

## Recognition of Polyadenylate RNA by the Poly(A)-Binding Protein

*S. Burley (Rockefeller U.) J. Bonanno and R. Deo (Howard Hughes Medical Institute) and N. Sonenberg (McGill U.)*

Abstract No. burl8733

Beamline(s): **X9B**

The co-crystal structure of human poly(A)-binding protein (PABP) has been determined at 2.6 Å resolution. PABP recognizes the 3' mRNA poly(A) tail and plays critical roles in eukaryotic translation initiation and mRNA stabilization/degradation. The minimal PABP used in this study consists of the N-terminal two RRM-type RNA-binding domains connected by a shortlinker (RRM1/2). These two RRM's form a continuous RNA-binding trough, lined by an antiparallel  $\beta$  sheet backed by four  $\alpha$  helices. The polyadenylate RNA adopts an extended conformation running the length of the molecular trough. Adenine recognition is primarily mediated by contacts with conserved residues found in the RNP motifs of the two RRM's. The convex dorsum of RRM1/2 displays a phylogenetically conserved hydrophobic/acidic portion, which may interact with translation initiation factors and regulatory proteins.