

A human homologue of the *Escherichia coli* DnaJ heat-shock protein

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Three *E. coli* heat shock proteins, DnaJ, DnaK and GrpE, are essential for replication of the bacteriophage lambda chromosome *in vivo* (1). *In vitro* studies have shown that the binding of DnaJ and DnaK is one of the final steps in the formation of the ori initiation complex (2, 3). The DnaJ protein is probably a molecular chaperon that mediates and/or alters the folding of polypeptides (4). To date, no mammalian DnaJ homologues have been reported. Recently, however, four yeast genes encoding proteins with similarity to DnaJ have been isolated. SEC63 appears to be involved in transport of nascent polypeptides to the endoplasmic reticulum and nucleus (5). YDJ1, which appears to be associated with the nucleus, is required for normal growth (6). Another, S1S1, is believed to be important for nuclear assembly (7), while the fourth, SCJ1, may be a mitochondrial protein that can influence intracellular protein sorting (8).

We report here the isolation of a cDNA encoding a human homologue of the *E. coli* DnaJ protein. Using monoclonal antibodies obtained from mice injected with partially purified HeLa cell poly(A) polymerase, a human placenta cDNA expression library in λ gt11 was immunoscreened. Four cDNA clones of nearly identical restriction patterns and lengths (~1.5 kb) were isolated and one was sequenced in its entirety. A 1017 bp open reading frame encoding a 339 residue protein with over 20% identity (31% similarity) to the 376 residue *E. coli* DnaJ protein (9, 10) was detected (Figure 1). The similarity is greatest in the N-terminal third of the protein, a property shared with all four of the yeast homologues. We name the corresponding gene Human DnaJ 1 (HDJ-1). Subsequent analysis indicated that the protein is most likely not involved in polyadenylation, and its function is unknown. Biochemical fractionation experiments suggest that the protein is localized in, or associated with, the nucleus. Given the multiplicity of DnaJ-like proteins in yeast, we anticipate that additional mammalian homologues will be identified.

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HDJ-1  MGLDYQYQTGLA--AALGRGQAGLPPPLGLRYHPDLNL--EPGAELFLEIAEAYDVLSPF
      :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
dnaJ  MAKQDYELLGVSKTAEEREIRKAYKRLAMKYHPDRNQDKEAEAKFKEIKEAYEVLTD
      10      20      30      40      50      60

HDJ-1  RLREIFDRYLEEGLKGGSPGG--TAEEMPVLSATHSMETLMPCLLSSVVAEIPITPF-
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
dnaJ  QKRAAYDQYGHAAFEQGGMGGGGFGGGADFSDIFGDFVFDIFGGGGRQRAARGADLRYN
      70      80      90      100     110     120

HDJ-1  LGSSTGRKAWTLMTHSLASLWNGMGFTNVNFGRSQAQ--PARKKQDPPVTHDLRVSL
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
dnaJ  MELTLEEAVRGVTKIIRIPIPTLEECVCHGSGAKPTGPTQPTCTCHGSGGQVQRQGFVAQ
      130     140     150     160     170     180

HDJ-1  EIYSGCTKR--TKISHKRLNPDGKSIERNEDKILTEVKKGWKEGKTIFFPKEGQTSNNIP
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
dnaJ  QTCPHCQGRGTLIKDPCNCKHGHGRVRSKTLVSKIPAGVDTDGRIRLAGEGEAGEHGAP
      190     200     210     220     230     240

HDJ-1  ADIVFV--LKDKEHDFIKRGGSDVIYPARISREALCGCTVNVPTLDGRTIPVVFQVIRP
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
dnaJ  AGDLVQVQVKQHPIFEREENLYCEVFINFAMAALGGEIEVPTLDGR--VLLKVPGETQT
      250     260     270     280     290

HDJ-1  GMRRKVPGEGLPLPKTPEKRGDLIEFEAIFPERIPQTSRTVLEQVLP I
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
dnaJ  GKLFMRGKGVKSVRG--GAQGDLLCRVVVETPFVGLNERQQLLQELQESFGGPTGEHNSP
      300     310     320     330     340     350

dnaJ  RSKSFFDGVKVFDDLTR
      360     370

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Figure 1. Amino acid sequence of the human DnaJ homologue. The single letter amino acid code is used. Identities between HDJ-1 and DnaJ are marked with double dots, similarities with single dots. Similar residues were defined by the following rules: I=L=V=M; K=R; D=E; S=T; and F=Y. The region of the human protein with the strongest homology to DnaJ encompasses the N-terminal 79 residues, which are 37% identical and 46% similar. The C-terminal half of HDJ-1 (residues 178–339) is 24% identical and 38% similar to the corresponding region of DnaJ, while residues 80 to 177 show no significant homology.

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