



Special issue: Biomolecular Modelling and Simulation

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Computational biomolecular simulation has been demonstrating its value to study the insights of a range of different systems of biotechnological and biomedical interest. The application of molecular modelling methods to address a wide array of topics ranging from viruses to prokaryotes and eukaryotes were collected in this special issue. The use of sequence alignment, phylogenetic analysis, protein structure modelling, virtual drug screening, molecular docking, and molecular dynamics simulation with different algorithms is widely demonstrated. These methods enabled the elucidation and identification of evolutionary relationships, biomolecular conformation/folding, protein–ligand/protein interactions, inhibitor, and vaccine design. The new knowledge generated with the integration of experimental data will be

useful to further rapidly increase the development of biomolecular simulation in the future.

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