

ne nitrogen is the one most easily broken. For the fast proton $\Delta H^\ddagger = 9.9$ Kcal/M and $\Delta S^\ddagger = -28$ eu. For the slower reacting proton $\Delta H^\ddagger = 14.5$ Kcal/M and $\Delta S^\ddagger = -17$ eu. This shows that the stereochemistry of the schiff base plays an important role in the reactivity of the amino acid substituents and that proper orientation of the bond to be broken results in a lower barrier for the reaction and shows how the enzyme might bring about its rapid rates of reaction.

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PS5.13 — MO

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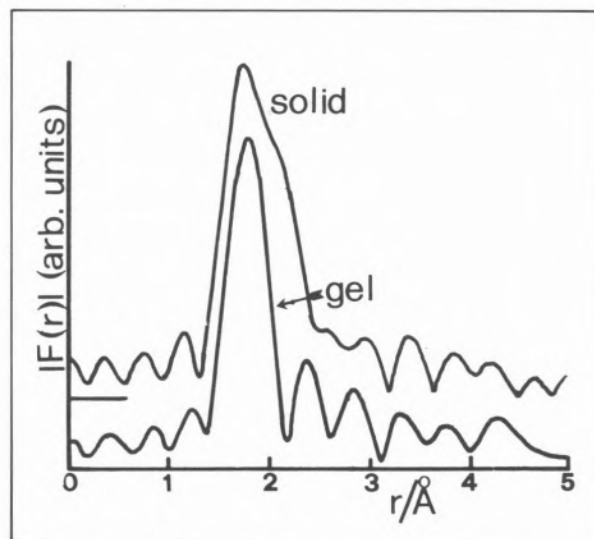
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EXAFS STUDIES OF GEL AND SOLID FORMS OF Ca^{2+} - α -D-POLYGALACTURONATE

Knowledge of the structural assemblies involved in the biologically important Ca^{2+} polysaccharides is still fragmentary. We have measured the EXAFS spectra of the gel and solid forms of Ca^{2+} - α -D-polygalacturonate, the major intercellular component of deacetylated pectin [1]. Calcium ascorbate

dihydrate and the 2-keto-D-gluconate were used as model compounds [2]. Filtered Fourier transforms of the extracted EXAFS (widest common k range possible; k^3 -weighted; not phase-shift corrected) are shown in the figure.



The first shell peak is clearly different in the two materials, *i.e.* the Ca-O bond distance distributions differ. The gel gives a well-defined peak, whereas the solid has a shoulder at higher Ca-O distance. (EXAFS of the models confirm that an asymmetry can be identified when the spread of Ca-O bond distances is at least 0.2 Å, as in the 2-keto-D-gluconate).

Further structure is visible out to 3.5 Å, and is again different in the two forms. Full parameter fits are in course and should provide information on the possible 2_1 and 3_1 configurations put forward in the literature [3].

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PS5.14 — TU

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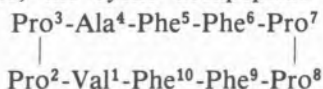
MODES OF COMPLEXATION OF CYCLIC PEPTIDES WITH LIGHT METAL IONS

The structures and conformations of a number of free cyclic peptides and the same peptides complexed with Li^+ , Na^+ , K^+ or Mg^{2+} ions have been established by X-ray diffraction analyses of single crystals. The different modes of complexation that have been found are: 1) an infinite sandwich in which the metal ion and the cyclic peptide alternate [1]; 2) a discrete sandwich in which the metal ion is between two cyclic peptide molecules [2-4]; 3) incomplete encapsulation of the metal ion by one peptide molecule [5,6]; 4) complete encapsulation by one peptide molecule [7,8]; and 5) the metal ion partially *exo* to the polar cavity formed by the peptide [9]. Modes 1-4) appear to be a function of the size of the cyclic peptide, beginning with a pentapeptide for 1) and progressing to a dodecapeptide for 4). Mode 5) can occur when the size of the metal ion is mismatched with the size of the cyclic peptide.

The complexation of cyclic oligopeptides with metal ions requires the formation of ligands between the metal ion and carbonyl oxygens. If the peptide is too small, even acting in pairs, then the incomplete coordination sphere about the metal ion is completed by ligands to the oxygens of water molecules [1] or to O or N atoms of solvent molecules [5,6] such as CH_3CN , $\text{C}_2\text{H}_5\text{OH}$, $(\text{CH}_3)_2\text{CO}$ or to counterions [1] such as SCN^- . The Mg^{2+} ion has shown an almost exclusive preference for octahedral coordination [1,2], with all O- Mg^{2+} -X angles (X=O or N) very near to 90° . The Li^+ and Na^+ ions adjust their coordination to the local geometry, as for example, in the complexes with antamanide and antamanide analogs, the Li^+ and

Na^+ ions have pentacoordination with ligands to four carbonyl O atoms in a square array and the fifth ligand to a polar atom of a solvent molecule at the apex of the coordination pyramid [5,6]. In every case, the ligands to O or N atoms radiate from the metal ion in all directions and a polar envelope about the metal ion is provided that separates it from the lipophilic regions of the peptide.

The free cyclic peptide is not in a conformation ready to accept and encapsulate a metal ion. Severe conformational changes occur upon complexation. To demonstrate that complexation is responsible for the conformational changes rather than other changes in the crystal environment such as packing, intermolecular interactions, and/or solvent inclusion, a number of crystal structure analyses were performed on the uncomplexed peptides, or closely related analogs of the peptide. To illustrate, the cyclic decapeptide antamanide



and the biologically active analog [$\text{Phe}^4, \text{Val}^6$] antamanide were crystallized from solutions containing water and common organic solvents such as $\text{C}_2\text{H}_5\text{OH}$, CH_3CN , acetone, DMFA, *etc.*, and from completely nonpolar solvents such as *n*-hexane. The resulting crystals had different packing arrangements of the peptides, different solvent inclusions (both polar and nonpolar) and several different side chains on the peptides. Nevertheless, the folding of the backbone and the twisting of the side chains are almost identical in all the crystals [10-12]. Similarly, the conformations of the cyclic pentapeptides (Gly-Pro-Gly-D-Ala-Pro) and (D-Phe-Pro-Gly-D-Ala-Pro) are superimposable despite a different side chain and different packing in the respective crystals [13,14]. Similarly, uncomplexed valinomycin crystallized from different solvents and occurring in different crystalline packing arrangements has a unique elongated conformation [15-17].

The process of forming complexes with Li^+ , Na^+ and Mg^{2+} with each of the cyclic peptides involves major changes such as the rotation of one or more peptide units by as much as 180° . On complexation in antamanide, not only does the flattened elongated cyclic backbone become folded, but sequences 4,5,6 and 9,10,1 turn inside out so that