



HCK (NM_002110.5) - cDNA + Protein - 2024-12-22

ACCACGTCCC TGGTCCCAGC TCGGGAGCAC ATCAGAGGCT TAGAGGCGAG -134

TGGGAAGGGA CTCAGACAGT GCAGGACGAG AAACGCCCGC GGCACCAAAG -84

CCCCTCAGAG CGTCGCCCCC GCCTCTAGTT CTAGAAAGTC AGTTTCCCGG -34

CACTGGCACC CCGGAACCTC AGGGGCTGCC GAGCTGGGGG GCGCTCAAG 17

MetGlyG lyArgSerSe 6

CTGCGAGGAT CCGGGCTGCC CGCGAGACGA GGAGCGGGCG CCCAGGATGG 67

rCysGluAsp ProGlyCysP roArgAspGl uGluArgAla ProArgMetG 23

GGTGCATGAA GTCCAAGTTC CTCCAGGTCG GAGGCAATAC ATTCTCAAAA 117

lyCysMetLy sSerLysPhe LeuGlnValG lyGlyAsnTh rPheSerLys 39

ACTGAAACCA GCGCCAGCCC ACACTGTCTT GTGTACGTGC CGGATCCCAC 167

ThrGluThrs erAlaSerPr oHisCysPro ValTyrValP roAspProTh 56

ATCCACCATC AAGCCGGGGC CTAATAGCCA CAACAGCAAC ACACCAGGAA 217

rSerThrIle LysProGlyP roAsnSerHi sAsnSerAsn ThrProGlyI 73

TCAGGGAGGC AGGCTCTGAG GACATCATCG TGGTTGCCCT GTATGATTAC 267

leArgGluAl aGlySerGlu AspIleIleV alValAlaLe uTyrAspTyr 89

GAGGCCATTC ACCACGAAGA CCTCAGCTTC CAGAAGGGGG ACCAGATGGT 317

GluAlaIleH isHisGluAs pLeuSerPhe GlnLysGlyA spGlnMetVa 106

GGTCCTAGAG GAATCCGGGG AGTGGTGGAA GGCTCGATCC CTGGCCACCC 367

lValLeuGlu GluSerGlyG luTrpTrpLy sAlaArgSer LeuAlaThrA 123

GGAAGGAGGG CTACATCCCA AGCAACTATG TCGCCCGCGT TGACTIONCTG 417

rgLysGluGl yTyrIlePro SerAsnTyrV alAlaArgVa lAspSerLeu 139

GAGACAGAGG AGTGGTTTTT CAAGGGCATC AGCCGGAAGG ACGCAGAGCG 467

GluThrGluG luTrpPhePh eLysGlyIle SerArgLysA spAlaGluAr 156

CCAACTGCTG GCTCCCGGCA ACATGCTGGG CTCCTTCATG ATCCGGGATA 517

gGlnLeuLeu AlaProGlyA snMetLeuGl ySerPheMet IleArgAspS 173

GCGAGACCAC TAAAGGAAGC TACTCTTTGT CCGTGCGAGA CTACGACCCT 567

erGluThrTh rLysGlySer TyrSerLeuS erValArgAs pTyrAspPro 189

CGGCAGGGAG ATACCGTGAA ACATTACAAG ATCCGGACCC TGGACAACGG 617

ArgGlnGlyA spThrValLy sHisTyrLys IleArgThrL euAspAsnGl 206

GGGCTTCTAC ATATCCCCC GAAGCACCTT CAGCACTCTG CAGGAGCTGG 667

yGlyPheTyr IleSerProA rgSerThrPh eSerThrLeu GlnGluLeuV 223

TGGACCACTA CAAGAAGGGG AACGACGGGC TCTGCCAGAA ACTGTCCGGTG 717

alAspHisTy rLysLysGly AsnAspGlyL euCysGlnLy sLeuSerVal 239

CCCTGCATGT CTTCCAAGCC CCAGAAGCCT TGGGAGAAAAG ATGCCTGGGA 767

ProCysMetS erSerLysPr oGlnLysPro TrpGluLysA spAlaTrpGl 256

GATCCCTCGG GAATCCCTCA AGCTGGAGAA GAAACTTGGG GCTGGGCAGT 817
uIleProArg GluSerLeuL ysLeuGluLy sLysLeuGly AlaGlyGlnP 273

