Dear Crick,

I have just read your paper with Griffith and Orgel in the P.N.A.S. and your paper 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,

A. Lwoff

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