



*RBCK1* (NM\_031229.4) - cDNA + Protein - 2025-04-02

ACTTTCACTT TCTCTTCCGC CGAAGCCGCT CCCCTTGCGA AGAACTGGGG -410 [c.ex1\\_ex4del](#)  
CCTCCCGGGA GGAGAGAGGG CTTTGCCTTG AAACCCGGGA CGCCAGGGGC -360  
GCTCCCGCAA GTGGGGGTCC TCCGGGACTT GGAACGCCCC GGCTGGGTGG -310  
TGTCCGGGCG TCCTTTCCCC GCTTCTTCCC ACCTCGGCTG GTCCCGTTTC -260  
CTCCTGCGCC CAGTGC GGAC CTGTCTCGGC GCCCGCTGCC CTCTCACC GC -210  
CCCACGCAGG ATCCCGGCCT GGTCAACGGG CAGTGTGATG CTTCCCGACT -160  
GCCGCGGGGA CAGCGAGGCA CACACAGGGC TTGGGCGCG CCGGAGGCCA -110  
CACGGCCTGG CTGAGTTGCT CCTGGTCTCC CGCCTCTCCC AGGCGACCCG -60  
GAGGTAGCAT TTCCAGGAG GCACGGTCCC CCCAGGGGG ATGGGCACAG -10  
CCACGCCAGA **TGGACGAGAA** **GACCAAGAAA** **GCAGAGGAAA** **TGGCCCTGAG** 41  
M etAspGluLy sThrLysLys AlaGluGluM etAlaLeuSe 14  
  
CCTCACCCGA GCAGTGGCGG GCGGGGATGA ACAGGTGGCA ATGAAGTGTG 91 [c.52G>C](#)  
rLeuThrArg AlaValAlaG lyGlyAspGl uGlnValAla MetLysCysA 31  
  
CCATCTGGCT GGCAGAGCAA CGGGTGCCCC TGAGTGTGCA ACTGAAGCCT 141 [L41fsX7](#)  
laIleTrpLe uAlaGluGln ArgValProL euSerValGl nLeuLysPro 47  
  
GAGGTCTCCC CAACGCAGGA CATCAGGCTG TGGGTGAGCG TGGAGGATGC 191  
GluValSerP roThrGlnAs pIleArgLeu TrpValSerV alGluAspAl 64  
  
TCAGATGCAC ACCGTCACCA TCTGGCTCAC AGTGCGCCCT GATATGACAG 241

aGlnMetHis ThrValThrI leTrpLeuTh rValArgPro AspMetThrV 81

TGGCGTCTCT CAAGGACATG GTTTTTCTGG ACTATGGCTT CCCACCAGTC 291

alAlaSerLe uLysAspMet ValPheLeuA spTyrGlyPh eProProVal 97

TTGCAGCAGT GGGTGATTGG GCAGCGGCTG GCACGAGACC AGGAGACCCT 341

LeuGlnGlnT rpValIleGl yGlnArgLeu AlaArgAspG lnGluThrLe 114

GCACTCCCAT GGGGTGCGGC AGAATGGGGA CAGTGCCTAC CTCTATCTGC 391 [N122H](#)

uHisSerHis GlyValArgG lnAsnGlyAs pSerAlaTyr LeuTyrLeuL 131

TGTCAGCCCG CAACACCTCC CTCAACCCTC AGGAGCTGCA GCGGGAGCGG 441

euSerAlaAr gAsnThrSer LeuAsnProG lnGluLeuGl nArgGluArg 147

CAGCTGCGGA TGCTGGAAGA TCTGGGCTTC AAGGACCTCA CGCTGCAGCC 491 [c.456+1G>C](#)

GlnLeuArgM etLeuGluAs pLeuGlyPhe LysAspLeuT hrLeuGlnPr 164

GCGGGGCCCT CTGGAGCCAG GCCCCCCAA GCCCCGGGTC CCCCAGGAAC 541 [c.494delG](#)

oArgGlyPro LeuGluProG lyProProLy sProGlyVal ProGlnGluP 181

CCGGACGGGG GCAGCCAGAT GCAGTGCCTG AGCCCCACC GGTGGGCTGG 591 [Q185X](#)

roGlyArgGl yGlnProAsp AlaValProG luProProPr oValGlyTrp 197

CAGTGCCCGG GGTGCACCTT CATCAACAAG CCCACGCGGC CTGGCTGTGA 641

GlnCysProG lyCysThrPh eIleAsnLys ProThrArgP roGlyCysGl 214

GATGTGCTGC CGGGCGCGCC CCGAGGCCTA CCAGGTCCCC GCCTCATACC 691 [Q231Sfs\\*45](#)

uMetCysCys ArgAlaArgP roGluAlaTy rGlnValPro AlaSerTyrG 231

AGCCCGACGA GGAGGAGCGA GCGCGCCTGG CGGGCGGAGGA GGAGGCGCTG 741 P190fs c.722del c.727\_728insGGCG c.727G>T  
lnProAspGl uGluGluArg AlaArgLeuA laGlyGluGl uGluAlaLeu 247

