Special Issue

Novel Approaches in Protein Structure Prediction

Message from the Guest Editors

Computer modeling of the structure of biological macromolecules, especially proteins, is growing in importance. Knowledge of the structure and motions characteristics of these molecules is a necessary condition to learn about their functions and malfunctioning and, consequently, to design effective drugs and therapies against such lethal diseases as, e.g., cancer and neurodegenerative diseases. With thousands of new protein sequences discovered every year, experimental methods of structure determination are insufficient and theoretical methods for protein–structure predictions have become one of the pillars of structural biology. This Special Issue will comprise papers about state-of-the art methods for the prediction of protein structures, such as comparative modeling, fragment assembly, threading, and physics-based methods, as well as combinations of these methods. Prediction of disordered regions of proteins and prediction assisted by sparse NMR, SAXS, and cryomicroscopy data, as well as prediction assisted by residue-residue contacts will also be addressed.
Sincerely, Prof. Adam Liwo

Guest Editors

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Deadline for manuscript submissions

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

Editor-in-Chief

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