the protein-ligand complex and collected data set at resolution of 3 Å, structure solution and refinement is on the way. Based on the structure further biochemistry experiments were carried out to identify the cause of the retinal degenerative disorders by mutation of CRALBP.

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Keywords: vitamin A; crystal structure; retinitis pigmentosa

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Conserved Binding Mode of Single-Stranded DNA and RNA to Cold-Shock Domains. Udo Heinemann[a], Klaas E. A. Max[a]. [a]*Max-Delbrueck Center for Molecular Medicine, Berlin, Germany.*
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Cold-shock domains occur ubiquitously in proteins from all kingdoms of life. They occur in proteins that function in transcriptional and/or translational control of gene expression. Bacterial cold-shock domains are autonomous, small proteins, whereas their eukaryal orthologs usually occur as structural units in larger proteins. Some, but not all bacterial cold-shock proteins are upregulated under cold-shock conditions and are thought to mediate cold-stress-response functions.
Already the first crystal structure of a bacterial cold-shock protein suggested a possible mode of DNA or RNA single-strand binding to a basic protein surface with conspicuously exposed aromatic side chains [1]. It was not until recently, however, that this binding mode was proven by crystal structure analysis of oligothymidine strands bound to the major cold shock proteins *Bs*-CspB of *Bacillus subtilis* and *Bc*-Csp of *Bacillus caldolyticus* [2, 3]. These structures identified seven subsites for nucleotide binding and, combined with fluorescence-based DNA binding studies, suggested the consensus sequence NTCTTTN (N = any nucleotide) for DNA binding to the *Bacillus* cold-shock proteins. This consensus was confirmed by DNA microarray studies [4].
The crystal structure of the *Bc*-Csp:dT_7 complex showed a domain-swapped dimeric structure of the cold-shock domain [3]. Domain swapping has never been observed before in a series of crystal structures of bacterial cold-shock proteins [5-9] and thus extends the range of structural polymorphs populated by cold-shock domains.
Recently, we extended the structural characterization of cold-shock domains by studying the binding of ribooligonucleotides to cold-shock domains from human Y-box factors by fluorescence-based assays and crystal structure analysis. We find a conservation of the general binding mode observed before, but there is significant variation in subsite interactions which may be functionally relevant.

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Decoding the Structural Basis for the *cis*-Regulatory Logic of Early Developmental Switches. Ralf Jauch[a], Andrew Hutchins[a], Nithya Baburajendran[a], Kamesh Narasimhan[a], Calista KL Ng[a], Prasanna Kolatkar[a]. [a]*Stem Cell Biology, Genome Institute of Singapore.*
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The basis for differential gene regulation is the selective recognition of /cis/-regulatory DNA sequences by sequence-specific transcription factors (TFs).TF binding sites (TFBS), however, are short, degenerate and have strong affinities for highly homologous yet functionally antagonistic proteins. Also, genome-wide TFBS mapping studies in embryonic stem cells and other tissues showed that key regulators such as Nanog, Sox2/17, Oct4 and Smad1 co-occupy thousands of binding sites and gene activity prediction based on such data is poor. How then are gene expression programs executed and how are cell fate decisions made? We use genome wide TFBS datasets to retrieve candidate motifs that may lead to the differential assembly of TFs and thereby act as, developmental enhancer'. By using biochemical and biophysical assays as well as by determining crystal structures of protein-DNA complexes we study the basis for TF function and assess contributions of individual sequence specificities, TF induced DNA deformations and co-factor recruitment. I will present structural and biochemical data of proteins from the Sox and Smad families that provide a mechanistic perspective on the decision making during the earliest stages of mammalian development.

Keywords: transcription; protein-DNA; gnomics