CGTCAGTACC AGCAGCGGAA GCAGCAGCAG CAGGAGGGGA ACTACCTGCA 791 Q222X  
ArgGlnTyrG lnGlnArgLy sGlnGlnGln GlnGluGlyA snTyrLeuGl 264

GCACGTCCAG CTGGACCAGA GGAGCCTGGT GCTGAACACG GAGCCCGCCG 841 Q267\* L273Pfs\*27  
nHisValGln LeuAspGlnA rgSerLeuVa lLeuAsnThr GluProAlaG 281

AGTGCCCGT GTGCTACTCG GTGCTGGCGC CCGGCGAGGC CGTGGTGCTG 891 V295L  
luCysProVa lCysTyrSer ValLeuAlaP roGlyGluAl aValValLeu 297

CGTGAGTGTC TGCACACCTT CTGCAGGGAG TGCCTGCAGG GCACCATCCG 941 c.896\_899del C305F  
ArgGluCysL euHisThrPh eCysArgGlu CysLeuGlnG lyThrIleAr 314

CAACAGCCAG GAGGCGGAGG TCTCCTGCCC CTTCATTGAC AACACCTACT 991 A319V  
gAsnSerGln GluAlaGluV alSerCysPr oPheIleAsp AsnThrTyrS 331

CGTGCTCGGG CAAGCTGCTG GAGAGGGAGA TCAAGGCGCT CCTGACCCCT 1041  
erCysSerGl yLysLeuLeu GluArgGluI leLysAlaLe uLeuThrPro 347

GAGGATTACC AGCGATTTCT AGACCTGGGC ATCTCCATTG CTGAAAACCG 1091 c.1054C>T  
GluAspTyrG lnArgPheLe uAspLeuGly ileSerIleA laGluAsnAr 364

CAGTGCC TTC AGCTACCATT GCAAGACCCC AGATTGCAAG GGATGGTGCT 1141  
gSerAlaPhe SerTyrHisC ysLysThrPr oAspCysLys GlyTrpCysP 381

TCTTTGAGGA TGATGTCA<sup>A</sup>T GAGTTCACCT GCCCTGTGTG TTTCCACGTC 1191 [c.1160A>G](#)

hePheGluAs pAspValAsn GluPheThrC ysProValCy sPheHisVal 397

AACTGCCTGC TCTGCAAGGC CATCCATGAG CAGATGAACT GCAAGGAGTA 1241

AsnCysLeuL euCysLysAl aIleHisGlu GlnMetAsnC ysLysGluTy 414

TCAGGAGGAC CTGGCCCTGC GGGCTCAGAA CGATGTGGCT GCCCGGCAGA 1291

rGlnGluAsp LeuAlaLeuA rgAlaGlnAs nAspValAla AlaArgGlnT 431

CGACAGAGAT GCTGAAGGTG ATGCTGCAGC AGGGCGAGGC CATGCGCTGC 1341

hrThrGluMe tLeuLysVal MetLeuGlnG lnGlyGluAl aMetArgCys 447

CCCCAGTGCC AGATCGTGGT ACAGAAGAAG GACGGCTGCG ACTGGATCCG 1391

ProGlnCysG lnIleValVa lGlnLysLys AspGlyCysA spTrpIleAr 464

CTGCACCGTC TGCCACA<sup>CCG</sup> AGATCTGCTG GGTCAACAAG GGCCACGCT 1441 [T470S](#) [E471K](#)

gCysThrVal CysHisThrG luIleCysTr pValThrLys GlyProArgT 481

GGGGCCCTGG GGGCCCAGGA GAC<sup>A</sup>CCAGCG GGGGCTGCCG CTGCAGGGTA 1491 [T489Pfs\\*9](#)

rpGlyProGl yGlyProGly AspThrSerG lyGlyCysAr gCysArgVal 497

AATGGGATTC CTTGCCACCC AAGCTGTCTAG <sup>A</sup>ACTGCCACT GAGCTAAAGA \*8 [N508Pfs\\*4](#)

