

Sequence of a cDNA clone encoding chicken ribosomal protein S17

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Sequences of eukaryotic ribosomal proteins are of particular interest for evolutionary studies because ribosomes from different organisms show remarkable similarities in subunit structure and function. We report here the sequence of a cloned cDNA that encodes chicken ribosomal protein S17. This cDNA contains 387 nucleotides of the coding sequence corresponding to amino acid residues 7-135, 43 nucleotides of the 3' untranslated region and a short poly(A) tail. Our attempts to isolate a cDNA for the 5' untranslated region have not been successful so far. The predicted amino acid sequence is identical to that of man and hamster except for the two residues at the carboxyl terminus (Ala-Leu as compared to Pro-Val and Ala-Val) (1). On the nucleotide level, the chicken sequence is 82% homologous to the sequences of man, hamster and rat (1, 2). In the figure below the human nucleotide sequence (1) is included wherever it differs from the chicken sequence.

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ATG GGC CGC GTT CGC ACC A C C C A A
1 .... .... .... .... AAG ACG GTG AAG AAG GCG GCG CGG GTG ATC ATC GAG AAG TAC
.... .... .... .... Lys Thr Val Lys Lys Ala Ala Arg Val Ile Ile Glu Lys Tyr

G C G T
61 TAC ACC CGT CTG GGC AAC GAC TTC CAC ACC AAC AAG CGC GTG TGC GAG GAG ATC GCC ATC
Tyr Thr Arg Leu Gly Asn Asp Phe His Thr Asn Lys Arg Val Cys Glu Glu Ile Ala Ile

A C A A T C G T A
121 ATC CCC AGC AAG AAG CTG CGC AAC AAC AAG ATC GCG GGG TAT GTC ACC CAC CTG ATG AAG CGC
Ile Pro Ser Lys Leu Arg Asn Lys Ile Ala Gly Tyr Val Thr His Leu Met Lys Arg

T A A A A A A A C A A A G
181 ATC CAG CGG GGC CCC GTC CGG GGT ATC TCC ATT AAG CTG CAG GAG GAG AGG GAG CGC
Ile Gln Arg Gly Pro Val Arg Gly Ile Ser Ile Lys Leu Gln Glu Glu Arg Glu Arg

A A T T T T A C T G T A T T
241 CGG GAC AAC TAC GTG CCC GAG GTC TCT GCT CTC GAT CAG GAG ATC ATT GAA GTG GAC CCG
Arg Asp Asn Tyr Val Pro Glu Val Ser Ala Leu Asp Gln Gln Ile Ile Glu Val Asp Pro

T T T T T T A T T T
301 GAC ACC AAG GAA ATG CTG AAG CTC CTG GAC TTC GGC AGC CTG TCC AAC CTG CAG GTC ACG
Asp Thr Lys Glu Met Leu Lys Leu Leu Asp Phe Gly Ser Leu Ser Asn Leu Gln Val Thr

T A T T T G A C G T TTTTTTG A GC
361 CAG CCC ACC GTG GGG ATG AAC TTC AAA ACG CCG CGA GGC GCT CTC TGA...GCCGCTCGTTAT
Gln Pro Thr Val Gly Met Asn Phe Lys Thr Pro Arg Gly Ala Leu

ATT A T T C C A
425 GTTGCTTTACAATAAACGTGGGAAACC (A)21

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