the $^2B_2$ level with the $^2E_\pm$ levels which yields a triclinic electron distribution. The $^2E_\pm$ levels admix to the $^6A_1$ ground state by spin–orbit coupling. The electron distribution is therefore predominantly spherically symmetric with a small rhombic component C_{2v}. Ferric low spin Fe in Mb(CN) has for C_{4v} symmetry a ^2E ground state and low lying $^2E_2$ and $^4A_2$ levels at about 300 and 800 cm^{-1}. A triclinic perturbation splits the ^2E doublet into $^2E_+$ and the new ground state $^2E_-$. The electron distribution is therefore always of rhombic symmetry C_{2v}.

It is intended to discuss also the symmetry properties of hemes and heme proteins for the $3d^6$ configuration of Fe.

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B9

Jack Bean Urease: the First Nickel Enzyme

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Jack bean urease is the first example of a nickel metalloenzyme [1–3]. Reassessment of the molecular properties of the enzyme shows that the native enzyme has a molecular weight (M_r) of 590,000 ± 30,000, and that under denaturing conditions, urease breaks down to identical subunits with M_r = 90,000–100,000 [4]. The molecular weight of subunits is 96,600, as determined by titration with radioactive inhibitors (acetohydroxamic acid [5] and phosphoramidate) [2, 4]. Thus the native enzyme consists of six identical subunits, and these are arranged in the form of a regular octahedron [6]. Each subunit contains one cystine disulfide bond and a total of fifteen cysteine residues [7].

Each subunit contains 2.0 ± 0.1 very tightly bound nickel ions [1, 2, 8–10]. After the electronic absorption spectrum of native urease has been corrected for effects of light scattering, the peaks associated with nickel ion (λ_{max}: ~407 nm, 745 nm, 1060 nm) are consistent with Ni(II) in an octahedral environment [6, 11]. β-Mercaptoethanol binds rapidly and reversibly to urease to produce marked reversible changes in the absorption spectrum of the enzyme [12]. New absorption peaks in the difference spectrum (324 nm, 1550 M^{-1} cm^{-1}; 380 nm, 890 M^{-1} cm^{-1}; 420sh nm, 460 M^{-1} cm^{-1}) are consistent with charge transfer transitions of a thiolate anion coordinated to Ni(II).

A detailed mechanism was developed in which urea is activated towards nucleophilic attack by virtue of O-coordination to Ni(II) ion [13], and has been subsequently successfully modelled [14].

The competitive inhibitors acetohydroxamic acid, phosphoramidate and fluoride [4, 12, 15], produce small, reversible changes near 400 nm in the absorption spectrum of urease, consistently with their direct coordination to Ni(II) ion.

These and other aspects of the chemistry of this system will be discussed.

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B10

Ions and Ionophores

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It will be shown using typical examples that it is possible to account, by explicit computations, for the complexing preferences of ionophores for certain cations. In the case of valinomycine, the preference observed for complexing the alkali cations is in the order $Rb^+ \sim> K^+ > Cs^+ \gg Na^+$, and can be accounted for by making an energy balance between the ener-

gies of binding of the cation to the ionophore, assumed to remain a rigid bracelet-like cage, and the desolvation energies of the cation: the calculated values of the complexation energies are in the order $Na^+ > K^+ > Rb^+ > Cs^+$; the energies required to desolvate the ions decrease in the same order, but the numerical values are such as to bring the balance between the two quantities into the experimentally observed order.

In the case of nonactine, a much more flexible molecule, the computations show that, in the observed preference $K^+ > Na^+$, the complexation energies largely favor Na^+ and that the substraction of the desolvation energies does not suffice to reverse the order of the two cations. In that case the determining factor stems from the intramolecular repulsions between the oxygenated ligands inside the cavity, repulsions appreciably larger in the conformation of the Na^+ cavity than in that of the K^+ cavity, so that the total balance favors K^+. An attempt to account for the preference $NH_4^+ > K^+$ was made, assuming that the conformational changes between the two complexes can be neglected: there, the computed complexations energy largely favors NH_4^+, the preferred cation, and the substraction of the desolvation energy does not modify the order. The optimized computed position for NH_4^+ shows very interesting differences with respect to K^+, confirming some inferences made on the basis of early experimental infrared measurements in solution.

