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Nucleotide sequence of rat hsp60 (chaperonin, GroEL homolog) cDNA

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The 60 kDa heat shock family of protein (hsp 60) comprise major antigens of pathogenic bacteria (e.g. *Mycobacterium tuberculosis, M. leprae*) (1). Autoimmune response to hsp 60 has been implicated in a number of autoimmune diseases (e.g. rheumatoid arthritis) (2). This report describes the cloning and sequencing of rat hsp60 cDNA. A λgt11 cDNA library from rat kidney was screened using cDNA probes derived from Chinese hamster hsp60 cDNA (3). For the clones obtained both DNA strands were sequenced using oligonucleotide primers. The clones obtained lacked the 5′- leader sequence as well as the mitochondrial targeting sequence. However, the entire coding sequence for the mature hsp60 protein (amino acids 1−547) could be deduced. The deduced sequence of rat hsp60 protein differed from the corresponding proteins from human and Chinese hamster cells in *13* and *6* amino acids, respectively, most of which are conservative replacements (3, 4).

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1       GCC AAA GAT GTA AAA TTT GGT GCG GAT GCT CGA GCC TTA ATG CTT CAA GGT GTA GAC CTT TTA GCC GAT GCT GTA GCT GTT ACA ATG GGG
         A   K   D   V   K   F   G   A   D   A   R   A   L   M   L   Q   G   V   D   L   L   A   D   A   V   A   V   T   M   G   30
91      CCA AAG GGA AGA ACA GTG ATT ATT GAA CAG AGT TGG GGA AGT CCC AAA GTA ACA AAA GAT GGG GTC ACT GTT GCA AAG TCA ATT GAT TTA
         P   K   G   R   T   V   I   I   E   Q   S   W   G   S   P   K   V   T   K   D   G   V   T   V   A   K   S   I   D   L   60
181     AAG GAT AAA TAC AAA AAT ATC GGA GCT AAG CTT GTT CAG GAT GTT GCC AAT AAC ACA AAT GAA GAG GCT GGG GAT GGC ACC ACC ACT GCC
         K   D   K   Y   K   N   I   G   A   K   L   V   Q   D   V   A   N   N   T   N   E   E   A   G   D   G   T   T   T   A   90
271     ACT GTT CTG GCA CGG TCT ATT GCC AAG GAG GGC TTT GAG AAG ATC AGC AAA GGG GCT AAT CCA GTG GAA ATC CGG AGA GGT GTG ATG TTG
         T   V   L   A   R   S   I   A   K   E   G   F   E   K   I   S   K   G   A   N   P   V   E   I   R   R   G   V   M   L   120
361     GCT GTT GAT GCT GTA ATT GCT GAA CTT AAG AAA CAA TCT AAA CCT GTG ACA ACC CCT GAA GAA ATT GCT CAG GTT GCT ACA ATT TCT GCA
         A   V   D   A   V   I   A   E   L   K   K   Q   S   K   P   V   T   T   P   E   E   I   A   Q   V   A   T   I   S   A   150
451     AAC GGA GAC AAA GAC ATT GGG AAC ATC ATT TCT GAT GCA ATG AAG AAG GTT GGA AGA AAG GGT GTC ATC ACA GTG AAG GAT GGA AAA ACC
         N   G   D   K   D   I   G   N   I   I   S   D   A   M   K   K   V   G   R   K   G   V   I   T   V   K   D   G   K   T   180
541     CTG AAT GAT GAG CTA GAA ATT ATT GAA GGC ATG AAG TTT GAT AGA GGA TAT ATT TCC CCA TAT TTT ATT AAC ACA TCA AAA GGT CAA AAA
         L   N   D   E   L   E   I   I   E   G   M   K   F   D   R   G   Y   I   S   P   Y   F   I   N   T   S   K   G   Q   K   210
631     TGT GAA TTC CAA GAT GCC TAT GTT TTG TTG AGT GAA AAG AAA ATT TCT AGT GTT CAG TCC ATT GTA CCT GCT CTT GAA ATT GCC AAT GCT
         C   E   F   Q   D   A   Y   V   L   L   S   E   K   K   I   S   S   V   Q   S   I   V   P   A   L   E   I   A   N   A   240
