REGIONAL CENTRE FOR BIOTECHNOLOGY
Seminar series

Regulation of Transcription Initiation in Prokaryotes: Structures and Mechanisms

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Wednesday, June 19, 2013
11:00 am
Seminar Room

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Abstract

The ability to perceive stimulus and respond appropriately is the hallmark of any living organism. In many instances, such responses are regulated through modulation of transcription of appropriate genes in response to physiological and environmental stimuli. A key strategy utilized by bacteria to regulate transcription is through the use of modulators that can positively (activators) or negatively (repressors) affect transcription. The tetrameric activator cII from bacteriophage lambda has been used as a model system to study transcription activation in prokaryotes. cII activates transcription from three phage promoters P(RE), P(I), and P(AQ) by binding to two direct repeats that flank the promoter -35 element. I will present the crystal structures of activator alone (2.8Å) and in complex with its DNA operator P(RE) (1.7Å) and RNAP subunits (2.3Å) which point to the key role for the alpha-subunit C-terminal domain of RNAP in cII dependent activation.

The repressors on the other hand bind to operator sites that are overlapping with the promoter and thereby occlude the binding of RNAP to DNA. AraR, is a repressor (*Bacillus subtilis*) of genes associated with arabinose metabolism. It binds to eight different operators present in five promoters with distinct affinities through a DNA binding domain at the N-terminus. I will present high resolution crystal structures of the DNA binding domain of the AraR in complex with four different natural operators. The study reveals the diverse structural strategies utilized by this repressor to achieve specific binding to different operators. This observed plasticity probably allows optimal calibration of repression of different genes in the regulatory circuit involving AraR.