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Novel Approaches in Protein Structure Prediction

Guest Editors:

Prof. Dr. Jozef Adam Liwo

Faculty of Chemistry, University
of Gdansk, 80-308 Gdansk,
Poland

Prof. Dr. Cezary Czaplewski

Department of Theoretical
Chemistry, Faculty of Chemistry,
University of Gdańsk, 80-308
Gdańsk, Poland

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Message from the Guest Editors

Dear Colleagues,

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

Prof. Cezary Czaplewski

Guest Editors



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Special Issue



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Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan

Department of Pathology, The
University of Alabama at
Birmingham, 1825 University
Blvd, SHEL 814, Birmingham, AL
35294-2182, USA

Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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Genes Editorial Office
MDPI, St. Alban-Anlage 66
4052 Basel, Switzerland

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