



BioMed Research International

Special Issue on  
**Network Proteomics: From Protein Structure to  
Protein-Protein Interaction**

CALL FOR PAPERS

With the emergence of high-throughput “omics” data, network theory is being increasingly used to analyze biomolecular systems. Combined with traditional computational methods, such as molecular dynamics (MD) simulation and normal mode analysis (NMA), the representation of proteins as amino acid networks provides an effective method to quantitatively investigate protein structures through network descriptors, as well as studying allostery in proteins in terms of pathway analysis. Accordingly, network languages decipher new information in the paradigm from structure to function. In fact, proteins, as the basic units for biological functions, rarely act alone, which prompted the arrival of proteomics. “Network proteomics” is just defined as the research area that introduce network theory to investigate biological networks ranging from protein structure networks to protein interaction networks, including protein-protein and protein-DNA/RNA interactions. This area lies somewhere between structural biology and systems biology, which can be rapidly moving towards full biological network analysis. In addition, the application of network proteomics in biomedical fields has increased significantly. For example, the study of allosteric sites and hotspots could help us to understand molecular mechanisms of various diseases, as well as providing putative new therapeutic targets.

This special issue intends to collect contributions, not only focusing on the state of the art of methodology in “network proteomics” itself, but also focusing on the current status and future direction of their applications in translational medical informatics.

Potential topics include, but are not limited to:

- ▶ Advances in amino acid network (or protein contact network, protein structure network, and residue interaction network)
- ▶ Elastic network model for proteins
- ▶ Dynamic network analysis for proteins
- ▶ Protein-protein interaction network and disease
- ▶ Biological networks analysis (i.e., transcriptional networks and metabolic networks)
- ▶ Network-based drug design
- ▶ Network biomarkers in proteomics

Authors can submit their manuscripts via the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/computational.biology/pspp/>.

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