGG ATCCCGGCCT GGTCACCGGG CAGTGTGATG CTTCCCGACT -160

GCCGCGGGGA CAGCGAGGCA CACACAGGGC TTGGGCCGCG CCGGAGGCCA -110

CACGGCCTGG CTGAGTTGCT CCTGGTCTCC CGCCTCTCCC AGGCGACCCG -60

GAGGTAGCAT TTCCCAGGAG GCACGGTCCC CCCCAGGGGG ATGGGCACAG -10

CCACGCCAGA TGGACGAGAA GACCAAGAAA GCAGAGGAAA TGGCCCTGAG 41

CCTCACCCGA GCAGTGGCGG GCGGGGATGA ACAGGTGGCA ATGAAGTGTG 91    c.52G>C

CCATCTGGCT GGCAGAGCAA CGGGTGCCCC TGAGTGTGCA ACTGAAGCCT 141   L41fsX7

GAGGTCTCCC CAACGCAGGA CATCAGGCTG TGGGTGAGCG TGGAGGATGC 191

TCAGATGCAC ACCGTCACCA TCTGGCTCAC AGTGCGCCCT GATATGACAG 241

TGGCGTCTCT CAAGGACATG GTTTTTCTGG ACTATGGCTT CCCACCAGTC 291

TTGCAGCAGT GGGTGATTGG GCAGCGGCTG GCACGAGACC AGGAGACCCT 341

GCACTCCCAT GGGGTGCGGC AGAATGGGGA CAGTGCCTAC CTCTATCTGC 391   N122H

TGTCAGCCCG CAACACCTCC CTCAACCCTC AGGAGCTGCA GCGGGAGCGG 441

CAGCTGCGGA TGCTGGAAGA TCTGGGCTTC AAGGACCTCA CGCTGCAGCC 491   c.456+1G>C

GCGGGGCCCT CTGGAGCCAG GCCCCCCAAA GCCCGGGGTC CCCCAGGAAC 541   c.494delG

CCGGACGGGG GCAGCCAGAT GCAGTGCCTG AGCCCCCACC GGTGGGCTGG 591   Q185X

CAGTGCCCCG GGTGCACCTT CATCAACAAG CCCACGCGGC CTGGCTGTGA 641
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GATGTGCTGC CGGGCGCGCC CCGAGGCCTA CCAGGTCCCC GCCTCATACC 691   Q231Sfs*45

AGCCCGACGA GGAGGAGCGA GCGCGCCTGG CGGGCGAGGA GGAGGCGCTG 741   P190fs c.722del c.727_728insGGCG c.727G>T

CGTCAGTACC AGCAGCGGAA GCAGCAGCAG CAGGAGGGGA ACTACCTGCA 791   Q222X

GCACGTCCAG CTGGACCAGA GGAGCCTGGT GCTGAACACG GAGCCCGCCG 841   Q267* L273Pfs*27

AGTGCCCCGT GTGCTACTCG GTGCTGGCGC CCGGCGAGGC CGTGGTGCTG 891   V295L

CGTGAGTGTC TGCACACCTT CTGCAGGGAG TGCCTGCAGG GCACCATCCG 941   c.896_899del C305F

CAACAGCCAG GAGGCGGAGG TCTCCTGCCC CTTCATTGAC AACACCTACT 991   A319V

CGTGCTCGGG CAAGCTGCTG GAGAGGGAGA TCAAGGCGCT CCTGACCCCT 1041

GAGGATTACC AGCGATTTCT AGACCTGGGC ATCTCCATTG CTGAAAACCG 1091   c.1054C>T

CAGTGCCTTC AGCTACCATT GCAAGACCCC AGATTGCAAG GGATGGTGCT 1141

TCTTTGAGGA TGATGTCAAT GAGTTCACCT GCCCTGTGTG TTTCCACGTC 1191   c.1160A>G

AACTGCCTGC TCTGCAAGGC CATCCATGAG CAGATGAACT GCAAGGAGTA 1241

TCAGGAGGAC CTGGCCCTGC GGGCTCAGAA CGATGTGGCT GCCCGGCAGA 1291

CGACAGAGAT GCTGAAGGTG ATGCTGCAGC AGGGCGAGGC CATGCGCTGC 1341

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CTGCACCGTC TGCCACACCG AGATCTGCTG GGTCACCAAG GGCCCACGCT 1441   T470S E471K