AsnGlyIleP roCysHisPr oSerCysGln AsnCysHisS top

TGGTGGGGCC ACATGCTGAC CCAGCCCCAC ATCCACATTC TGTTAGAATG \*58

TAGCTCAGGG AGCTTCGTGG ACGGCCTTGC TTGCTGTAGC GTTGTAGGGG \*108

CCCTGCCTGC ACTGCGGTTG TCCACGGTCA CATCTGCCCC AGTGCCTTTG \*158

TCCTTCCCTT GGGGCTTGCC GGCCAGACTT CTCTCCCCTG CGGCTCCCAC \*208

CTCTGCCCTGA CCCAGCCCTT AACATAGCC CCTGGCCAGA GGCCTTGCTG \*258  
GGTGGAGCCT CTGTGTGACT CCATACCTCT CCCACCACAA CACTCATCTG \*308  
TCAAACACCA AGCACTCTCA GCCTCCCCGC CTTCAGCTGT CAGCTTTCTG \*358  
GGGCTAACTT CTCTGCCTTT GTGGTTGGAG GCCTGAGGCC TCTTGGAAct \*408  
CTTGCTAACC TGTTGAGAGC CAGGAAGGAG ACTGCACAGT TTTGAAAGCA \*458  
CAGCCCGTCA GGTCCGGCTC TCGTCTCCC TCTCTGCAGC CTGTGTAAGC \*508  
TATTATAATT AAAATGGTTT TCCGGGAAGG GATGAGTGTG ATGTCCTTGA \*558  
GAGGAAATGA ATGTCCTGGC CTGGGACTCT ACACACAGGC AGGATCCTGA \*608  
GGTCTCTGGG AACTGCATCA GAAAGTTGAC TTGTCAGTCC ATCTGTGGTA \*658  
GAATGAGGCT GTGACTGAGC ACTGGGACCT TTCTACCAGA TGTGGACCCC \*708  
ATGCCAGCC TCAGGGGCAA GGATGCTCTT GGGTCACCGT CAGCCAGGAC \*758  
AGGTGGAGTG TGCAGTGTGT CAAGTCTGCA GAGAAGGATG GGCTTAGGGG \*808  
CGGGAGGGGA AGTCTTGCCA CTCCTGCTCC CTTTTGACCT CTCAGCAGGC \*858  
ATCTAGGGTT GGCAGGTAGA TAGTTCAAGA AGGAACGAAG CTGCTGCAGT \*908  
TGAGGGGTGG GGTGTCCAT CCTATTTTCT CGTCTCAAGC AAGATGGCAC \*958  
AGTATCGATT CAGCAGTATT TACTAGAACC CACTCTGTGC TGGTCGGAGG \*1008  
TTACTAAGAC AGGGTCCTGG GATGTTTATT CTCTAAGTCT TTCCTCCGCT \*1058  
CTGTGACCCA CCCTCCTTCC CTTTTGAGA TCTGGTATTT GATGCCCAAC \*1108  
ACATTGTCCA CGCTGTGACG TGACCATCAT CATAGCAGGC AGAGGGCGCC \*1158  
TCTGCTGCTG AAGCCCTGTG ATTTTGTGGG GAAGGGCCTG TTCTAGCAAC \*1208  
TGAAAAGGCA CTGCCACCTG CCGTTGGATG CCAGGACTCA AGAGCTGGCC \*1258  
CCAGTCACTG TGCAGCAGAGC TGTCTGAGAA TGTGTGAGTG GACTGGGTCC \*1308  
TTCGGCACTG CCTGCATTGG CTCAGGGCAG TCAACCGTCG CAGAGGATGA \*1358  
GGGGCACACT CAGGCAGCCT CCCCAGCCCT GGAGGCAGAA AGGCCAGGC \*1408  
AGAACCCTG ACTGGGAGGA AACAGAAAA GCAGAGGAGA GCCAGGCTGC \*1458  
AGGCGTGTGG ATGGGACCAG CTCAGGCAGA CGCTGTCTCA TACCCACTCT \*1508  
CCCCTCTCTT GCCAGGGCCT GGCTGGTGT CTCTCAGGAG CCTGGGCATG \*1558  
AGACAAAAGC AGAGATTGTT CTCTTGTGGT ACCACAGGCT GTAACCAGTC \*1608

CACCCAGTGT TGTTTTAGAA ATTTAAATCG GTTGCCCATC TTTTAAATT \*1658

GGCAACATCG TTTACCACAT TAAAATCTAG ATGCCCTGCT TCTCTTGAAA \*1708

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*RBCK1* (NM\_031229.4) - cDNA + Protein - 2025-04-02

