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# Predicting Drug Targets Using Bioinformatics Methods

Guest Editor:

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## Message from the Guest Editor

Dear Colleagues,

The function of protein molecules is influenced by their structure and participation in various aspects of life activities. The emergence of a series of bioinformatics methods such as AlphaFold has improved the efficiency of protein structure analysis and functional annotation. Bioinformatics methods and tools are accelerating the development of proteomics and pharmacomics. In addition, the function of protein molecules can also affect their networks, including protein–protein interaction networks, drug–protein interactions, DNA–protein interactions, and non-coding RNA–protein interactions. A protein's function and its network complement each other in analyzing, predicting, and guiding experiments. This Special Issue focuses on analyzing and predicting the function and network of protein molecules using bioinformatics methods. The relevant content includes, but is not limited to:

- Protein–protein interaction recognition and analysis;
- Identification and analysis of drug–protein interactions;
- RNA/DNA–protein interaction analysis;
- Identification and analysis of protein structure and function.