Structural studies of a nucleosome remodeling factor

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Nucleosome remodeling factors confer dynamic properties to chromatin and render nucleosomal DNA accessible for interacting factors. The presence of the ATPase ISWI characterizes one subgroup of remodeling complexes, which comprises the remodeling complexes NURF, ACF and CHRAC [1]. We are focusing on the structural analysis of the *Drosophila* CHRAC complex which consists of the two large subunits ACF1 and ISWI and the two smaller subunits CHRAC-16 and CHRAC-14.

The ISWI ATPase forms the enzymatic core of the CHRAC complex. ISWI belongs to the SWI2/SNF2 subfamily of DEAD/H helicases and contains two SANT related modules at its C-terminal end. We have crystallized a 300 amino acid residues C-terminal fragment of ISWI (ISWI-C), solved the structure using selenomethionine substituted protein at ESRF beamlines and refined it using data at 1.9 Å resolution [2]. The crystal structure consists of three domains: a four-helix-domain with a novel fold named HAND and the two α-helical domains SANT and SLIDE (SANT-like domain) which are linked by a long spacer helix. SANT and SLIDE domains are both structurally related to the DNA-binding modules of the transcription factor c-Myc. However, a more detailed structural and functional analysis suggests that only the SLIDE domain interacts with nucleosomal DNA.
Based on our analysis and taking into account the overall shape of ISWI-C we will discuss a model how ISWI-C might interact with nucleosomal substrates.

References

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