The structure consists of an unexpected, irregular (β/α) barrel with a tightly attached C-terminal zinc-containing subdomain. The packing of the subdomain to the barrel is mediated by an α-helix, located close to the C-terminus, which displaces the eighth helix of the barrel. This structure represents the first example of a (β/α) barrel protein interacting specifically with a nucleic-acid.

We also solved the structure of TGT in complex with preQ1 which suggests a binding mode for tRNA where the phosphate backbone is recognized by the zinc subdomain, and the U33G34U35 sequence by the barrel. This model for tRNA binding is consistent with a base exchange mechanism involving a covalent tRNA-enzyme intermediate.

MS04.06.06 PyrR, A BIFUNCTIONAL RNA-BINDING TRANSCRIPTION ATTENUATION PROTEIN AND URACIL PHOSPHORIBOSYLTRANSFERASE

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*Bacillus subtilis* PyrR regulates the transcription of the pyrimidine nucleotide biosynthetic operon (pyr) via an attenuation mechanism, in response to exogenous pyrimidine levels. UMP-bound PyrR effects regulation at three antitermination/terminator points in the pyr mRNA by binding to the 5' end of an antitermination stem-loop structure, which permits the formation of the downstream factor-independent transcription terminator stem-loop.

Transcription is thus converted from a readthrough mode with expression of the downstream biosynthetic genes, to a termination mode with reduced expression of the downstream genes. An approximately 50-nucleotide conserved sequence has been identified as the PyrR binding site to the pyr mRNA. While PyrR displays no recognized RNA-binding sequence motif, it contains a short sequence that is characteristic of PRPP binding enzymes, and is a uracil phosphoribosyltransferase. The relevance of this enzymatic activity to transcriptional attenuation is as yet unproven.

Structures of PyrR in two oligomerization states will be presented. A dimeric form of the enzyme was obtained as a Sm3+ cosubstrate. The structure was solved via MAD from data collected at energies around the LII edge of Sm on beamline 19 at the ESRF. Initial phasing was via the program MLPHARE and the atomic model was refined to 1.6 Å. The physiologically relevant hexameric form of PyrR crystallized in the space group R32 (dmin of 2.3 Å) and was solved via molecular replacement. The structure of a Mg2+/UMP complex of PyrR will also be presented.

An analysis of the potential RNA-binding site(s) of PyrR and mechanism of transcriptional attenuation will be presented, as well as a comparison of the enzyme to other phosphoribosyltransferase structures.

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MS04.06.07 U1A SPLICEOSOMAL PROTEIN BINDS TO TWO DIFFERENT DNA TARGETS USING THE SAME STRATEGY

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U1A spliceosomal protein binds to hairpin II of U1 small nuclear RNA and, together with other proteins, forms the U1 snRNP essential in pre-mRNA splicing. It also binds to the 3' untranslated region (3' UTR) of its pre-mRNA and controls its own production through inhibition of polyadenylation at the 3' end of mRNA. The crystal structure of U1A protein bound to a 21 nucleotide RNA hairpin, representing its binding site in U1 snRNP, was solved at 1.92 Å resolution using a single isomorphous derivative. The AUUGAC sequence within the ten nucleotide loop fits tightly into the groove on the surface of the protein and the bases of the heptanucleotide are splayed out. The bases of the heptanucleotide and the C/G base pair, which closes the loop, stack onto an aromatic protein side chain, an adjacent base or both. These bases also form an extensive hydrogen bond network with protein side chains, main chain amide and carbonyl groups. Bases of the last three nucleotide in the loop have no apparent interaction with the protein.

The 3' UTR of U1A protein mRNA folds into an evolutionarily conserved secondary structure with two internal loops containing the sequence AUUGAC, found in hairpin II of U1 snRNA, and its variant AUUG/AC. The C/G base pair is also found at the equivalent positions in the 3' UTR binding site. The conservation of the heptanucleotide and the C/G base pair strongly suggests that they form identical protein contacts in the 3' UTR complex. Based on this assumption and the 2-fold symmetry in the 3' UTR binding site we have been able to model of the 3' UTR complex in which two molecules of U1A protein form a dimer.

U2B" protein, a component of U2 snRNP, shares a high sequence homology with U1A protein and binds to hairpin IV of U2 snRNA only when it is complexed with U2A' protein which contains the Leu-rich sequence repeats. We have been able to grow crystals of a ternary complex between U2B'/U2A' proteins and the cognate binding site and its crystallographic analysis is underway. This structure will reveal how U1A and U2B" proteins bind their cognate binding sites.

(2) Jovine, L. et al. Structure in press

PS04.06.08 CRYSTAL STRUCTURES OF SIGNAL RECOGNITION PARTICLE (SRP) SRP PROTEIN AND SRP0149/FUSION PROTEIN

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The mammalian Signal Recognition Particle (SRP) is a cytoplasmic ribonucleoprotein particle (RNP) that plays an essential role in the targeting of secretory and membrane proteins to the rough endoplasmic reticulum (RER). Targeting occurs co-translationally and translocation across the RER membrane begins before polypeptide synthesis is complete.

The mammalian SRP is an 11S cytoplasmic RNP which consists of six polypeptides (SRP9, SRP14, SRP19, SRP54, SRP68, SRP72) and a single RNA molecule.

SRP9 protein has been crystallized in the point group P6222 with cell parameters a=b=64.0 Å, c=110.5 Å. Using synchrotron radiation on single flash-frozen crystals, a complete data set showing diffraction beyond 2.3 Å resolution with a Rsym on intensities of 4.5% was collected. MAD data at four wavelengths was collected and the cognate binding site and its crystallographic analysis is underway.

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PS04.06.09 CRYSTALLOGRAPHY OF BIOLOGICAL MACROMOLECULES