Using Synthetic Chemistry to Understand Copper Protein Active Sites

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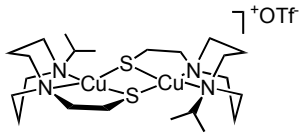
Proteins that contain copper ions in their active sites represent a large and functionally significant class of metallobiomolecules. The Cu sites may be involved in inter- and intraprotein electron transfer, dioxygen binding and activation, and nitrogen oxide reduction, among other roles. This functional diversity of copper proteins is matched by variability in active site geometric, electronic structural, and spectroscopic features. In this lecture, fundamental chemical insights into copper protein structure and function will be described, which were obtained through the synthetic modeling approach wherein low molecular weight complexes designed to replicate metalloprotein active site properties are characterized and their reactivity studied. The diverse utility of such model studies for addressing bioinorganic problems will be illustrated. For example, key aspects of the electronic structure of the "Cu_A" and "type 1" copper-containing electron transfer centers have been revealed through studies of novel copper-thiolate complexes such as **1** and **2**. Possible pathways of dioxygen and nitrogen oxide activation by copper protein active sites have been discovered through detailed examination of the reactivity of Cu(I) complexes with O_2 and NO_x species. As a result, novel reactive intermediates such as **3** have been characterized through structural, spectroscopic, and kinetic studies, in conjunction with theoretical calculations. Recent progress in O_2 activation by mono- and multicopper complexes and in copper-sulfide chemistry relevant to the unique "Cu_Z" site of nitrous oxide reductase will augment perspectives obtained from previously published work.



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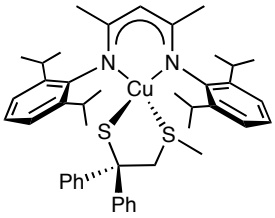

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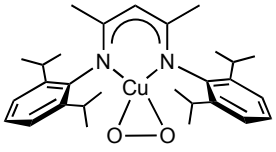

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