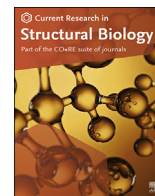


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Current Research in Structural Biology

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Structural biology - Painting the mechanistic landscape of biomolecules

As joint Editors, we are very pleased to present a joint Virtual Special Issue of *Current Research in Structural Biology* (CRSB) and the *Journal of Molecular Biology* (JMB).

JMB was founded in 1959 by Sir John Kendrew and was the first journal devoted to the emerging discipline of molecular biology. From the outset, JMB has published seminal papers that helped build the foundations of structural biology and molecular genetics. The early volumes featured classic articles that exploited the emerging knowledge of proteins and protein structure, such as the 1963 paper by G. N. Ramachandran on the stereochemistry of polypeptide chain configurations (Ramachandran et al., 1963) and the 1965 paper of Monod, Wyman and Changeux on the nature of allosteric transitions (Monod et al. 1965). Ten years later in another highly cited article, on the detection of specific sequences among DNA fragments, E.M. Southern presented the first description of nucleic acid blotting in 1975 (Southern, 1975). The journal has continued over more recent decades to document the dramatic growth of structural biology through advances in X-ray crystallography, NMR, and electron microscopy, and to publish articles that have had major impact, for example, that from the laboratory of David Lipman describing the search algorithm, BLAST, a basic local alignment tool for protein homology (Altschul et al., 1990).

On the other hand, *Current Research in Structural Biology* had a very different and later origin. It developed from the influence and success of the journal, *Current Opinion in Structural Biology*, which focused on reviews. However, this journal frequently received articles that described original research on structural biology, some of them very publishable and interesting. It seemed sensible to develop a further journal in parallel that would publish experimental and computational structural biology research with original research data rather than reviews. This led to the *Current Research in Structural Biology*.

Both Journals reflect the influence that the understanding of structure has had on biochemistry, molecular and cell biology over the years and have reflected the two resolution revolutions, the first in the 1960's using X-rays to define three dimensional structures and the second, more recently, the development of cryo-electron microscopy, a revolution that had been emerging over the previous decades. Although electron microscopes had been available for many years, the recent developments in processing of the data now allow the new cryo-EM instruments,

developed in the early 2000's, to play a huge and impactful role in understanding macromolecular structures and assemblies.

This joint issue of the two Journals reflects these changes not only in experimental methods but also in computational aspects, particularly involving conformational change. These developments were applied not only to protein, DNA and RNA structures, but also to the study of macromolecular assemblies and small-molecule ligand binding, including the conformational changes to allow interactions to develop.

Here we bring together some papers reflecting current developments, apparently a heterogeneous group of papers but nevertheless reflecting the ongoing advances in our understanding of macromolecules and their functions.

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