

## Prof M Carr - Molecular basis of the control of eukaryotic gene expression.

Research in my group is focussed on determining the structures, functions, interactions and mechanisms of action of proteins and protein complexes involved in key biological processes of significant medical importance. A major component of this work has been the successful use of NMR-based methods to determine new protein structures and to investigate protein-drug, protein-protein and protein-DNA interactions. The ongoing research in my group aims to integrate the information obtained from molecular, cellular and structural biology-based approaches to provide a detailed understanding of the function of proteins involved in disease states, which is an essential prerequisite for a rational, knowledge-based approach to drug discovery and development. In addition, through close collaboration with pharmaceutical companies such as UCB-Celltech we aim to make a major contribution to the design and development of important new drugs, such as therapeutic antibodies targeted at secreted signalling proteins (cytokines, chemokines, etc.) or cell surface receptors.

Control of eukaryotic gene expression is dependent upon the assembly of a diverse range of protein-protein and protein-nucleic acid complexes, which are formed in a dynamic and highly regulated process. The main focus of current work in my group is the highly conserved, eukaryotic protein Pdc4, which has recently emerged as a key regulator of both transcription and translation, mediated via specific protein-protein and perhaps protein-RNA interactions. Pdc4 has also been identified as an important new type of tumour suppressor in mammalian cells and has very recently been shown to play an essential role in cellular responses to DNA damage. The overall aim of ongoing work is to determine the molecular basis of the cellular functions of Pdc4, which should lead to a clearer picture of the functions associated with its role as a tumour suppressor. A major aspect of this work will be the determination of high resolution structures for functional domains of Pdc4 and tight complexes formed with functional partners, such as eIF4A, eIF4G, c-Jun and p300. This will also be complemented by structure-guided mutagenesis studies aimed at associating interesting surface features of Pdc4 (potential functional sites) with specific cellular functions, such as its role in DNA damage response. This research programme forms part of a successful and long-term collaboration with Prof. Karl-Heinz Klempnauer's group at the University of Münster in Germany.

### References.

1. Wilkinson, I.C., Hall, C.J., Veverka, V., Shi, J.Y., Muskett, F.W., Stephens, P.E., Taylor, R.J., Henry, A.J. and **Carr, M.D.** (2009) A high resolution NMR-based model for the structure of a scFv-IL-1 $\beta$  complex: potential for NMR as a key tool in therapeutic antibody design and development. *J. Biol. Chem.* In press.
2. Ilghari, D., Waters, L.C., Veverka, V., Muskett, F.W. and **Carr, M.D.** (2009)  $^{15}\text{N}$ ,  $^{13}\text{C}$  and  $^1\text{H}$  resonance assignments and secondary structure determination of the *Mycobacterium tuberculosis* RV0287-Rv0288 protein complex. *J. Biomol. NMR Assign.* In press, DOI 10.1007/s12104-009-9167-3.
3. Veverka, V., Henry, A.J., Slocombe, P.M., Ventom, A., Mulloy, B., Muskett, F.W., Muzylak, M., Greenslade, K., Moore, A., Zhang, L., Gong, J., Qian, X., Paszty, C., Taylor, R.J., Robinson, M.K. and **Carr, M.D.** (2009) Characterization of the structural features and interactions of

sclerostin: molecular insight into a key regulator of Wnt-mediated bone formation. *J. Biol. Chem.* **284**, 10890-10900.

4. Lightbody, K.L., Ilghari, D., Waters, L.C., Carey, G., Bailey, M.A., Williamson, R.A., Renshaw, P.S. and **Carr, M.D.** (2008) Molecular features governing the stability and specificity of functional complex formation by *Mycobacterium tuberculosis* CFP-10/ESAT-6 family proteins. *J. Biol. Chem.* **283**, 17681-17690.
5. Veverka, V., Crabbe, T., Bird, I., Lennie, G., Muskett, F.W., Taylor, R.J. and **Carr, M.D.** (2008) Structural characterization of the interaction of mTOR with phosphatidic acid and a novel class of inhibitor: compelling evidence for a central role of the FRB domain in small molecule-mediated regulation of mTOR. *Oncogene* **27**, 585-595.
6. Waters, L.C., Veverka, V., Böhm, M., Schmedt, T., Choong, P.T., Muskett, F.W., Klempnauer, K.-H. and **Carr, M.D.** (2007) Structure of the C-terminal MA-3 domain of the tumour suppressor protein Pcd4 and characterisation of its interaction with eIF4A. *Oncogene* **26**, 4941-4950.
7. Waters, L., Yue, B., Veverka, V., Renshaw, P., Bramham, J., Matsuda, S., Frenkiel, T., Kelly, G., Muskett, F.W., **Carr, M.D.** and Heery, D.M. (2006) Structural diversity in p160/CREB-binding protein coactivator complexes. *J. Biol. Chem.* **281**, 14787-14795.
8. Waters, L.C., Böhm, M., Veverka, V., Muskett, F.W., Frenkiel, T.A., Kelly, G.P., Prescott, A., Dosanjh, N.S., Klempnauer, K.-H. and **Carr, M.D.** (2006) NMR assignment and secondary structure determination of the C-terminal MA-3 domain of the tumour suppressor protein Pcd4. *J. Biomol. NMR* **36**, S5, 18.
9. Veverka, V., Gregor, L., Crabbe, T., Bird, I., Taylor, R.J. and **Carr, M.D.** (2006) Letter to the Editor: NMR assignment of the mTOR domain responsible for rapamycin binding. *J. Biomol. NMR* **36**, S5, 3.
10. Renshaw, P.S., Lightbody, K.L., Veverka, V., Muskett, F.W., Kelly, G., Frenkiel, T.A., Gordon, S.V., Hewinson, R.G., Burke, B., Norman, J., Williamson, R.A. and **Carr, M.D.** (2005) Structure and function of the complex formed by the tuberculosis virulence factors CFP-10 and ESAT-6. *EMBO J.* **24**, 2491-2498.
11. Marei, A., Ghaemmaghami, A., Renshaw, P., Wiselka, M., Barer, M., **Carr, M.D.** and Ziegler-Heitbrock, L. (2005) Superior T cell activation by ESAT-6 as compared with the ESAT-6·CFP-10 complex. *Int. Immunol.* **17**, 1439-1446.