

Solution structure of the complex between complement C3d and full length complement receptor Type 2

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Complement receptor type 2 (CR2, CD21) is a cell surface protein that links the innate and adaptive immune response during the activation of B cells. The extracellular portion of CR2 comprises 15 or 16 short complement regulator (SCR) domains. Its overall domain structure in solution was recently determined by constrained X-ray scattering and analytical ultracentrifugation (AUC) modeling to be a partially folded back but flexible structure (Gilbert et al. (2006) *J. Mol. Biol.* **362**, 1132-1147). To examine the effects of ligand binding to this structure, we have expressed C3d in *E. coli* and CR2 in baculovirus and are studying their complex by both X-ray scattering data and analytical ultracentrifugation (AUC). The X-ray radius of gyration of free CR2 was determined to be 11.5 ± 0.9 nm, and that of its cross-section was 1.8 ± 0.1 nm. An X-ray data set for the 1:1 complex between CR2 and C3d was collected at ESRF. This showed evidence for complex formation. Analytical ultracentrifugation experiments to verify these results are in progress.