

Corrigenda

**The human apolipoprotein A-II gene: complete nucleic acid sequence and genomic organization**

by Karl J.Lackner, Simon W.Law and H.Bryan Brewer,Jr.

*Nucleic Acids Research*, 13, 4597-4608 (1985)

Due to a typographical error in the preparation of Fig. 3, there is a error in the DNA sequence. The sequence of the first intron contains a 13 bp segment in duplicate. The sequence from residue 226 to 260 should read as follows:

GGCTAGGTAAGATAAGGAGGCAAGATGTTGTGAGCA.

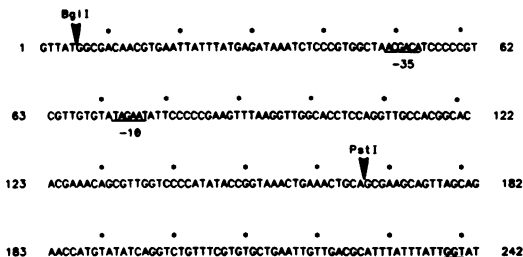
The first intron is 169 bp in length.

**The DNA sequence of the gene (*rnc*) encoding ribonuclease III of *Escherichia coli***

by Paul E.March, Joohong Ahnn and Masayori Inouye

*Nucleic Acids Research*, 13, 4677-4685 (1985)

We have found that the T originally reported at positions 746, 789 and 832 of the rnc gene DNA sequence are not present. As a result the amino acid sequence between amino acid residue number 167 and 196 is altered and there is one less codon overall (226). These changes are incorporated in the accompanying figure and table. This DNA sequence reveals that RNase III possesses 60 charged residues of which 29 are basic and 31 are acidic, giving the protein an estimated pI of 6.8. The calculated molecular weight is 25,550.



243 CGCATGAACCCCATCGTAATTAATGGCTTCAACGGGAAGCTGGGCTACACTTTTAATCAT 302  
MetAsnProIleValIleAsnArgLeuGlnArgLysLeuGlyTyrThrPheAsnHis  
1 10

303 CAGGAACCTGTTCACAGCCATTAACTCATCGTAGTCCAGCAGTAACATAACGAGCGT 362  
GlnGluLeuLeuGlnGlnAlaLeuThrHisArgSerAlaSerSerLysHisAsnGluArg  
20 30

363 TTAGAATTTTAAAGCGACTCTATTCTGAGCTACGTTATCGCCAATCGCCTTTATCACCGT 422  
LeuGluPheLeuGlyAspSerIleLeuSerTyrValIleAlaAsnAlaLeuTyrHisArg  
40 50

423 TTCCTCGTGTGGATGAAGGGATATGAGCCGGATGCGCCCAAGCTGGTCCGTGGCAAT 482  
PheProArgValAspGluGlyAspMetSerArgMetArgAlaThrLeuValArgGlyAsn  
60 70

483 ACGCTGGGGAACTGGCGGGGAATTTGAGTTAAGCGAGTCTACGTTTAAAGCCAGGT 542  
ThrLeuAlaGluLeuAlaArgGluPheGluLeuGlyGluCysLeuArgLeuGlyProGly  
80 90

543 GAACCTAAAAGCGGTGGATTCGTCGTGAGTCAATTCGCGCCAGCCGTCGAAGCATT 602  
GluLeuLysSerGlyGlyPheArgArgGluSerIleLeuAlaAspThrValGluAlaLeu  
100 110

603 ATTGGTGGCTATTCTCGACAGTGATTAACACCGTCGAGAAATTAATCCTCAACTGG 662  
IleGlyGlyValPheLeuAspSerAspIleGlnThrValGluLysLeuIleLeuAsnTrp  
120 130

663 TATCAAACCTGGTTGGACGAAATTAAGCCAGGCGATAAACAANAAGATCGAAAACCGCC 722  
TyrGlnThrArgLeuAspGluIleSerProGlyAspLysGlnLysAspProLysThrArg  
140 150

