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Fingerprinting redox/ligand states and driving catalysis in protein single crystals

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Single crystal spectroscopic analysis may be used to gain a complete and accurate identification of the redox and ligation states of metal (redox) centres in protein crystals [1,2]. Combining this approach with controlled X-ray radiolysis can allow the generation and characterisation of functional species and intermediates [3].

Cytochrome *c*' (CYT*c*) is a haem protein with the remarkable ability to discriminate between NO and CO by binding them to opposite faces of the haem while excluding O₂ [4]. The binding of NO to CYT*c* provides a model for the activation of soluble guanylate cyclase. We will describe the use of UV-visible absorption and resonance Raman spectroscopies to monitor radiolysis and 'fingerprint' key redox and ligand states in crystals of native and mutant CYT*c*, from which high resolution crystal structures have been determined. We will also describe the radiolysis-driven conversion of substrate-to-product in crystals of copper nitrite reductase.

1. Ellis, M. J. et al. (2008) *J. Synchrotron Rad.* 15, 433-439.
2. Antonyuk, S. V. & Hough, M. A. (2011) *BBA Proteins and Proteomics* 1814, 778-784.
3. Hough, M. A. et al. (2008) *J. Mol. Biol.* 378, 353-361.
4. Hough M. A. et al, (2011) *J. Mol. Biol.* 405, 395-409.

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