GGGGCCCTGG GGGCCCAGGA GACACCAGCG GGGGCTGCCG CTGCAGGGTA 1491   T489Pfs*9

AATGGGATTC CTTGCCACCC AAGCTGTCAG AACTGCCACT GAGCTAAAGA *8   N508Pfs*4

TGGTGGGGCC ACATGCTGAC CCAGCCCCAC ATCCACATTC TGTTAGAATG *58

TAGCTCAGGG AGCTTCGTGG ACGGCCTTGC TTGCTGTAGC GTTGTAGGGG *108

CCCTGCCTGC ACTGCGGTTG TCCACGGTCA CATCTGCCCC AGTGCCTTTG *158

TCCTTCCCTT GGGGCTTGCC GGCCAGACTT CTCTCCCCTG CGGCTCCCAC *208

CTCTGCCTGA CCCCAGCCTT AAACATAGCC CCTGGCCAGA GGCCTTGCTG *258

GGTGGAGCCT CTGTGTGACT CCATACTCCT CCCACCACAA CACTCATCTG *308

TCAAACACCA AGCACTCTCA GCCTCCCCGC CTTCAGCTGT CAGCTTTCTG *358

GGGCTAACTT CTCTGCCTTT GTGGTTGGAG GCCTGAGGCC TCTTGGAACT *408

CTTGCTAACC TGTTCAGAGC CAGGAAGGAG ACTGCACAGT TTTGAAAGCA *458

CAGCCCGTCA GGTCCGGCTC TGCGTCTCCC TCTCTGCAGC CTGTGTAAGC *508

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TATTATAATT AAAATGGTTT TCCGGGAAGG GATGAGTGTG ATGTCCTTGA *558

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GGTCTCTGGG AACTGCATCA GAAAGTTGAC TTGTCAGTCC ATCTGTGGTA *658

GAATGAGGCT GTGACTGAGC ACTGGGACCT TTCTACCAGA TGTGGACCCC *708

ATGCCCAGCC TCAGGGGCAA GGATGCTCTT GGGTCACCGT CAGCCAGGAC *758

AGGTGGAGTG TGCAGTGTGT CAAGTCTGCA GAGAAGGATG GGCTTAGGGG *808

CGGGAGGGGA AGTCTTGCCA CTCCTGCTCC CTTTTGACCT CTCAGCAGGC *858

ATCTAGGGTT GGCAGGTAGA TAGTTCAAGA AGGAACGAAG CTGCTGCAGT *908

TGAGGGGTGG GGTTGTCCAT CCTATTTTCT CGTCTCAAGC AAGATGGCAC *958

AGTATCGATT CAGCAGTATT TACTAGAACC CACTCTGTGC TGGTCGGAGG *1008

TTACTAAGAC AGGGTCCTGG GATGTTCATT CTCTAAGTCT TTCCTCCGCT *1058

CTGTGACCCA CCCTCCTTCC CCTTTTGAGA TCTGGTATTT GATGCCCAAC *1108

ACATTGTCCA CGCTGTGACG TGACCATCAT CATAGCAGGC AGAGGGCGCC *1158

TCTGCTGCTG AAGGCCTGTG ATTTTGTGGG GAAGGGCCTG TTCTAGCAAC *1208

TGGAAAGGCA CTGCCACCTG CCGTTGGATG CCAGGACTCA AGAGCTGGCC *1258

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