Tentative Outline
Special Issue for CURRENT PROTEIN & PEPTIDE SCIENCE
Guest Editor: Xing Chen

Aims & Scope:

Identifying drug–target interactions based on heterogeneous biological data is critical not only for better understanding of the various interactions and biological processes, but also for the development of novel drugs and improvement of human medicines. There are about 6000–8000 targets of pharmacological interest in the human genome, but only a small number of them have been identified to be related to approved drugs so far. In the past, drug research followed the one-disease, one-target, one-drug paradigm which hasn't accelerated the discovery of drugs as expected, since multiple targets are often involved in the same disease. Recently, much attention has been paid to the development of multiple-target drugs in order to increase the drug efficacy and overcome drug resistance. As is well-known, the experimental determination of drug–target interactions is still time-consuming, expensive, and limited to small-scale research. Computational methods can provide new predictions for experimental scientists and narrow the scope of candidate targets to accelerate drug discovery. Therefore, there is a strong incentive to develop powerful computational methods that are capable of detecting potential drug–protein interactions effectively in a genome-wide way. For the potential drug-target interactions with high predictive scores, biological experiments were implemented for validation. The scope of special issue include: drug target interactions prediction method (specially, manuscripts with biological experiments validation are encouraged), reviews about computational models and (or) experimental methods of drug target interactions and related problems.

Schedule:

Manuscript submission deadline: April 30, 2015
Peer Review Due: June 31, 2015
Revision Due: July 31, 2015
Notification of acceptance by the Guest Editor: August 5, 2015
Final manuscripts due: August 10, 2015