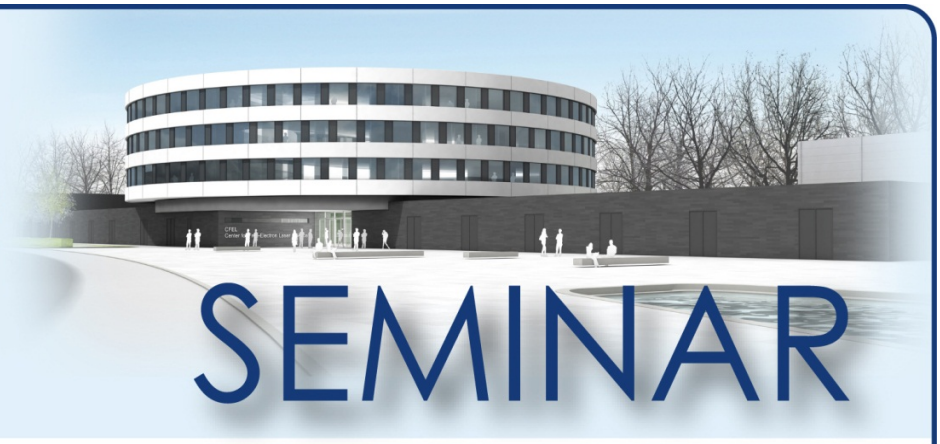
CFEL SCIENCE



SEMINAR

08th May 2012 - 11:00 am

DESY building 28c – FLASH Hall, seminar room

Holger Stark

Max Planck Institute for Biophysical Chemistry, Göttingen

Structure Determination of Dynamic Macromolecular Complexes by cryo-EM: The Ribosome in Motion

Macromolecular complexes are at the heart of central regulatory processes of the cell including translation, transcription, splicing, RNA processing, silencing, cell cycle regulation and repair of genes. Detailed understanding of such processes at a molecular level requires structural insights into large macromolecular assemblies consisting of many components such as proteins, RNA and DNA.

Single-particle electron cryomicroscopy is a powerful method for three-dimensional structure determination of macromolecular assemblies involved in these essential cellular processes. It is very often the only available technique to determine the 3D structure because of the challenges in purification of complexes in the amounts and quality required for X-ray crystallographic studies.

In recent years it was shown in a number of publications that it is possible to obtain near-atomic resolution structures of large and rigid macromolecules such as icosahedral viruses. Due to a number of methodological advances there are now also great perspectives for high-resolution single particle cryo-EM studies of large and dynamic macromolecules. Successful high-resolution structure determination of dynamic complexes requires new biochemical purification strategies and protocols as well as state of the art electron microscopes and high-performance computing. In the future cryo-EM will thus be able to provide structures at near-atomic resolution and information about the dynamic behavior of macromolecules simultaneously.

Host: Henry Chapman - Coherent Imaging Division