

## **SEMINAR ANNOUNCEMENT**

DATE: 4 April 2012, Wednesday

TIME / VENUE: 11:00AM @ Level 3, IMCB Seminar Room 3-46, Proteos, Biopolis

SPEAKER: Dr. Yonggui Gao

TITLE OF SEMINAR: Protein translation and bacterial cellulose biosynthesis



Understanding the detailed structure and function of ribosome is important not only as a fundamental issue in life science, but also because many clinically relevant antibiotics target the ribosome. The guanosine triphosphatase (GTPase) factors, IF2, EF-Tu/G, and RF3, catalyze all major steps of translation by bacterialribosome in a GTP-dependent manner. Ribosomal complexes with GTPase factorshave proven to be difficult to crystallize, and the reason was unraveled to be the structural clash of ribosomal protein L9 with factor binding in all published ribosome crystal forms. Recently, we succeeded in discovering a novel crystal form obtained from ribosome lacking L9, with which the structures of both EF-Tu/G bound to ribosome have been solved, providing insight into themechanism of decoding and translocation, as well as the mechanism of fusidic acid as an effective medicine. Moreover, the first structure of ribosome with a cognate tRNA in the E-site obtained by addition of EF-G and fusidic acid sheds light on the allosteric coupling of the A and E sites.

Cellulose, a linear homopolymer of D-glucopyranose linked by ß-1,4-glycosidic bond, is an abundant polysaccharide in nature, and over half of the total organic carbon in the earth's biosphere is in cellulose. As a kind of reproducible and biodegradable raw material, cellulose is widely used in industry. In contrast to the biological and commercial importance of cellulose, the mechanism of biosynthesis and regulation remains largely unknown due to the lack of the structure of individual subunit and the entire terminal complex. In this talk, I will be presenting our recent structure of one subunit of bacterial cellulose synthesizing complex, which provides the first basis for understanding of cellulose synthesis at atomic level, as well as nicely exemplifies the power of structural information in unraveling the functionality of a subunit of enzyme complex.

Host: Prof. Wanjin Hong