



Structure, Function and Dynamics in Proteins 2.0

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Message from the Guest Editor

This Special Issue continues on from the previous edition, “Structure, Function and Dynamics in Proteins”.

The structure–dynamics–function relationship plays crucial roles in the biological function of proteins. High-resolution protein structures can currently be obtained from X-ray crystallography (X-ray), nuclear magnetic resonance (NMR) and cryo-electron microscopy (Cryo-EM) techniques, as well as, under certain conditions, computer molecular modeling. Sometimes, three-dimensional protein structures fail to give a complete understanding of the concerned functional mechanisms. Protein dynamics and conformational transitions, in most biological functions, are the essential link that connects high-resolution structural details with cellular processes ranging from protein folding, enzymatic catalysis to signaling, solute transport and synaptic transmission. Over the last decades, experimental techniques such as NMR relaxation, fluorescence spectroscopy, time-resolved X-ray and molecular dynamics have made substantial progress in providing an accurate description, at an atomic level, of protein dynamics on timescales of nano- and microseconds.





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Message from the Editor-in-Chief

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