Structural basis for bacterial transcription activation

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Abstract

For most genes in most bacteria, the key regulatory step that modulates gene expression seems to be mediated by transcription factors (TFs), initiation σ factors, and RNA polymerase. The activating TFs increase gene expression by making direct interactions with promoter DNA, initiation σ factors, and/or RNAP. However, the underlying structural basis and molecular mechanism are largely unknow. We have solved cryo-EM structures of transcription activation complexes comprising bacterial RNA polymerase, initiation σ factors, promoter DNA, and three representative activating TFs. The structures visualize the global architecture of transcription machinery and TFs engaged with promoter DNA, and provide structural basis for understanding bacterial transcription activation.

Brief Biography

Yu Zhang is a principal investigator in Key laboratory of Synthetic Biology, Shanghai Institute of Plant Physiology and Ecology, Chinese Academy of Sciences (SIPPE, CAS). He joined the SIPPE, CAS in 2015 and leads a laboratory studying structural basis and molecular mechanism of bacterial transcription and transcription regulation.

Brief CV

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Education:

- B.S Biology, Fudan University, China, 2000
- Ph.D. Drug design, Shanghai Institute of Materia Medica, CAS, China, 2004

Research Interests:

- 1. Microbial Gene Regulation
- 2. RNA Polymerase Structure-Function
- 3. Discovery of novel bactericidal antibiotics

Selected publications

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