721     CAC CGG AAG CCC TTG GTC ATA ATT GCT GAA GAT GTT GAT GGA GAA GCT CTT AGC ACA CTG GTT TTG AAC AGG CTA AAA GTT GGT CTT CAG
         H   R   K   P   L   V   I   I   A   E   D   V   D   G   E   A   L   S   T   L   V   L   N   R   L   K   V   G   L   Q   270
811     GTT GTA GCA GTC AAA GCT CCA GGG TTT GGG GAC AAC AGG AAG AAC CAG CTT AAA GAT ATG GCT ATC GCT ACT GGT GGT GCG GTG TTT GGA
         V   V   A   V   K   A   P   G   F   G   D   N   R   K   N   Q   L   K   D   M   A   I   A   T   G   G   A   V   F   G   300
901     GAA GAG GGT TTG AAT CTA AAT CTT GAA GAT GTT CAA GCT CAT GAT TTA GGG AAA GTT GGA GAG GTC ATC GTC ACC AAA GAT GAT GCC ATG
         E   E   G   L   N   L   N   L   E   D   V   Q   A   H   D   L   G   K   V   G   E   V   I   V   T   K   D   D   A   M   330
991     CTT TTG AAA GGA AAA GGT GAC AAA GCT CAC ATT GAA AAA CGT ATT CAA GAA ATC ACT GAG CAG CTA GAC ATC ACA ACT AGT GAA TAT GAG
         L   L   K   G   K   G   D   K   A   H   I   E   K   R   I   Q   E   I   T   E   Q   L   D   I   T   T   S   E   Y   E   360
1081    AAG GAA AAG CTG AAC GAG CGA CTT GCT AAA CTC TCA GAT GGA GTA GCT GTG TTG AAG GTT GGA GGG ACA AGT GAT GTT GAA GTG AAT GAG
         K   E   K   L   N   E   R   L   A   K   L   S   D   G   V   A   V   L   K   V   G   G   T   S   D   V   E   V   N   E   390
1171    AAG AAA GAC AGA GTT ACA GAT GCT CTC AAT GCT ACA AGA GCA GCT GTT GAA GAA GGC ATT GTT CTA GGA GGG GGC TGT GCT CTA CTT CGG
         K   K   D   R   V   T   D   A   L   N   A   T   R   A   A   V   E   E   G   I   V   L   G   G   G   C   A   L   L   R   420
1261    TGC ATC CCA GCC TTG GAT TCA TTA AAG CCT GCT AAT GAA GAT CAG AAG ATA GGT ATA GAA ATT ATT AAA AGA GCA CTT AAA ATT CCT GCA
         C   I   P   A   L   D   S   L   K   P   A   N   E   D   Q   K   I   G   I   E   I   I   K   R   A   L   K   I   P   A   450
1351    ATG ACA ATT GCT AAG AAT GCA GGT GTT GAA GGA TCT TTG ATA GTT GAA AAA ATT CTG CAG AGT TCC TCA GAG GTT GGC TAT GAT GCC ATG
         M   T   I   A   K   N   A   G   V   E   G   S   L   I   V   E   K   I   L   Q   S   S   S   E   V   G   Y   D   A   M   480
1441    CTT GGA GAT TTT GTG AAC ATG GTG GAA AAG GGA ATC ATT GAT CCA ACA AAG GTT GTA AGA ACT GCT TTA CTG GAT GCT GCT GGG GTG GCC
         L   G   D   F   V   N   M   V   E   K   G   I   I   D   P   T   K   V   V   R   T   A   L   L   D   A   A   G   V   A   510
1531    TCC CTG CTA ACT ACA GCC GAA GCT GTA GTG ACA GAA ATT CCT AAA GAA GAG AAG GAC CCT GGA ATG GGT GCA ATG GGT GGA ATG GGA GGG
         S   L   L   T   T   A   E   A   V   V   T   E   I   P   K   E   E   K   D   P   G   M   G   A   M   G   G   M   G   G   540
1621    GGT ATG GGA GGT GGC ATG TTC TAA CTCCTAGAATAGTGCTTTGCCCTTATCAATGAACTGTGGCAGGAAGCTCAAGGCAGGTTCCTCACCAATAACTTCAGAGAAGTCACC
         G   M   G   G   G   M   F   *  547
1732    TGAAGAAAATGACTGAAGAGAAGGCTGGCTGATCACTGTAACCATCAGTTACTGGTTTCCTTTGACAATACATAATGGTTTACTGCTGTCATTGTCCATGCCTACAGATAATTTATTTT
1850    GTATTTTTGAATAAAGACATTTGTACATTCCTGATGCTGGGTGCAAGAGCCAGTGTCCTGCTTTCAACTTAAATCACTGAGGCATCTCTACTGTTCTGTTAGCATCAGGACTGTAGCGC
1969    TGTGTCACCACATGAGAAGTTCAGAAGCAGCCTTTCTGTGGAGGGTGAGAATGATTGTGTACAGAGTAGAGAAGTATCCAATTATGTGACAACCTTTGTGTAATAAAATTTTGTTTAAA
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