



Atomistic and Coarse-Grained Simulations in Biological Systems

Guest Editor:

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Deadline for manuscript
submissions:

closed (24 June 2019)

Message from the Guest Editor

Dear colleagues,

Classical molecular dynamics (MD) simulation of proteins has emerged as a complementary tool to experiments. Its appeal to fully describe biomolecular structures and dynamics at an atomistic level, combined with advancements in computer hardware and algorithms, have led to an ever-growing interest in simulations of increasing size and length.

As an expert in this field, we are very pleased to invite you to submit original papers, communications, and reviews for this Special Issue of *IJMS*, an MDPI open-access journal (IF 3.687). We have fixed a deadline for June 2019.

Thank you for your time and consideration, we look forward to hearing from you and receiving your contribution to this Special Issue.





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Message from the Editor-in-Chief

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