

P017 Calmodulin binding of mGluR7 target sequence using NMR
Stuart Findlow, Kate Holden-Dye, Joern Werner,
Matt Crump and Vincent O'Connor
SF, KH-D, JW & VO'C University of Southampton
MC University of Bristol

This work seeks to fast-track the identification of the binding mode adopted by the Ca^{2+} dependent complex formed between calmodulin and a novel peptide derived from metabotropic glutamate receptor 7 (mGluR7). mGluR7 is responsible for regulating the concentration of glutamate in the synaptic cavity providing feed-back inhibition of the glutamate release mechanism.

Calmodulin is capable of binding many different proteins in either a Ca^{2+} -bound or Ca^{2+} -free fashion. Structurally, several different binding modes have been observed leading to classifications being drawn up primarily based on sequence homology and are often based upon the spacing of two or more large hydrophobic amino acids which bind in hydrophobic cavities in calmodulin.

We will present our data on the free and peptide bound calmodulin characterising global and local changes in structure and dynamics of calmodulin using relaxation and residual dipolar coupling data. The results are expected to define the binding mode of this novel target peptide and may help refining the sequence based classification schemes.