

X-ray Absorption Spectroscopy as a Probe of Active Site Structure in Copper Enzymes and Copper Chaperones

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Copper is an essential trace element in biology. Copper enzymes are involved in a wide variety of cellular processes including respiration (cytochrome *c* oxidase), iron uptake and homeostasis (ceruloplasmin, hephaestin), pigmentation (tyrosinase), endocrine function (peptidylglycine monooxygenase), and free radical detoxification (superoxide dismutase). These enzymatic functions involve cycling between the two biologically accessible oxidation states of copper – Cu(II) and Cu(I). Another class of copper proteins are involved in the uptake and trafficking of this essential metal ion, and in these systems copper is found predominantly in the spectroscopically silent Cu(I) state. XAS is unique in its ability to provide detailed local structural information on both Cu(II) and Cu(I) forms, and has been pivotal as a probe of structure and function in both enzymes and transporters. In this presentation, the use of XAS in studying the reaction chemistry of a member of each group - peptidylglycine monooxygenase and the copper chaperone for superoxide dismutase – will be described.