Ascension—between feeding and breeding areas, but such migrations take place within one climatic zone. It is remarkable, as Mr Brongersma points out, that the animals should reach Northern Europe where the climate is unsuitable for a long stay, and where they cannot breed (the temperature is far too low).

Most of the animals found in British waters seem to come from the Western Atlantic Ocean and the Gulf of Mexico. Kemp's Ridley, *Lepidochelys Kempi* (Garman), one of the five species described in *British Turtles*, breeds only in the Gulf of Mexico, and may pass through the Florida Strait to the east coast of America. It sometimes continues its voyage from America to Europe, partly carried along by the Gulf Stream. The age of some of the specimens found suggests that hurricanes in the Caribbean area could sweep some very young turtles out into the ocean, where they lose their bearings and then just follow the current. Some specimens have lacked one of their front flippers, which implies that they would only have been able to swim in circles—clearly they must have been swept along by the current. The journey to Europe seems to take between thirteen and seventeen months. Although protected by their shells, the turtles are still in danger of having flippers bitten off by sharks or sliced off by propellers of ships, so that the specimens which finally reach the British Museum are not always complete.

Structure and Reactivity of Ribonuclease

from Professor E. A. Barnard

THE recent determinations of the three-dimensional structure of ribonuclease offer an unusual opportunity for insights into the molecular basis of enzyme action, and were the background for the international symposium held at the State University of New York at Buffalo between May 31 and June 1.

To begin with, there was a correlation of the determinations of the structure itself. Models and maps of the 2 Å structure of ribonuclease *A* due to G. Kartha, J. Bello and D. Harker and that of ribonuclease *S* due to H. W. Wyckoff and F. M. Richards (at 3·5 Å) were compared side by side. The very high degree of agreement between the structures was remarkable, considering the use of two protein forms in different heavy atom derivatives and in very different solvents. Most of the differences occur, as expected, in the regions on both sides of the bond (20–21) that is cleaved to form the ribonuclease *S* derivative. C. H. Carlisle who, using quite different derivatives, has obtained a map of ribonuclease *A* at 5·5 Å, showed that this was compatible with the Kartha's map with a transposition to a corresponding origin of co-ordinates: this map should lead to the same structure when taken to higher resolution.

A good deal of attention was paid to evidence on binding properties. Both the Roswell Park group (Kartha and colleagues) and the Yale group (Wyckoff, Richards and colleagues) showed that one bound ligand, defining the active centre regions, can be located in a cleft. The Yale workers specified the binding of inhibitors containing iodouracil. Several participants related the specific binding of di-anion inhibitors to interactions at a cluster of histidine and lysine side chains. G. G. Hammes interpreted evidence of relaxation rate to show discrete steps in the binding, involving histidines and (by presumption) a carboxyl.

There was much less agreement on the mechanism of catalysis. Different hypotheses by B. R. Rabin, G. G. Hammes and H. Witzel were separately put forward as consistent with the structure. It seems not to be possible to specify from the X-ray evidence the type and the extent of structural change which occurs on binding, chiefly because a ligand bound to the active site has so far always been necessary for crystallization. This, in itself, suggests a more motile structure for the free enzyme.

Some new directions of work became clear at this conference. H. A. Scheraga forecast the total computation of the structure of proteins such as ribonuclease and lysozyme, using their sequences and the minimization of energy. This bold approach has been applied so far to gramicidin *S*, oxytocin and, now, to two regions of ribonuclease. The method should yield the structure the proteins would possess if isolated, so that its validity has not yet been fully tested. In comparative studies, C. H. W. Hirs showed that pig pancreatic ribonuclease is a series of glycoproteins. E. A. Barnard, M. H. Gold and E. N. Zendzian reported a new study of the distribution of pancreatic ribonucleases through the vertebrates, and presented evidence of reactivity and specificity which shows that the active centre is similar. The active centre specific labellings they obtained point the way to phylogenetic sequence comparisons, but the time is clearly still distant when it will be possible to make a full comparison of three-dimensional structures in this series.

Circular DNA

from our Correspondent in Molecular Biology

MUCH interest has in recent years been generated by the discovery of circular DNA in viruses, and more recently in mitochondria from a variety of cells. This DNA is fully double stranded, and has been shown to be covalently cyclic. The properties innate in such a structure have been investigated by Vinograd and his associates. They arise from the topological restriction that, for a given molecular weight, the number of turns of the two-stranded helix is fixed. This confers on the molecule an enhanced resistance to denaturation, and hydrodynamic properties which differ from those of linear native DNA.

Good evidence was obtained earlier that the normal form of mitochondrial circular DNA is supercoiled, and shapes were observed in the electron microscope which were best described as being like pretzels. Vinograd and his group showed that when a single break is introduced in one strand, or when a small degree of denaturation is provoked, the supercoil is able to unwind and the molecule reverts to the untwisted circular form.

Radloff, Bauer and Vinograd (*Proc. US Nat. Acad. Sci.*, **57**, 1514; 1967) have now devised a striking method for the separation of intact circular DNA from the linear and the damaged circular species with which it is extracted from the cell. The principle involves the binding of a dye, ethidium bromide, which belongs to a class of planar conjugated molecules now generally held to be capable of intercalating, or sliding between adjacent bases, in a helical DNA. There is