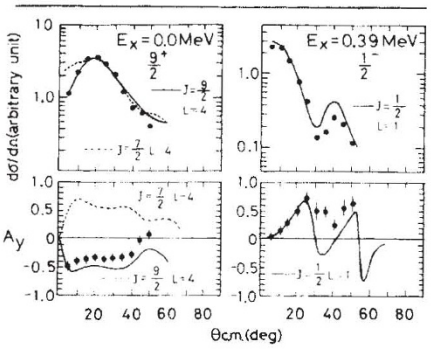
Nuclear spectroscopy with (p, α) reactions

from P. E. Hodgson

NUCLEON transfer reactions, in which a nucleon or group of nucleons is transferred from one nucleus to another, are already established as one of the most powerful ways of determining the properties of nuclear states. The angular distribution is usually sensitive to the transferred angular momentum L and this provides important information about the final state of the residual nucleus. The analysis is particularly simple if the target nucleus has no regular momentum, for then the angular momentum J of the final state is $L\pm\frac{1}{2}$, where L is the transferred orbital angular momentum and the $\frac{1}{2}$ is the spin angular momentum. If L is determined from the angular distribution there still remains the problem of deciding between $L+\frac{1}{2}$ and $L-\frac{1}{2}$. This can be done from theoretical considerations, but it is still desirable to have an experimental method of resolving this ambiguity.

This is provided by the measurement of the polarisation of the emitted particles or by a rather similar quantity, the asymmetry of the particles from a reaction initiated by polarised projectiles. The usefulness of this method has recently been studied for the (p, α) reaction with polarised protons by Mikumo and his colleagues at the University of Tsukuba in Japan (*Phys. Rev. Lett.* **41**, 16; 1978).



Scattering angle in degrees

Differential cross sections and asymmetries of the ^{116}Sn(p, α) ^{113}In reaction to the ground and 0.39 MeV states of the final nucleus, compared with distorted wave calculations with various values of J and L.

They irradiated ^{116}Sn and ^{112}Cd with 22 MeV polarised protons and measured the cross sections and asymmetries of the reactions leaving the residual nuclei in a number of different final states. Some of the results are shown in the figure, in which the cross sections and asymmetries are compared with distorted wave calculations for various values of J and L. In the case of the reaction to the ground state of ^{113}In, the calculated differential cross sections for $J=9/2$ and $J=7/2$ are very similar, but the asymmetries are quite different, so that it is possible to conclude that the state has $J=9/2$ without any ambiguity. In the same way the state at 0.39 MeV is found to have $J=\frac{1}{2}$.

The distorted wave calculations are made with the cluster approximation in which the three transferred nucleons are considered as a triton cluster, with the appropriate wavefunction. This is rather a drastic approximation, and the generally good agreement between theory and experiment is a confirmation of its validity for the (p, α) reaction. This is important for the use of the reaction in nuclear spectroscopy because if this approximation is not made it is necessary to consider the three transferred nucleons individually, and this makes the calculations impracticably complicated.

This new work shows that the analysing power of the (p, α) reaction is a sensitive way of determining the angular momenta of nuclear states, and the comparative simplicity of the analysis should may it widely useful.

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because it should indicate clearly where too few or too many atoms have been assigned to a particular side chain. For example, if, when interpreting the isomorphous map, a tyrosine is mistaken for a phenylalanine then the difference map should indicate that an additional atom—the oxygen of the terminal hydroxyl group—should be included (Steitz shows a nice example of just this effect). The process is comprehensive and iterative, so that the inclusion of the newly discovered hydroxyl group in the next difference map will improve features indicating the inclusion or exclusion of atoms in other residues, which in turn will improve the subsequent map, and so on. Effectively this enables errors due to poor isomorphous phasing to be progressively eliminated, and also enables the resolution to be increased without using heavy atom derivatives.

Clearly exhaustive use of refinement can result in a reasonably close approximation to the true electron density distribution, which means that the limitation to determining the amino acid sequence in this way is the number of residues that are intrinsically not well-ordered in the protein. Although Steitz has improved the amino acid identification from no better than 25% in the isomorphous map to 69–70% at the end of the refinement, it is evident that there are fewer Glx and Lys residues, and more Ala and Ser, than there should be. This is a consequence of the disordering of the longer residues and their inevitable misidentification as smaller residues. It is difficult to see how any conceivable X-ray method of sequencing can deal with the problem of mobile surface residues, and it would seem to present a fundamental limitation to the technique.

Nevertheless identification of 60–70% of the amino acids in a protein can be valuable on at least two counts. First the knowledge of the nature of particular side chains involved in substrate binding or catalysis in the active site is clearly important. Secondly, the identification of a proportion of the amino acids will facilitate the fitting of peptides, even very short ones, when they become available at the beginning of chemical sequence analysis, and should enable peptides to be correctly assembled in an end-to-end manner, making unnecessary the overlapping peptides normally used for ordering. □

Renewing the search for calcium pumps

from V. L. Lew

IT is now generally accepted that the maintenance of the large inward Ca^{2+} gradient across the plasma membranes of living cells is an essential condition for cell survival and for the various physiological roles of calcium as a trigger, signal-effect coupling agent or second messenger. What is not so clear is how these gradients are maintained.

The view most generally held at present is that in excitable cells and in many non-excitable cells as well, Ca extrusion is mediated by a Na : Ca countertransport mechanism which derives its energy from the electrochemical gradient of Na and perhaps also K. In red cells and certain cultured cells on the other hand an ATP-fuelled Ca pump is responsible for the uphill extrusion of Ca. Although the possibility has been raised that these apparently separate transport mechanisms reflect different operating

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