It will also be shown how the notions of molecular electrostatic potential, molecular electrostatic field, and atomic accessibilities can be useful in the domain of cation–ionophore interactions. Two examples will be given: a) the K^+-complex of valinomycine in connection with its ability to fix an anion, and the recently observed K^+–picrate–valinomycine complex; b) the uncomplexed form of valinomycine to propose arguments for a choice between two possible mechanisms recently suggested for initiating the ion capture.

Finally the case of divalent cations will be considered.

B11

Modeling the Molybdenum Sites of the Molybdenum Hydroxylases

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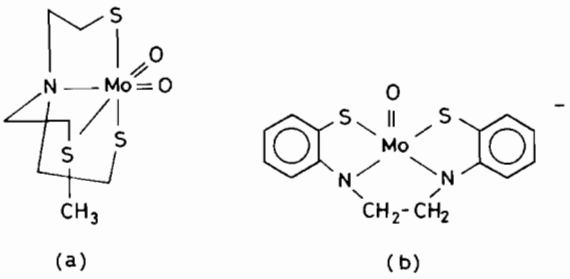
Molybdenum hydroxylases are multicomponent enzymes which catalyze two electron oxidations of purines, aldehydes, formate and sulfite in animals and microorganisms [1]. In addition, eukaryotic nitrate reductase [2] and several as yet poorly characterized molybdenum containing enzymes have properties similar to those of the hydroxylases.



(a) (b)

Fig. 1.

Recent EPR and EXAFS investigations indicate the presence of a terminal oxo and a terminal sulfido group on Mo in oxidized (Mo(VI)) xanthine oxidase and xanthine dehydrogenase and two oxo groups in oxidized sulfite oxidase [1, 3]. In the reduced state (Mo(V), (IV)) the sulfido group appears to be converted to SH (xanthine oxidase, xanthine dehydrogenase) or one oxo to OH (sulfite oxidase) [3]. In addition, 2-3 Mo thiolate sulfur ligands are present for both oxidized and reduced enzymes [3]. One or more of the thiolate ligands may be located on a side chain of a reduced pterin proposed to be the cofactor common to all Mo hydroxylases [4]. The reduction potentials of the Mo centers of the hydroxylases have been determined and are found to differ considerably between enzymes (–0.355 V for the Mo(VI)/(V) couple in xanthine oxidase [5], 0.038 V in sulfite oxidase [6], *e.g.*).

Recent model studies have concentrated on synthesis and structural characterization of dioxo-Mo(VI) complexes with N, S donor sets which mimic the EXAFS results [7] (Fig. 1a), on monomeric oxo-Mo(V) complexes having EPR parameters similar to those of the enzymes [8, 9] (Fig. 1b), and on oxo-Mo(VI), (V) and (IV) complexes which mimic the redox behavior of the enzymes [9, 10] (Fig. 1b). These results are briefly reviewed.

Current work in this laboratory is directed towards the synthesis and characterization of dioxo-Mo(VI) complexes with sterically bulky bi-, tri- and tetradentate ligands which may be electrochemically or chemically reduced to monomeric Mo(V)(O)(OH) complexes:

$$\left.\begin{matrix} MoO_2L_2 \\ MoO_2L'L'' \\ MoO_2L''' \end{matrix}\right\} \xrightarrow[H^+]{-e^-} \left\{\begin{matrix} MoO(OH)L_2 \\ MoO(OH)L'L'' \\ MoO(OH)L''' \end{matrix}\right.$$

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