Electron cryo-microscopy (cryo-EM) is emerging as a powerful method in determination of 3-D structure of large macromolecular machines and nano-particles. In contrast to crystallography, cryo-EM does not require diffracting crystals which are often difficult to obtain especially for large assemblies. Instead, cryo-EM can image directly particles frozen at random views in physiologically relevant buffer solution. A high resolution 3-D structure can be subsequently obtained by accurate determination of the relative views of different particles and then coherent merging of large number of 2-D images into a 3-D density map. The reconstruction is conceptually similar to the computed tomography (CT) is medical imaging. The Jiang group is interested in the technique development of cryo-EM into a high resolution and high throughput method that can be applied to broad range of applications in biology and bionanotechnology. In this presentation, I will overview the field, our recent near-atomic resolution 3-D reconstructions and novel asymmetric reconstructions with emphasis on the computational methods.

Bell Hall 130A
Friday, April 5, 2013, 10:30 AM
Wen Jiang received his B.S. degree in physics from Peking University in 1992, M.S. degree in biophysics from Institute of Biophysics, Chinese Academy of Sciences in 1995, and Ph.D. degree in structural biology in 2001 from Baylor College of Medicine. In 2005, Dr. Jiang became an assistant professor in the Markey Center for Structural Biology, Department of Biological Sciences, Purdue University. His group works on technique development of cryo-EM in the areas of sample preparation, imaging automation, image processing algorithm, and high throughput computing. His group also uses the cryo-EM technique to understand the structural basis of viral particle assembly, maturation, and genome packaging.

Selected publications relevant to the presentation