

重庆大学药学院

新药论坛

学术报告第一百七十三讲

报告题目：用于生物研究的超级计算机机器学习

报告人：Igor F. Tsigelny 教授（加州大学圣地亚哥分校）

时 间：2019年11月9日（周六）14:30

地 点：重庆大学药学院学术报告厅

报告人简介：

Igor F. Tsigelny is a Research Professor at the Department of Neurosciences, San Diego Supercomputer Center, and Moores Cancer Center. He is a world-known expert in structural biology, molecular modeling, bioinformatics, and structure-based drug design. He received his Ph. D. in Physics of Polymers from the Academy of Sciences of Ukraine, and was a postdoctoral fellow in the University of California from 1992-1995. Dr. Tsigelny has published over 200 papers, edited 4 scientific books, and applied 15 patents. The book “Protein Structure Prediction: Bioinformatic Approach” that he edited, has been called “The Bible of all current prediction techniques” by BioPlanet Bioinformatics Forums. Three drug-candidates developed by Dr. Tsigelny are licensed by UCSD to pharmaceutical companies and are in various stages of development.