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Computational Antibody and Antigen Design

Collection Editor:

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Message from the Collection Editor

Using computational modeling to help antibody engineering is complementary to traditional animal models and phage display methodologies, hopefully speeding up and providing additional variations into antibody design. Starting from antibody/antigen sequences, one can model the structures of antibody and antigen, predict antibody–antigen interactions through docking and/or molecular dynamics simulations, and provide computationally designed/optimized systems for experimental verification. In vaccine design, computational modeling can generate small and stable protein scaffolds, mimicking antigen epitopes to induce potent neutralizing antibodies. Even with this promising power, widely-integrated application of computational modeling in antibody engineering is still yet to arrive. This Special Issue will showcase various aspects of computational antibody and antigen design.

This Special Issue of Antibodies focuses on: (1) computational/structural characterization of antibody structures; (2) bioinformatics study of antibody and antigens; (3) computational algorithms in antibody and antigen design; and (4) applications of computational methods in antibody/antigen development.

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Message from the Editor-in-Chief

Antibodies is a relatively new journal with a major focus on quick dissemination of knowledge related to antibodies, especially how to quickly translate basic research results to therapeutic applications. Because it covers all areas related to antibodies unexpected connections between different areas could be made, leading to major discoveries and opening new fields of research and development. This is enhanced by the large readership of the many antibody-related areas of research. A specific priority area is human monoclonal antibodies for therapy of diseases and aging.

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