three-dimensional data. The orientation obtained from the
rotation function is in good agreement with that obtained
by Scoufoudi 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
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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 investiga-
tions 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-
t-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 ob-
served 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.
Tumanian, N. G. Esiyova 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 ≥20% concen-
trations), 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 di-
ensions and form could be determined using conventional
methods (Fournier, Porod, Kratky, Ptytyn 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 ob-
tained 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. Zeleznaja, B. K. Lematzkhn and G. M.
Frank, Institute of Biophysics of the Academy of Sciences
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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 poly-
merization 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 hetero-
genrety regions of the order of 0.1-1 mm. The X-ray
pattern of unoriented F actin solutions shows about 20
reflections (from 6 Å to 400 Å). A series of reflections from
55 Å to 400 Å have been obtained for the first time on
isolated actin. These reflections 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 fila-
ments, prove 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