Dr. F. H. C. Crick
Cavendish Laboratory
Free School Lane
Cambridge, England

Dear Francis:

I learned about Rosalind's death through an obituary in the Sunday New York Times and was profoundly saddened. I had known of her illness and as recently as last February had speculated with Hugh Huxley about the probable course of it, but nonetheless felt a considerable shock when it developed so rapidly. It was perhaps characteristic of Rosalind that she wrote me a letter just two weeks before her death in which she expressed a reasonably cheery confidence that she was now back to work again and hoping to get things moving. It is at such times that I feel the [redacted] mystery around most of our activities.

Most of this letter concerns poly A which David and I have been working on. We looked quite carefully at the coordinates which you had and felt that most of the configuration was quite suitable except the deviation of oxygen 6 from the pla~~in~~ne of the base. We have done two things in an attempt to bring it back to the pla~~in~~ne. The first one we perhaps described in the last letter, that is we introduced a distortion in the configuration of the phosphate group so that the Z value of oxygen 6 was decreased to the point where it lay below the phosphorous atom rather than above. This distortion diminished the outer pla~~in~~ne distance from 0.85 Å to 0.60 Å. In the enclosed sheet, you will see what this distortion has done to the angles around the phosphorous atom. One angle had been decreased to 102°, while another angle~~s~~ had been increased (07P06). We have noted on this sheet the same angles from dibenzylphosphate and feel that the variation in the angles around the phosphate in it is great enough to permit us to use the somewhat distorted angle in poly A. We do this with considerable reluctance, however, since we feel that the original angles that you had were preferable. However, we must compromise and decide whether we should confine a distortion to one parameter or distribute it among many parameters.

To overcome the remaining distance which 06 was out of pla~~in~~ne, we carried out a rotation of the adenine ring by rotating around an axis which passes through C^1_1 of ribose and C^2_3 of adenine~~, that is~~ this had the effect of lifting up the center part of the adenine pla~~in~~ne, so that the N^{10}_{10} comes closer to the O^6_6. We did this rotation by changing the Z coordinates as shown in the enclosure. This change has the effect of altering the tilt of the adenine base from the horizontal from a previous value of 13° to a new value of 9°. This altered tilt has several effects. It diminishes the deviation of O_6 from the pla~~in~~ne by about 0.25 Å so that the final O_6 is .36 Å from the pla~~in~~ne of the ring, that is it is about 7.6° out of plain. However, this rotation has the unfortunate effect of decreasing the N^{10} to O^6 distance so that it becomes 2.73 Å while at the same time it decreases the angle C^2, C^1, N^9 to 105.5° from its previous value of 106.8°. The adenine atoms are all still within 0.01 Å of the least square plain.

This tilt has the beneficial effect of modifying the transform in a somewhat favorable fashion, especially on the 8th and 9th layer lines as you can see in the enclosure. ~~It weakens the meridional contribution of~~. The 8th and 9th layer lines now have slightly larger peaks on them which is consonant with what is observed in the tilted diffraction pattern.

We have mixed feelings about the effect of all this fiddling on the structure. Several features of the structure have now changed in a somewhat unfavorable direction, but at the same time, others have become a little more favorable. It is our feeling, though, that it is not worthwhile continuing with modifications of the structure and think that we are in a position to proceed with drawing the figures and writing up the paper. Accordingly, we had started to make drawings for the paper and are thinking about a first draft. In the way of figures, we have in mind the following. 1.) A view of the structure looking down the axis which shows ~~both~~ a nucleotide unit on both chains; 2.) a somewhat ~~skolatic~~ schematic view from the side which shows two chains wrapped around each other with the appropriate screw; 3.) a diagram showing the calculated continuous transform ~~which is calculated~~ and the observed diffraction pattern ~~which~~ is plotted on the same graph, with semi-quantitative measurements of the observed intensities 4) A figure showing the diffraction pattern. ~~for a figure showing the diffraction pattern.~~ We do not have strong feelings about the desirability of a schematic diagram showing the angles and distances. There would, certainly, in addition to this, be a table of coordinates, and that is all we can think of at the moment.

David and I and Jim and I have discussed the question of the Morgan-Bear structure. We feel that it is probably not worth our while to write a separate note pointing out the essential incorrectness of their proposal. Instead, we think it would be worthwhile ~~putting~~ devoting/a small subsection of the present paper to a critical discussion of their structure and our reasons for believing it to be incorrect. We might consider putting in a table showing how incorrect some of their angles are. If this is concise enough, it would not represent too great a disturbance in the flow of this paper.

Have you decided yet on the dates of your visit to this country? I will be permanently in Boston by the first of June.

Best regards for now.

Sincerely yours,

Alex.

Alexander Rich

Please excuse the irregular typing.