723 TTGCAAGAATATTTGCAGGTCGCCATCTGCCGCTGCCGACTTATCTGCTAGTCCAGGT 781  
LeuGlnGluTyrLeuGlnGlyArgHisLeuProLeuProThrTyrLeuValValGlnVal  
160 170

782 ACGTGGCAGGCGCAGATCAGGAATTTACTATCCACTGCCAGGTGAGCGGCTGAGT 839  
IArgGlyGluAlaHisAspGlnGluPheThrIleHisCysGlnValSerGlyLeuSer  
180 190

840 GAACCGGTGGTTGGCACAGTTCAAGCGTCTAAGGCTGAGCAGCTGCCGCGGAACAG 899  
GluProValValGlyThrGlySerSerArgArgLysAlaGluGlnAlaAlaGluGln  
200 210

900 GCCTTGAAAAAAGTGGACCTGGAATGAGCATCGATAAAAGTTACTGGGATTTATTGCC 958  
AlaLeuLysLysLeuGluLeuGlu—  
220 MetSerIleAspLysSerTyrCysGlyPheIleAla  
1 10

959 ATCGTGGACGTCGAAAGCTTGGCAAAATCCACATTTGTTGAACAACCTGCTGGGCGAGAAA 1018  
IleValGlyArgProAsnValGlyLysSerThrLeuLeuAsnLysLeuLeuGlyGlnLys  
20 30

1019 ATCTCCATCACTCCCGCAAGCCGACAGACAACCTCGTACCGCATTGTGGGATCC 1073  
IleSerIleThrSerArgLysAlaGlnThrThrArgHisArgIleValGlyIle  
40 50  
BamHI

TABLE I  
Amino Acid Composition and Codon Usage

Amino Acid	Total Residues	Codon Number Used	% Codon Usage	* % Codon Usage	** % Codon Usage High Expression	Amino Acid	Total Residues	Codon Number Used	% Codon Usage	* % Codon Usage	** % Codon Usage High Expression		
Phe	7	TTT	5	71%	23%	Tyr	6	TAT	4	67%	17%		
		TTC	2	29	77			TAC	2	33	83		
Leu	31	TTA	8	25	3	His	7	CAT	4	57	32		
		TTG	5	16	4			CAC	3	43	68		
		CTT	3	10	4	Gln	14	CAA	5	36	14		
		CTC	3	10	3			CAG	9	64	86		
		CTA	0	0	0			Asn	7	AAT	4	57	5
CTG	12	39	86	AAC	3	43	95						
Ile	10	ATT	6	60	21	Lys	10	AAA	8	80	71		
		ATC	4	40	79			AAG	2	20	29		
		ATA	0	0	0	Asp	10	GAT	6	60	31		
Met	3	ATG	3	100	100			GAC	4	40	69		
		Val	13	GTT	2	15	44	Glu	21	GAA	14	67	75
				GTC	5	38	7			GAG	7	33	25
				GTA	4	31	31	Cys	2	TGT	0	0	20
GTC	2	15	17	TGC	2	100	80						
Ser	14	TCT	1	7	44	Trp	1	TGG	1	100	100		
		TCC	0	0	31			Arg	19	CGT	12	63	72
		TCA	2	14	2	CGC	4			21	26		
		TCC	0	0	0	CGA	0			0	0		
		AGT	4	29	6	CGG	3			16	0		
		AGC	7	50	17	AGA	0	0	0				
Pro	8	CCT	1	13	6	AGG	0	0	0				
		CCC	1	13	3	Gly	17	GGT	5	29	58		
		CCA	2	25	18			GGC	10	59	40		
		CCG	4	50	74			GGA	1	6	1		
Thr	11	ACT	5	45	48			GGG	1	6	1		
		ACC	2	18	41	Ala	15	GCT	2	13	50		
		ACA	1	9	7			GCC	6	40	6		
		ACG	3	27	3			GCA	2	13	26		
GCC	5	33	18	GCG	5			33	18				

\* % Codon Usage =  $\frac{\text{Number of occurrences of codon}}{\text{Total codons of a specific residue}}$

\*\* % Codon Usage High expression: calculated as described above, but for a typical highly expressed protein (calculated from data of Gouy and Gautier, 1982).