

Sequence of a cDNA coding for human IRF-1

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We have previously isolated and sequenced a cDNA clone encoding a mouse IFN regulatory factor 1 (IRF-1) (Miyamoto, M., Fujita, T., Kimura, Y., Maruyama, M., Harada, H., Sudo, Y., Miyata, T., and Taniguchi, T., 1988, Cell 54, 903-913). We have isolated a cDNA coding for human IRF-1 by cross-hybridization with the λ 28-8-derived mouse cDNA probe, using the Human T cell line, Jurkat-111 cDNA library. One of the positive clones, pHIRF31, contained the largest cDNA insert and its nucleotide sequence was determined. The cDNA includes 197bp of the 5'-untranslated, 975bp coding and 863bp 3'-untranslated regions. The deduced amino acid sequence of the 325 amino acid protein, shows 83% homology with mouse IRF-1; The amino-terminal half, spanning from amino acid residues 1 to 140 are highly conserved (95%) in the two species.

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1  CGAGCCCCCGAACCAGGCGCACCCGGAGCCGTGCCAGTCCAGCCGGCCGTGCCCGGGCCCTTAAGAACCAGGCAACCTCTGCCTTCTCCCTC
99  TTCCACTCGGAGTGGCGCTCCGGCGCCCTCACTAGCAGCCCTCGCTCGCGGGACCTCGCGGGCCAGCCGGAATGGCTCTCGCAGCAGCCAAAC
198  ATG CCC ATC ACT TGG ATG CGC ATG AGA CCC TGG CTA GAG ATG CAG ATT AAT TCC AAC CAA ATC CCG GGG CTC ATC
    Met Pro Ile Thr Trp Met Arg Met Arg Pro Trp Leu Glu Met Gln Ile Asn Ser Asn Gln Ile Pro Gly Leu Ile
273  TGG ATT AAT AAA GAG GAG ATG ATC TTG GAG ATC CCA TGG AAG CAT GCT GCC AAG CAT GGC TGG GAC ATC AAC AAG
    Trp Ile Asn Lys Glu Glu Met Ile Leu Glu Ile Pro Trp Lys His Ala Ala Lys His Gly Trp Asp Ile Asn Lys
348  GAT GCC TGT TTG TTC CGG AGC TGG GCC ATT CAC ACA GGC CGA TAC AAA GCA GGG GAA AAG GAG CCA GAT CCC AAG
    Asp Ala Cys Leu Phe Arg Ser Trp Ala Ile His Thr Gly Arg Tyr Lys Ala Gly Glu Lys Glu Pro Asp Pro Lys
423  ACG TGG AAG GCC AAC TTT CGC TGT GCC ATG AAC TCC CTG CCA GAT ATC GAG GAG GTG AAA GAC CAG AGC AGG AAC
    Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Gln Ser Arg Asn
498  AAG GGC AGC TCA GCT GTG CGA GTG TAC CGG ATG CTT CCA CCT CTC ACC AAG AAC CAG AGA AAA GAA AGA AAG TCG
    Lys Gly Ser Ser Ala Val Arg Val Tyr Arg Met Leu Pro Pro Leu Thr Lys Asn Gln Arg Lys Lys Glu Arg Lys Ser
573  AAG TCC AGC CGA GAT GCT AAG AGC AAG GCC AAG AGG AAG TCA TGT GGG GAT TCC AGC CCT GAT ACC TTC TCT GAT
    Lys Ser Ser Arg Asp Ala Lys Ser Lys Ala Lys Arg Lys Ser Cys Gly Asp Ser Ser Pro Asp Thr Phe Ser Asp
