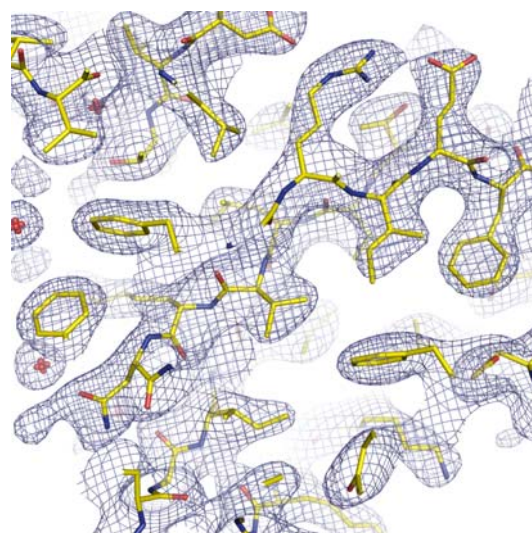
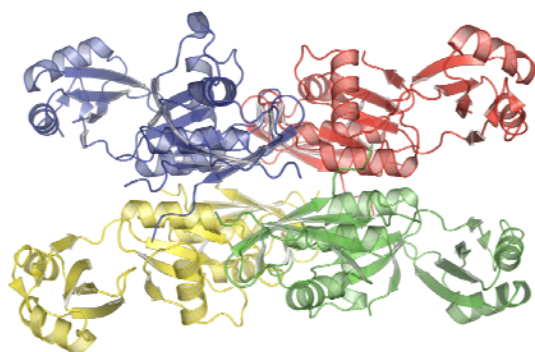


# Center for Eukaryotic Structural Genomics

## Protein Structure Initiative



<b>Target ID</b>	GO.74368	
<b>Source Organism</b>	<i>Saccharomyces cerevisiae</i>	
<b>Target Name</b>	N123	
<b>PDB Entry</b>	2GHP	Deposition: 26-Mar-2006
<b>Function</b>	n-terminal 3 RNA binding domains of the yeast splicing factor PRP24	
<b>Produced From</b>	<i>E. coli</i> B834 p(RARE2) pVP-16	
<b>Structure by X-ray</b>	Resolution: 2.70 Å	R-value (R-free): 21.3% (26.4%)
	No. of Residues/ASU: 1870	Monomers/ASU: 8
<b>Data Collected At</b>	Advanced Photon Source 22-ID 11-Oct-2005	
<b>Authors</b>	E. Bae, G.E. Wesenberg, G.N. Phillips, Jr., E. Bitto, C.A. Bingman	



### Structural Features

The essential *Saccharomyces cerevisiae* pre-messenger RNA splicing protein 24 (Prp24) has four RNA recognition motifs (RRMs) and facilitates U6 RNA base-pairing with U4 RNA during spliceosome assembly. Prp24 is a component of the free U6 small nuclear ribonucleoprotein particle (snRNP) but not the U4/U6 bi-snRNP, and so is thought to be displaced from U6 by U4/U6 base-pairing. The interaction partners of each of the four RRM of Prp24 and how these interactions direct U4/U6 pairing are not known. The crystal structure of the first three RRM of Prp24 has been solved at 2.70 Å resolution. Strikingly, RRM 2 forms extensive inter-domain contacts with RRM 1 and 3. These contacts occupy much of the canonical RNA-binding faces (beta-sheets) of RRM 1 and 2, but leave the beta-sheet of RRM 3 exposed. Previously identified substitutions in Prp24 that suppress mutations in U4 and U6 spliceosomal RNAs cluster primarily in the beta-sheet of RRM 3, but also in a conserved loop of RRM 2. RNA binding assays and chemical shift mapping indicate that a large basic patch evident on the surface of RRM 1 and 2 is part of a high affinity U6 RNA binding site. Our results suggest that Prp24 binds free U6 RNA primarily with RRM 1 and 2, which may remodel the U6 secondary structure. The beta-sheet of RRM 3 then influences U4/U6 pairing through interaction with an unidentified ligand.

*References:* (1) Bae, E., Reiter, N.J., Bingman, C.A., Kwan, S.S., Lee, D., Phillips, G.N., Jr, Butcher, S.E., Brow, D.A. (2007) Structure and interactions of the first three RNA recognition motifs of splicing factor prp24. *J Mol Biol* 367(5):1447-58.

<b>Percent Identity with Nearest PDB Structure at Time Solved</b>	25% (2CPD)
<b>Pfam Cluster</b>	RRM_1
<b>Sequence Cluster Size</b>	910

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