TTGGGGAAGT CTGGATGGCC ACCTACAACA AGCACACCAA GGTGGCAGTG 867
heGlyGluVa lTrpMetAla ThrTyrAsnL ysHisThrLy sValAlaVal 289

AAGACGATGA AGCCAGGGAG CATGTCGGTG GAGGCCTTCC TGGCAGAGGC 917
LysThrMetL ysProGlySe rMetSerVal GluAlaPheL euAlaGluAl 306

CAACGTGATG AAAACTCTGC AGCATGACAA GCTGGTCAA CTTTCATGCGG 967
aAsnValMet LysThrLeuG lnHisAspLy sLeuValLys LeuHisAlav 323

TGGTCACCAA GGAGCCCATC TACATCATCA CGGAGTTCAT GGCCAAAGGA 1017
alValThrLy sGluProIle TyrIleIleT hrGluPheMe tAlaLysGly 339

AGCTTGCTGG ACTTTCTGAA AAGTGATGAG GGCAGCAAGC AGCCATTGCC 1067
SerLeuLeuA spPheLeuLy sSerAspGlu GlySerLysG lnProLeuPr 356

AAAACTCATT GACTTCTCAG CCCAGATTGC AGAAGGCATG GCCTTCATCG 1117
oLysLeuIle AspPheSerA laGlnIleAl aGluGlyMet AlaPheIleG 373

AGCAGAGGAA CTACATCCAC CGAGACCTCC GAGCTGCCAA CATCTTGGTC 1167
luGlnArgAs nTyrIleHis ArgAspLeuA rgAlaAlaAs nIleLeuVal 389

TCTGCATCCC TGGTGTGTAA GATTGCTGAC TTTGGCCTGG CCCGGGTCAT 1217
SerAlaSerL euValCysLy sIleAlaAsp PheGlyLeuA laArgValIl 406

TGAGGACAAC GAGTACACGG CTCGGGAAGG GGCCAAGTTC CCCATCAAGT 1267

eGluAspAsn GluTyrThrA laArgGluGl yAlaLysPhe ProIleLysT 423

GGACAGCTCC TGAAGCCATC AACTTTGGCT CCTTCACCAT CAAGTCAGAC 1317

rpThrAlaPr oGluAlaIle AsnPheGlyS erPheThrIl eLysSerAsp 439

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ValTrpSerP heGlyIleLe uLeuMetGlu ileValThrT yrGlyArgIl 456

CCCTTACCCA GGGATGTCAA ACCCTGAAGT GATCCGAGCT CTGGAGCGTG 1417

eProTyrPro GlyMetSerA snProGluVa lIleArgAla LeuGluArgG 473

GATACCGGAT GCCTCGCCCA GAGAACTGCC CAGAGGAGCT CTACAACATC 1467

lyTyrArgMe tProArgPro GluAsnCysP roGluGluLe uTyrAsnIle 489

ATGATGCGCT GCTGGAAAAA CCGTCCGGAG GAGCGGCCGA CCTTCGAATA 1517

MetMetArgC ysTrpLysAs nArgProGlu GluArgProT hrPheGluTy 506

CATCCAGAGT GTGCTGGATG ACTTCTA_CAC GGCCACAGAG AGCCAGTACC 1567 [Y515*](#)

rIleGlnSer ValLeuAspA spPheTyrTh rAlaThrGlu SerGlnTyrG 523

AACAGCAGCC ATGATAGGGA GGACCAGGGC AGGGCCAGGG GGTGCCCAGG *36

lnGlnGlnPr oStop

TGGTGGCTGC AAGGTGGCTC CAGCACCATC CGCCAGGGCC CACACCCCCT *86

TCCTACTCCC AGACACCCAC CCTCGCTTCA GCCACAGTTT CCTCATCTGT *136

CCAGTGGGTA GGTGGACTG GAAAATCTCT TTTTGACTCT TGCAATCCAC *186

AATCTGACAT TCTCAGGAAG CCCCAGTT GATATTTCTA TTCCTGGAA *236

TGGTTGGATT TTAGTTACAG CTGTGATTG GAAGGAAAC TTTCAAATA *286

GTGAAATGAA TATTAAATA AAAGATATAA ATGCCAAAGT CTTTACCAA *336

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