



IFIH1 (NM_022168.4) - cDNA + Protein - 2026-10-31

CAAACTCTGT AAGAACTGCC TGACAGAAAG CTGGACTCAA AGCTCCTACC -328
CGAGTGTGCA GCAGGATCGC CCCGGTCCGG GACCCCAGGC GCACACCGCA -278
GAGTCCAAAG TGCCGCGCCT GCCGGCCGCA CCTGCCTGCC GCGGCCCCGC -228
GCGCCGCCCC GCTGCCCACC TGCCGCGCTG CCCACCTGCC CAGGTGCGAG -178
TGCAGCCCCG CGCGCCGGCC TGAGAGCCCT GTGGACAACC TCGTCATTGT -128
CAGGCACAGA GCGGTAGACC CTGCTTCTCT AAGTGGGCAG CGGACAGCGG -78
CACGCACATT TCACCTGTCC CGCAGACAAC AGCACCATCT GCTTGGGAGA -28
ACCCTCTCCC TTCTCTGAGA AAGAAAGATG TCGAATGGGT ATTCCACAGA 23

Met SerAsnGlyT yrSerThrAs 8

CGAGAATTTTC CGCTATCTCA TCTCGTGCTT CAGGGCCAGG GTGAAAATGT 73
pGluAsnPhe ArgTyrLeuI leSerCysPh eArgAlaArg ValLysMetT 25

ACATCCAGGT GGAGCCTGTG CTGGACTACC TGACCTTTCT GCCTGCAGAG 123
yrIleGlnVa lGluProVal LeuAspTyrL euThrPheLe uProAlaGlu 41

GTGAAGGAGC AGATTCAGAG GACAGTCGCC ACCTCCGGGA ACATGCAGGC 173
ValLysGluG lnIleGlnAr gThrValAla ThrSerGlyA snMetGlnAl 58

AGTTGAACTG CTGCTGAGCA CCTTGGAGAA GGGAGTCTGG CACCTTGGTT 223
aValGluLeu LeuLeuSerT hrLeuGluLy sGlyValTrp HisLeuGlyT 75

GGACTCGGGA ATTCGTGGAG GCCCTCCGGA GAACCGGCAG CCCTCTGGCC 273
rpThrArgGl uPheValGlu AlaLeuArgA rgThrGlySe rProLeuAla 91

GCCCGCTACA TGAACCCTGA GCTCACGGAC TTGCCCTCTC CATCGTTTGA 323
AlaArgTyrM etAsnProGl uLeuThrAsp LeuProSerP roSerPheGl 108

GAACGCTCAT GATGAATATC TCCAACGCT GAACCTCCTT CAGCCCCTC 373
uAsnAlaHis AspGluTyrL euGlnLeuLe uAsnLeuLeu GlnProThrL 125

TGGTGGACAA GCTTCTAGTT AGAGACGTCT TGGATAAGTG CATGGAGGAG 423
euValAspLy sLeuLeuVal ArgAspValL euAspLysCy sMetGluGlu 141

GAACTGTTGA CAATTGAAGA CAGAAACCGG ATTGCTGCTG CAGAAAACAA 473
GluLeuLeuT hrIleGluAs pArgAsnArg IleAlaAlaA laGluAsnAs 158

TGGAAATGAA TCAGGTGTAA GAGAGCTACT AAAAAGGATT GTGCAGAAAG 523
nGlyAsnGlu SerGlyValA rgGluLeuLe uLysArgIle ValGlnLysG 175

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luAsnTrpPh eSerAlaPhe LeuAsnValL euArgGlnTh rGlyAsnAsn 191

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GluLeuValG lnGluLeuTh rGlySerAsp CysSerGluS erAsnAlaGl 208

GATTGAGAAT TTATCACAAG TTGATGGTCC TCAAGTGGAA GAGCAACTTC 673
uIleGluAsn LeuSerGlnV alAspGlyPr oGlnValGlu GluGlnLeuL 225

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euSerThrTh rValGlnPro AsnLeuGluL ysGluValTr pGlyMetGlu 241

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AsnAsnSerS erGluSerSe rPheAlaAsp SerSerValV alSerGluSe 258

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rAspThrSer LeuAlaGluG lySerValSe rCysLeuAsp GluSerLeuG 275

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lyHisAsnSe rAsnMetGly SerAspSerG lyThrMetGl ySerAspSer 291

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CAGGCCTTAC CAAATGGAAG TTGCCAGCC AGCCTTGGA GGAAGAATA 973

uArgProTyr GlnMetGluV alAlaGlnPr oAlaLeuGlu GlyLysAsnI 325

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IleAlaLysA spHisLeuAs pLysLysLys LysAlaSerG luProGlyLy 358

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sValIleVal LeuValAsnL ysValLeuLe uValGluGln LeuPheArgL 375

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GluAspAspS erAspGluGl yGlyAspAsp GluTyrCysA spGlyAspGl 658

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ATTAGCACTT GATTGAAGAT TCTTTTAAAA TACTATCAGT TAAACATTTA *45

spStop

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