



## Protein Structural Landscapes: From Structure to Function through Correlative Structural Biology

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### Message from the Guest Editor

The determination of the structure of proteins is crucial to discover how these biomolecules work. As of today, the most common route for determining a protein structure is to crystallize it and determine its 3D structure from its X-ray diffraction data. Nevertheless, these images of the protein do not fully represent how the protein really looks like, as it is in fact dynamic and more indistinct. Moreover, some proteins are very hard if not impossible to crystallize.

Other methods, such as solution or solid-state NMR, Cryo-EM, ET or MS, give different points of view of proteins at different scales. The integration of the structural data derived from such different technologies helps understand how proteins, protein complexes or whole pathogens interact dynamically with their functional environment. This fundamental understanding will in turn allow to provide new therapeutics to tackle the main challenges of a continuously ageing society, public health and global pandemics.

This [Special Issue](#) will welcome papers dealing with an integration of the abovementioned techniques and showing a synergistic approach to biological problems.





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