Aims & Scope: 
During the past decades, computational method has become an important strategy in the understand and study of biological sciences. With the more and more proteomics data generation, it is urgent to develop and apply various computational resources and methods to handle these protein data. We invite authors to contribute review articles and research papers on computational resources and methods for all aspects of protein structure and function studies. The special issue aims to provide an open, multidisciplinary forum for protein databases, web services, standalone programs, relevant algorithms and methods for data mining and knowledge discovery in proteins. Potential topics include the development and application of computational resources and methods to proteomics data.

Keywords: Recombinant proteins, pharmaceutical proteins, chloroplasts, edible.

Subtopics: 
The subtopics to be covered within this issue are listed below:

- The development and application of computational method for protein function and function prediction
- Feature selection technique to improve prediction accuracy of computational method
- New biological database or lasting database with substantial updates for proteomics analysis
- The comparison of prediction performance among different computational methods
- New web services or existing web services with substantial updates for proteomics analysis
- New or better standalone biological programs and tools for proteomics analysis

Schedule: 
- Manuscript submission deadline: February 2019
- Peer Review Due: May 2019
- Revision Due: June 2019
- Announcement of acceptance by the Guest Editors: July 2019
- Final manuscripts due: September 2019

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