

# Institut Pasteur

25, RUE DU DOCTEUR ROUX  
(XV<sup>e</sup> Arrond<sup>t</sup>)

Téléphone : SÉGUR 01-10

Paris, le 13 septembre 1957

Dr. F.H.C. CRICK  
Cavendish Laboratory  
CAMBRIDGE

Dear Crick,

I have just read your paper with Griffith and Orgel in the P.N.A.S. and ~~Symour Benzer's~~ one in the same journal. One thing is for me difficult to understand. Let us consider the four bases A, B, C, D in which A-C and B-D are complementary.

Let us now consider a sequence of triplets in helix 1 and the complementary sequence in helix 2.

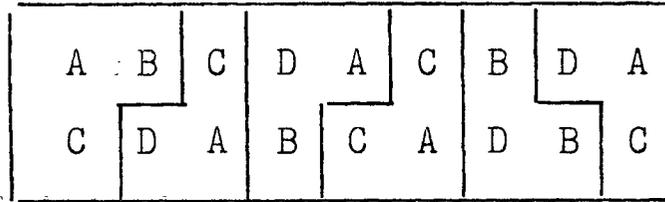
1) A B C	D A C	B D A
2) C D A	B C A	D B C

Unless it is assumed that A = C and B = D, which is an impossible hypothesis, it is clear that

ABC	is different from	CDA	and	ADC
DAC	"	"	"	BCA and ACB
BDA	"	"	"	DBC and CBD

If this is true and we assume that each single helix 1 and 2 organizes one molecule of protein, then a double helix would produce two different protein molecules. This seems unlikely.

I see two ways out possibilities : a) the two sequences formed on helix 1 and 2 get stuck and thus form a molecule ; b) each amino acid is taken care by three bases, one of which is located on ~~one~~ helix, the other two on the other.



For esthetical reasons, b seems more likely than a. It is satisfactory to visualize the double helix functioning as a whole when directing syntheses. As a matter of fact, it is probably why a double helix exists. Otherwise, a single helix 1 would produce a complementary helix 2. One organism would inherit helix 1 and the other helix 2, and each one would produce different protein molecules.

I am somewhat worried because either this could be completely idiotic or very interesting, or perhaps very well known, and I would be grateful if you could clarify the situation for me.

Sincerely yours,

*Ausloeff*

A. LWOFF

*P. S. I apologize for the bad state of this letter, but I have no possibility to have it retyped.*