The primary structure of rat ribosomal protein L32

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The amino acid sequence of rat ribosomal protein L32 was deduced from the sequence of nucleotides in a recombinant cDNA and confirmed from the sequence of amino acids at the NH_2-terminus of the protein. A single synthetic DNA oligonucleotide (30-mer) encoding 10 of the amino acids in human ribosomal protein L32 (1) was used to screen a rat cDNA library. A number of clones were identified and the sequence of nucleotides in one, pL32-17, was determined. The open reading frame in pL32-17 is 405 nucleotides in length and encodes a protein containing 135 residues. The sequence of amino acids at the NH_2-terminus of rat L32 determined from the protein is AALRPLVK. This corresponds precisely to the sequence encoded in pL32-17 except that the NH_2-terminal methionine is removed after translation of the mRNA. Thus, the molecular weight of mature rat L32 is 15,730. Protein L32 has 39 basic residues and only 9 acid ones; 37 of the 134 amino acids are hydrophobic; and there are 6 prolys. Thus, L32 is very basic and quite hydrophobic.

Rat L32 is homologous with ribosomal proteins from other eukaryotic species: with L32 from humans (1); L32 from mouse (2); and rp49 from Drosophila melanogaster (3). The amino acid sequences of rat, mouse, and human L32 are identical. In the comparison of D. melanogaster rp49 and rat L32 there are 84 identities out of 123 possible matches (68%).

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                                        30                                  60
GGC ATC ATG GCT GCC CTT CGG CCT CTG GTG AAG CCC AAG ATC GTC AAA AAG AGG ACC AAG
       MET ALA ALA LEU ARG PRO LEU VAL LYS PRO LYS ILE VAL LYS LYS ARG THR LYS
         1                                  10

                                        90                                 120
AAG TTC ATC AGG CAC CAG TCG GAC CGA TAT GTG AAA ATT AAG CGA AAC TGG CGG AAA CCC
LYS PHE ILE ARG HIS GLN SER ASP ARG TYR VAL LYS ILE LYS ARG ASN TRP ARG LYS PRO
     20                                 30

                                       150                                 180
AGA GGC ATC GAC AAC AGG GTG CGG AGA AGA TTC AAG GGC CAG ATC CTG ATG CCC AAC ATT
ARG GLY ILE ASP ASN ARG VAL ARG ARG ARG PHE LYS GLY GLN ILE LEU MET PRO ASN ILE
     40                                 50

                                       210                                 240
GGT TAC GGG AGT AAC AAG AAA ACC AAG CAC ATG CTG CCT AGC GGC TTC CGG AAG TTT CTG
GLY TYR GLY SER ASN LYS LYS THR LYS HIS MET LEU PRO SER GLY PHE ARG LYS PHE LEU
     60                                 70

                                       270                                 300
GTC CAC AAT GTC AAG GAG CTG GAA GTG CTG CTG ATG TGC AAC AAA TCT TAC TGT GCT GAG
VAL HIS ASN VAL LYS GLU LEU GLU VAL LEU LEU MET CYS ASN LYS SER TYR CYS ALA GLU
     80                                 90

                                       330                                 360
ATT GCT CAC AAT GTG TCC TCT AAG AAC CGA AAA GCC ATC GTA GAA AGA GCA GCA CAG CTG
ILE ALA HIS ASN VAL SER SER LYS ASN ARG LYS ALA ILE VAL GLU ARG ALA ALA GLN LEU
    100                                110

                                       390                                 420
GCC ATC AGA GTC ACC AAT CCC AAC GCC AGG CTA CGC AGC GAA GAG AAT GAA TAG ATG GCT
ALA ILE ARG VAL THR ASN PRO ASN ALA ARG LEU ARG SER GLU GLU ASN GLU END
    120                                130

TGT GTG CCT GTT TTG TGT TCA AAT AAA ACC ACA AAA ACT GCC AAA
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