



IKBKG (NM_003639.4) - cDNA + Protein - 2026-02-28

AGCCCGTTCC TGCTCCGCGC TTCTGGAGCA CTGGCCAAGG CGGGCCGATT -209
CAGGACCCAG GTTACTTGGG CGGCGAGCTG GACTGTTTCT ACTCCTCCCT -159
CCTCCTCCAC TGCGGGGTCT GACCCTACTC CTTGTGTGAG GACTCCTCTA -109
G TTCAGAGAC ATATTCTGTT CACCAAAC TT GACTGCGCTC TATCGAGGTC -59
GT TAAAT TCT TCGGAAATGC CTCACATATA GTTTGGCAGC TAGCCCTTGC -9
CCTGTTGGAT GAATAGGCAC CTCTGGAAGA GCCAACTGTG TGAGATGGTG 42
Me tAsnArgHis LeuTrpLysS erGlnLeuCy sGluMetVal 14

CAGCCCAGTG GTGGCCCGGC AGCAGATCAG GACG TACTGG 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

TTTCCAAGCC AGCCAGAGGG AGGAGAAGGA GTTCCTCATG TGCAAGTTCC 292
sPheGlnAla SerGlnArgG luGluLysGl uPheLeuMet CysLysPheG 98

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lnGluAlaAr gLysLeuVal GluArgLeuG lyLeuGluLy sLeuAspLeu 114

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LysArgGlnL ysGluGlnAl aLeuArgGlu ValGluHisL euLysArgCy 131

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

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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*](#)
lnValAspGl nLeuArgMet GlnGlyGlnS erValGluAl aAlaLeuArg 214

ATGGAGCGCC AGGCCGCCCTC GGAGGAGAAG AGGAAGCTGG CCCAGTTGCA 692
MetGluArgG lnAlaAlaSe rGluGluLys ArgLysLeuA laGlnLeuGl 231

GGTGGCCTAT CACCAGCTCT TCCAAGAATA CGACAACCAC ATCAAGAGCA 742
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eAspLysLeu LysGluGluA laGluGlnHi sLysIleVal MetGluThrV 298

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alProValLe uLysAlaGln AlaAspIleT yrLysAlaAs pPheGlnAla 314

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GCAGCTGGAG CAGCTGCAGA GGGAGTACAG CAACTGAAG GCCAGCTGTC 1042
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lnGluSerAl aArgIleGlu AspMetArgL ysArgHisVa lGluValSer 364

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GlnAlaProL euProProAl aProAlaTyr LeuSerSerP roLeuAlaLe 381

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uProSerGln ArgArgSerP roProGluGl uProProAsp PheCysCysP 398

CCAAGTGCCA GTATCAGGCC CCTGATATGG ACACCCTGCA GATACATGTC 1242

roLysCysGl nTyrGlnAla ProAspMetA spThrLeuGl nIleHisVal 414

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MetGluCysI leGluStop

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TCCCATCTTT TTGTTACCAT AAATAATGGC ATAGTAAAAA TCCTTGTGCA *582

TTA

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