

20 May 1970

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Dear Jerry

Thank you for your letter of May 6. I am amused to see from it that, as I suspected, you have not appreciated the point about the dyads in the DNA model.

Of course, it is quite possible to make errors with centric Fouriers, but it is the general experience of crystallographers, and I am sure it is yours, that it is much easier to do so with acentric structures. I think you have quite failed to appreciate the significance of this difference and also that it is far harder to get false structures from polymers than from single crystals of small molecules. You are only likely to get an "acceptable" false structure if its Patterson is similar to the Patterson of the real structure, and the much greater restrictions imposed by a polymer make this condition more difficult to satisfy.

Would you please explain to me the following odd circumstances, which must have struck the attentive reader of Science? Whenever the King's College group do a difference synthesis it shows clearly the direction the groups of atoms should be moved. Whenever you publish the ~~difference~~ synthesis of one of your imaginary structures of base pairs, it is difficult to distinguish the false solution from the true one and the difference synthesis does not show clearly how the groups of atoms should be moved. I feel that I can explain this rather remarkable difference. *Can you?*

I look forward with interest to your reply.

F. H. C. Crick