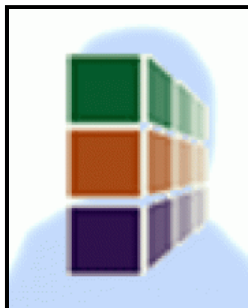




## Events

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## Special Guest Lectures

**Ligand Homology Modeling as a new computational platform to support modern drug discovery****Michal Brylinski, Georgia Institute of Technology, Atlanta**

Research Scientist II, Center for the Study of Systems Biology

Johnston Hall 338  
May 10, 2011 - 10:00 am**Abstract:**

As an integral part of drug development, high-throughput virtual screening is a widely used tool that could in principle significantly reduce the cost and time needed to discover new pharmaceuticals. In practice, virtual screening algorithms suffer from a number of limitations and the development of new methodologies is required. In this talk, I will discuss the ideas of Ligand Homology Modeling (LHM), which is likely one of the first approaches in Cheminformatics that successfully extends template-based techniques, commonly used in proteins structure prediction, to the modeling of protein-ligand interactions. Our intensive research in this field culminated in the development of a novel virtual screening approach, which appears as a powerful compound prioritization technique applicable to the early stages of proteome-scale drug design projects. As an example, I will describe the application of LHM to all kinase domains in humans, which has provided the scientific community with a very extensive structural and functional characterization of the human kinome to support the discovery of novel kinase inhibitors.

**Speaker's Bio:**

Michal Brylinski currently works at the Center for the Study of Systems Biology, Georgia Institute of Technology, as a senior research scientist. Brylinski received his Ph.D. in Chemistry from Jagiellonian University, Krakow, Poland (2006); and his M.S. in Pharmacy from Wroclaw Medical University, Poland (2000). His research interests are: systems biology, chemical systems biology and cheminformatics; drug discovery and design; low-resolution ligand docking; ligand comparative modeling; protein function inference; protein structure prediction; protein evolution; and engineering and simulation of life.