648  GGA CTC AGC AGC TCC ACT CTG CCT GAT GAC CAC AGC AGC TAC ACA GTT CCA GGC TAC ATG CAG GAC TTG GAG GTG
    Gly Leu Ser Ser Ser Thr Leu Pro Asp Asp His Ser Ser Tyr Thr Val Pro Gly Tyr Met Gln Asp Glu Leu Val
723  GAG CAG GCC CTG ACT CCA GCA CTG TCG CCA TGT GCT CTC AGC AGC ACT CTC CCC GAC TGG CAC ATC CCA GTG GAA
    Glu Gln Ala Leu Thr Pro Cys Ala Val Ser Ser Thr Leu Pro Ser Ser Thr Ile Pro Val Glu
798  GTT GTG CCG GAC AGC ACC AGT GAT CTG TAC AAC TTC CAG GTG TCA CCC ATG CCC TCC ATC TCT GAA GCT ACA ACA
    Val Val Pro Asp Ser Thr Ser Asp Leu Tyr Asn Phe Gln Val Ser Pro Met Pro Ser Ile Ser Glu Ala Thr Thr
873  GAT GAG GAT GAG GAA GGG AAA TTA CCT GAG GAC ATC ATG AAG CTC TTG GAG CAG TCG GAG TGG CAG CCA ACA AAC
    Asp Glu Asp Glu Glu Gly Lys Leu Pro Glu Asp Ile Met Lys Leu Leu Glu Gln Ser Glu Trp Gln Pro Thr Asn
948  GTG GAT GGG AAG GGG TAC CTA CTC AAT GAA CCT GGA GTC CAG CCC ACC TCT GTC TAT GGA GAC TTT AGC TGT AAG
    Val Asp Gly Lys Gly Tyr Leu Leu Asn Glu Pro Gly Val Gln Pro Thr Ser Val Tyr Gty Asp Phe Ser Cys Lys
1023  GAG GAG CCA GAA ATT GAC AGC CCA GGG GGG GAT ATT GGG CTG AGT CTA CAG GGT GTC TTY ACA GAT CTG AAG AAC
    Glu Glu Pro Glu Ile Asp Ser Pro Gly Gly Asp Ile Gly Leu Ser Leu Gln Arg Val Phe Thr Asp Leu Lys Asn
1098  ATG GAT GCC ACC TGG CTG GAC AGC CTG CTG ACC CCA GTC CGG TTG CCC TCC ATC CAG GCC ATT CCC TGT GCA CCG
    Met Asp Ala Thr Trp Leu Asp Ser Leu Leu Thr Pro Val Arg Leu Pro Ser Ile Gln Ala Ile Pro Cys Ala Pro
1173  TAG CAGGGCCCCGGGCCCTCTTATTCCTTAGGCAAGCAGGACCTGGCATATGTTGGATATGGTGCAGAGAAGCTGGACTCTGTGGGGCCCTCA
1271  ACAGCCAAGTGTGACCCCACTGCCAAGTGGGGATGGCCCTCCTCTTGGGTCAATTGACCTCTCAGGCCCTGGCAGGCCAATGTCTGGGTTTTCCTGT
1370  GGTGTAAGACTGGCCCTGCTCCCTGGGAAGTATGAGTCTGTAGACCAAGTATCAGGTCAGGGACTTGGACAGGAGTACAGTCTGGCTTTTCTCTGT
1469  AGCCCACTCCCTGGAGAGGGTCTCGCTGTCACTGGCTGGCTCCTTAGGGGAACAGACAGCCAGTACCCAGAAAAGTAAACCAATCCAGGGCTGGCT
1568  CTCACATAAGCGAAATGTCACTAAATGAATCTCGTCCAAAGAACTACCCCTTTTTCAGTGTAGCCCTGGGGAGTGTCCAAAGCCAGTGAATGTGAAG
1667  GAAACTCCCTCCTTTCGGGGCAATGCTCCCTCAGCCTCAGAGGAGCTTACCCCTGCTCCCTGCTTTGGCTGAGGGGCTTGGGAAAAAACTTGGCACTT
1766  TTTCGTGTGATCTTGCACATTTCTGATCAGAGGGTACACTAACATTTCCCCCGAGCTCTTGGCTTTGCAATTTATATACAGTGCCTTGTCTGGG
1865  GCCCACACCCCTCAAGCCCAAGCAGCCCTCAACAGGCCAGGGAGGAAGTGTGAGCGCTCTGGTATGACTTAAATTTGGAAATGTCACTCAACCAT
1964  TAAGTCATGTGTGAACCATAGGACCGTGTGTAATATGTACATTTGTCTTTTATAAAAAGTAAAAATTGTT 2035
    
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