ERRATUM

Re: 'The Evolution of the Protein Synthesis System. I. *A Model of a Primitive Protein Synthesis System*', by H. Mizutani *et al.*, *Origins of Life*, 8, 183 (1977)

On page 188, the extreme left hand edge of the page was not printed, so the complete page is now reprinted overleaf.

TABLE I
Grading of the components

Grade	A-polymerase and N-polymerase	A-gene and N-gene
1	No activity	Produce grade 1 polymerase ^a
2	Random polymerization	Produce grade 2 polymerase ^a
3	The lowest selectivity	Produce grade 3 polymerase ^a
4	The 2nd lowest selectivity	Produce grade 4 polymerase ^a
	and so forth	

^a Assuming no errors during the translation.

code grade j polymerase under the given coding table will be considered as grade j genes. Table I summarizes the grading system. Note that the grading system shown in Table I concerns only the activity and the selectivity. Therefore, it is quite possible that two sequence-wisely different molecules may be assigned the same grade. The accuracies are connected with the selectivities by Equations (5) and (6).

2.2 MODEL I

Model I is schematically shown in Figure 1. In Model I, we assume that either the longevity of the polynucleotide is long enough or its replication is rapid so that the template can remain in the system during the course of its evolution. Considering the stability of the helical form of polynucleotides, this assumption may not be so unreasonable as a first order approximation.

The model consists of activated amino acids, A-polymerase, and a template polynucleotide. A-polymerase of $(i-1)$ th generation catalyzes the polymerization reaction of activated amino acids, which eventually produces polypeptides of i th generation. A-polymerase serves as a polymerase of certain forms of activated amino acids, and the selectivity of A-polymerases includes their selective preference for different

Fig. 1. Schematic representation of Model I.