Poster Presentation

MS93.P01

Structural studies of Mot1 and NC2 in transcription initiation process

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Regulation of protein—nucleic acid interactions plays a key role in various cellular processes. The SNF2/SWI2 protein family forms a large and diverse class of proteins and multiprotein assemblies, which use energy derived from ATP hydrolysis to disrupt or modify protein-DNA interactions. They possess a conserved helicase-like domain accompanied by protein-specific targeting and regulation regions. The SNF2/SWI2 family member Mot1 (Modifier of transcription 1, also known as BTAF1) is a single polypeptide ATP-dependent remodeler. Mot1 acts directly on TBP (TATA-box binding protein) regulating RNA polymerase II preinitiation complex formation in the first stages. Global distribution of TBP on promoter regions is also modulated by NC2 (Negative Cofactor 2). It has been suggested that Mot1 and NC2 can co occupy the same promoter sites influencing the assembly of the transcription machinery simultaneously. Our understanding of the molecular mechanism of SWI2/SNF2 family ATPases is very limited. Previously, we have reported the crystal structure of the complex of Encephalitozoon cuniculi N terminal domain of Mot1 (Mot1NTD) with its substrate, TBP [1]. Here we present the crystal structure of the TBP NC2 Mot1NTD complex bound to a promoter DNA fragment at 3.9Å resolution. In our studies we have applied a combined structural biology approach using crystallography, electron microscopy reconstructions and chemical cross-linking. We probed the conformational changes of the complex during the ATP hydrolysis cycle and unveiled the structural basis of the Mot1—NC2 interplay. Our findings greatly contribute not only to our limited understanding of Mot1 action, but all SNF2/SWI2 family remodeling enzymes.

[1] *P. Wollmann, S. Cui, et al, Nature, 2011, 475, 403-407*

Keywords: transcription, SNF2/SWI2