

three-dimensional data. The orientation obtained from the rotation function is in good agreement with that obtained by Scouloudi from an examination of the two-dimensional projection.

In order to develop techniques to solve the structures of a number of related proteins once one of the group is known, attempts are being made to develop the techniques of the Q functions (Tollin, A.C.A. meeting, Gatlinburg, 1965) to determine the known member of the group once the rotation function has determined their angular relationship. It is hoped to present the results at the meeting.

10-41. **Structural studies of some polytripeptides related to collagen.** By W. TRAUB and A. YONATH, *Weizmann Institute of Science, P.O. Box 26, Rehovoth, Israel*. Probable journal *Journal of Molecular Biology*.

Collagen, the main protein of connective tissue, is generally believed to have a three-stranded helical structure. However, the elucidation of structural details, including the mode of interchain hydrogen bonding, is made difficult by the complexity of the amino-acid sequence of collagen and the limited detail of its X-ray pattern. X-ray investigations have therefore been undertaken of several possible poly-tripeptide models for collagen with, like the protein, every third residue glycine and a large proportion of imino acids.

Poly(L-prolyl-glycyl-glycine) has been found to form helices which resemble the individual strands of collagen, but are not coiled about each other. Poly(L-prolyl-glycyl-L-proline), however, shows an X-ray pattern which has all the main features of the collagen pattern and is appreciably sharper in detail. As in collagen, water absorption leads to an increase in the equatorial, but not in the meridional, spacings. Analysis of the pattern shows it to have the same helical parameters as have been found for collagen, but, of the structures that have been proposed for the protein, only modified versions of collagen II and the closely similar alternate Madras structure are compatible with the observed X-ray spacings.

Poly(L-prolyl-L-alanyl-glycine) and poly(L-prolyl-glycyl-O-acetyl-L-hydroxyproline) also show X-ray patterns which resemble that of collagen, including the characteristic 2.9 Å spacing.

The detailed analysis of the polytripeptide structures and their implications with respect to the structure of collagen will be discussed.

10-42. **X-ray diffraction study of transfer RNA.** By V. G. TUMANJAN, N. G. ESİPOVA and L. L. KISELEV, *Institute of Biophysics and Institute of Molecular Biology of the Academy of Sciences of the U.S.S.R., Profsoyuznaya Street 7, Moscow, U.S.S.R.* Probable journal not stated.

Total (unfractionated) valine- and alanine-specific transfer RNAs from yeast have been studied in a wide range of concentrations and ionic strengths. At low ionic strength tRNA molecules organize (at $\geq 20\%$ concentrations), forming liquid crystals which give diffraction in a range of angles up to 1° .

With an increase in ionic strength the regularity of the liquid-crystalline type disappears and the molecular dimensions and form could be determined using conventional methods (Fournet, Porod, Kratky, Pitytzy and Fedorov). The molecule is approximated well enough by a circular cylinder or ellipsoid of revolution with an asymmetry of about 4 and diameter of 25 Å. Treatment of the curves obtained with individual fractions leads to the idea of the close similarity in general pattern of molecular structure of different tRNAs.

An analysis of diffraction patterns obtained on gels and filaments of tRNA has been performed at small and large angles. A conclusion was drawn about the direction of orientation of the basic period which is characteristic of the liquid-crystalline state in relation to the direction of the RNA double helix.

10-43. **A study of the actin structure.** By A. A. VAZINA, L. A. ŽELEZNAJA, B. K. LEMAŽIKHIN and G. M. FRANK, *Institute of Biophysics of the Academy of Sciences of the U.S.S.R., Profsoyuznaya Street 7, Moscow, U.S.S.R.* Probable journal not stated.

The study of physiological processes at the molecular level becomes more and more popular. The muscle-contraction problem is one of the principal problems of contemporary molecular biology. The structure of muscle proteins is of great importance for the interpretation of the muscle-contraction mechanism.

The paper presents the results of investigation of the F-actin structure by small-angle X-ray scattering and X-ray diffraction. It is known that F actin is formed by polymerization of individual globular actin (G actin) molecules.

In 1964 we found highly organized structures of the liquid-crystalline type in concentrated F actin solutions (10–15%). In the polarizing microscope between crossed nicols the gels examined look like polycrystals with heterogeneity regions of the order of 0.1–1 mm. The X-ray pattern of unoriented F actin solutions shows about 20 reflexions (from 6 Å to 400 Å). A series of reflexions from 55 Å to 400 Å have been obtained for the first time on isolated actin. These reflexions are due to the periodicity along the actin filament. (The liquid-crystalline structure allows F actin to be examined under nearly physiological conditions.)

The method of small-angle X-ray scattering has been used for the determination of the cross-section of F actin in dilute solution. The value obtained (80 ± 15 Å) agrees well with the electron-microscopical data.

We succeeded in obtaining fine oriented filaments from the concentrated F actin gels. Small-angle X-ray patterns of these filaments are typical for the helical structure.

An analysis of the X-ray patterns of F actin concentrated solutions and dilute solutions, as well as of oriented filaments, proves the two-helical F actin model, suggested by Selby and Bear (1956) on the basis of X-ray analysis of muscle. In this helical model each G actin molecule is bound with four neighbouring ones by two types of bonds.

According to the model two structural forms of fibrillar