

Poster Presentation

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Crystal structures of 2OG oxygenases involved in ribosomal protein hydroxylation

S. Horita^{1,2}, J. Scotti¹, M. McDonough¹, R. Sekirnik¹, R. Chowdhury¹, T. Krojer³, A. Thalhammer¹, W. Aik¹, U. Oppermann³, C. Schofield¹

¹University of Oxford, Chemistry Research Laboratory, Department of Chemistry, Oxford, UK, ²University of Oxford, Department of Physiology, Anatomy and Genetics, , Oxford, UK, ³University of Oxford, Structural Genomics Consortium, University of Oxford, Oxford, UK

Post-translational modifications play diverse biological functions. Hydroxylation of collagen proteins has long been a recognised post-translational modification in eukaryotes. In the case of collagen, hydroxylation of prolyl residues, by 2-oxoglutarate and iron dependent enzymes (2OG oxygenases), in collagen proteins allows for the stabilisation of the collagen triple helix structure through conformational restraint and through the addition of a hydrogen bond donor. Additionally, hydroxylation of lysine side chains of collagen is required for cross-linking collagen (and possibly other proteins) in the extra-cellular matrix. Post-translational prolyl hydroxylation also plays a pivotal role in transcriptional regulation of the hypoxic response, as catalyzed by the hypoxia inducible factor / HIF prolyl hydroxylases (PHDs or EGLN enzymes). Recently, ribosomal protein hydroxylation catalyzed by 2OG- and Fe(II)-dependent oxygenases has been found to be a highly conserved post-translational modification in eukaryotes and prokaryotes (Ge et al and Loenarz et al). We present several crystal structures of 2OG oxygenases involved in ribosomal protein hydroxylation.

[1] W. Ge, et al., 2012, *Nat Chem Biol* 8, 860-962., [2] C. Loenarz, et al., 2013, *Proc Natl Acad Sci U S A* (in press)

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