too close for accurate measurement and the c axial length is derived from the axial ratio. The dimensions of the cell may still be multiples of this. Using the density measured on fresh material[2] as 1·32 (our measurements gave 1·28), the cell molecular weight is 478,000, which is twelve times 40,000, almost exactly Svedberg's value arrived at by sedimentation in the ultracentrifuge. This agreement may however be quite fortuitous as we have found that the crystals contain about 50 per cent of water removable at room temperature. But this would still lead to a large molecular weight, with possibly fewer molecules in the unit cell.

Not only do these measurements confirm such large molecular weights but they also give considerable information as to the nature of the protein molecules and will certainly give much more when the analysis is pushed further. From the intensity of the spots near the centre, we can infer that the protein molecules are relatively dense globular bodies, perhaps joined together by valency bridges, but in any event separated by relatively large spaces which contain water. From the intensity of the more distant spots, it can be inferred that the arrangement of atoms inside the protein molecule is also of a perfectly definite kind, although without the periodicities characterising the fibrous proteins. The observations are compatible with oblate spheroidal molecules of diameters about 25 A. and 35 A., arranged in hexagonal nets, which are related to each other by a hexagonal screw-axis. With this model we may imagine degeneration to take place by the linking up of amino acid residues in such molecules to form chains as in the ring-chain polymerisation of polyoxy methylenes. Peptide chains in the ordinary sense may exist only in the more highly condensed or fibrous proteins, while the molecules of the primary soluble proteins may have their constituent parts grouped more symmetrically around a prosthetic nucleus.

At this stage, such ideas are merely speculative, but now that a crystalline protein has been made to give X-ray photographs, it is clear that we have the means of checking them and, by examining the structure of all crystalline proteins, arriving at far more detailed conclusions about protein structure than previous physical or chemical methods have been able to give.

J. D. BERNAL.
D. CROWFOOT.

Department of Mineralogy and Petrology,
Cambridge.
May 17.

[1] G. L. Clark and K. E. Korrigan (*Phys. Rev.*, (ii), **40**, 639; 1932) describe long spacings found from crystalline insulin, but no details have been published.

[2] J. H. Northrop, *J. Gen. Physiol.*, **13**, 739; 1930.

IT is now some time since we first took X-ray powder photographs of crystalline pepsin kindly sent by Prof. J. H. Northrop, but no really satisfactory interpretation of these photographs presented itself because they show features which we have learnt recently to associate with the fibrous proteins[1]: even single crystals, so far as we could judge with the minute crystals available, appeared to give results similar to those produced by many crystals in random orientation. The two chief rings have spacings of about 11·5 A. and 4·6 A. at ordinary humidity, corresponding to the 'side-chain spacing' and the 'backbone spacing', respectively, of an extended polypeptide[1].

It was difficult, of course, to reconcile such findings with external morphology and the Law of Rational Indices, but the photographs of Bernal and Miss Crowfoot, taken before the degeneration which we now see the crystals must have undergone on drying, clear up this long-standing problem at once. Furthermore, their photographs tend to confirm the suggestion[2] that the numbers 2, 3, 4, and 6 occurring in Svedberg's multiple particle weights are fundamentally of *crystallographic* significance, even though their conclusions to date appear to be against the chain mechanism proposed for the building-up of the various crystallographic groups[2].

We are left now with the paradox that the pepsin molecule is both globular[3] and also a real, or potential, polypeptide chain system, and the immediate question is whether the chains are formed by metamorphosis and linking-up of the globular molecules, or whether the initial unit is the chain itself, which is afterwards folded in some neat manner which is merely an elaboration of the intra-molecular folding that has been observed in the keratin transformation[1]. What is either an exceedingly valuable clue or else only a fantastic coincidence is found in the fibre photograph of feather keratin[4], a study of which will be published shortly; for if, as Bernal thinks, the pepsin molecules are piled, perhaps in a screw, along the hexad axis, their length in this direction is 140/6, that is, about 23½ A., which is almost exactly the strongest period along the fibre-axis of feather keratin, a period which is again repeated probably six (or a multiple of six) times before the fundamental period is completed! The innermost equatorial spot of the feather photograph also corresponds to a side-spacing of about 33 A. (though this is probably not the maximum side-spacing), which again is in simple relation to the side dimensions of the pepsin unit cell. As just said, these resemblances may be only accidental, but we cannot afford to overlook anything in such a difficult field, and it is not impossible that we have here an indication of how very long, *but periodic*, polypeptide chains can arise by the degeneration and linking-up of originally globular molecules.

W. T. ASTBURY.
R. LOMAX.

Textile Physics Laboratory,
University of Leeds.

[1] W. T. Astbury, *Trans. Faraday Soc.*, **29**, 193; 1933. W. T. Astbury and A. Street, *Phil. Trans. Roy. Soc.*, A, **230**, 75; 1931. W. T. Astbury and H. J. Woods, NATURE, **126**, 913, Dec. 13, 1930. *Phil. Trans. Roy. Soc.*, A, **232**, 333; 1933. W. T. Astbury and W. R. Atkin, NATURE, **132**, 348, Sept. 2, 1933.

[2] W. T. Astbury and H. J. Woods, NATURE, **127**, 663, May 2, 1931.

[3] J. St. L. Philpot and Inga-Britta Eriksson-Quensel, NATURE, **132**, 932, Dec. 16, 1933.

[4] W. T. Astbury and T. C. Marwick, NATURE, **130**, 309, Aug. 27, 1932.

Transitions to Optical Levels in the Argon *L* X-Ray Absorption Spectrum

THE so-called fine structure of X-ray absorption edges is caused by the possibility of transition of an inner electron to *different* upper levels, these levels being more or less discrete for the lowest energies and approximately continuous for the higher ones. In the ordinary X-ray region, the fine structure observed with crystalline absorbers usually extends over more than 100 v. from the main edge. It was pointed out by Kronig[1] that in this case the discrete character of the upper states may be considered as due to the wave character of the motion of a 'free' electron in