Copy of a printed diagram referenced as "Antiparallel chain structure. Pleated sheet"

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as the arrangement of the peptide [illegible]
apparent. The differences between the relations of corresponding groups in adjacent chains are also apparent. This picture is essentially in harmony with the earlier model proposed by Astbury and illustrated in Fig. 10; but it goes further by proposing precise positions for all the atomic coordinates in the repeating unit of structure. Given such precise coordinates, X-ray diffraction patterns can be calculated, and the intensity of

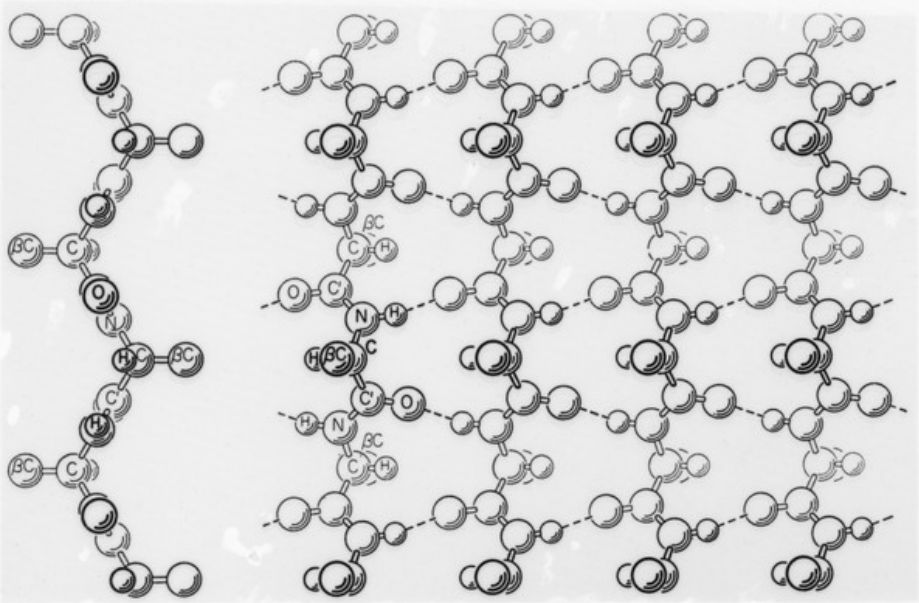

FIG. 11. The parallel chain pleated sheet structure of Pauling and Corey.

the observed reflections compared with the calculations. This is essentially what Marsh *et al.* (1955) have done for silk fibroin, as we have discussed above, with highly encouraging results. In β-keratin the problem is more difficult for two reasons: (1) The side chains are far more various than in silk fibroin; almost every kind of amino acid residue is present in significant amounts; and only a fragmentary knowledge of the sequence of [illegible] (2) There are large amorphous regions