IKBKG (NM_003639.4) - cDNA + Protein - 2025-04-02

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AGCCCGTTCC TGCTCCGCGC TTCTGGAGCA CTGGCCAAGG CGGGCCGATT -209
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GTTCAGAGAC ATATTCTGTT CACCAAACTT GACTGCGCTC TATCGAGGTC -59
GTTAAATTCT TCGGAAATGC CTCACATATA GTTTGGCAGC TAGCCCTTGC -9
CCTGTTGGAT GAATAGGCAC CTCTGGAAGA GCCAACTGTG TGAGATGGTG 42
        Me tAsnArgHis LeuTrpLysS erGlnLeuCy sGluMetVal 14

CAGCCCAGTG GTGGCCCGGC AGCAGATCAG GACGTACTGG GCGAAGAGTC 92
GlnProSerG lyGlyProAl aAlaAspGln AspValLeuG lyGluGluSe 31

TCCTCTGGGG AAGCCAGCCA TGCTGCACCT GCCTTCAGAA CAGGGCGCTC 142
rProLeuGly LysProAlaM etLeuHisLe uProSerGlu GlnGlyAlaP 48

CTGAGACCCT CCAGCGCTGC CTGGAGGAGA ATCAAGAGCT CCGAGATGCC 192
roGluThrLe uGlnArgCys LeuGluGluA snGlnGluLe uArgAspAla 64

ATCCGGCAGA GCAACCAGAT TCTGCGGGAG CGCTGCGAGG AGCTTCTGCA 242
IleArgGlnS erAsnGlnIl eLeuArgGlu ArgCysGluG luLeuLeuHi 81

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sPheGlnAla SerGlnArgG luGluLysGl uPheLeuMet CysLysPheG 98
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LysArgGlnL ysGluGlnAl aLeuArgGlu ValGluHisL euLysArgCy 131

CCAGCAGCAG ATGGCTGAGG ACAAGGCCTC TGTGAAAGCC CAGGTGACGT 442
sGlnGlnGln MetAlaGluA spLysAlaSe rValLysAla GlnValThrS 148

CCTTGCTCGG GGAGCTGCAG GAGAGCCAGA GTCGCTTGGA GGCTGCCACT 492
erLeuLeuGl yGluLeuGln GluSerGlnS erArgLeuGl uAlaAlaThr 164

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LysGluCysG lnAlaLeuGl uGlyArgAla ArgAlaAlaS erGluGlnAl 181

GCGGCAGCTG GAGAGTGAGC GCGAGGCGCT GCAGCAGCAG CACAGCGTGC 592
aArgGlnLeu GluSerGluA rgGluAlaLe uGlnGlnGln HisSerValG 198

AGGTGGACCA GCTGCGCATG CAGGGCCAGA GCGTGGAGGC CGCGCTCCGC 642  V199V Q205*
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MetGluArgG lnAlaAlaSe rGluGluLys ArgLysLeuA laGlnLeuGl 231

GGTGGCCTAT CACCAGCTCT TCCAAGAATA CGACAACCAC ATCAAGAGCA 742
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GlnGlnLeuG lnGlnAlaGl uGluAlaLeu ValAlaLysG lnGluValIl 281

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eAspLysLeu LysGluGluA laGluGlnHi sLysIleVal MetGluThrV 298

TTCCGGTGCT GAAGGCCCAG GCGGATATCT ACAAGGCGGA CTTCCAGGCT 942
alProValLe uLysAlaGln AlaAspIleT yrLysAlaAs pPheGlnAla 314

GAGAGGCAGG CCCGGGAGAA GCTGGCCGAG AAGAAGGAGC TCCTGCAGGA 992
GluArgGlnA laArgGluLy sLeuAlaGlu LysLysGluL euLeuGlnGl 331

GCAGCTGGAG CAGCTGCAGA GGGAGTACAG CAAACTGAAG GCCAGCTGTC 1042
uGlnLeuGlu GlnLeuGlnA rgGluTyrSe rLysLeuLys AlaSerCysG 348

AGGAGTCGGC CAGGATCGAG GACATGAGGA AGCGGCATGT CGAGGTCTCC 1092
lnGluSerAl aArgIleGlu AspMetArgL ysArgHisVa lGluValSer 364

CAGGCCCCCT TGCCCCCCGC CCCTGCCTAC CTCTCCTCTC CCCTGGCCCT 1142
GlnAlaProL euProProAl aProAlaTyr LeuSerSerP roLeuAlaLe 381

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roLysCysGl nTyrGlnAla ProAspMetA spThrLeuGl nIleHisVal 414

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CCAGGATGAA GGGCTGGGTG GCCACAACTG GGATGCCACC TGGAGCCCCA *132
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TTTGTTCCCT TCTGTCTGCT CGAACCACTT GCCTCGGGCT AATCCCTCCC *282
TCTTCCTCCA CCCGGCACTG GGGAAGTCAA GAATGGGGCC TGGGGCTCTC *332
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CGGACACCGA CCCGCCCGCT GCTGTGCCCT GGGAGTGCTG CCCTCTTACC *432
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CAGACCGATG TGTATTTAAC CAGTCACTAT TGATGGACAT TTGGGTTGTT *532
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TTA
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