

Celebrating 20 Years of *Structure*

This issue marks 20 years since the first issue of *Structure* was published, becoming the first journal exclusively devoted to structural biology. The cover of the first issues in 1993 prominently featured the journal's motto: "Form and function in modern biology" (Figure 1). This motto, now printed on the journal's masthead, continues to capture the emphasis *Structure* places on publishing studies that provide critical structural insights into biological function, mechanism, and evolution. The journal was launched in a visionary effort by Wayne A. Hendrickson and Carl-Ivar Brändén, who served as its editors and later joined by Alan Fersht. This editorial team led the journal for a number of years and through several major changes. In 1998, another journal, *Folding and Design*, was integrated into *Structure*, and for the next couple of years the journal was entitled *Structure with Folding and Design*. In the early 2000s, *Structure with Folding and Design* became part of Cell Press as *Structure*, reinstating the original name of the journal. In 2003, Andrej Sali, Christopher D. Lima, and Jody Puglisi were recruited as scientific editors for *Structure*, reinforcing Cell Press' strong position that editorial decisions for the journal should be influenced by academic scientists whose areas of expertise span a broad swath of structural biology. Lima and Sali remain with the journal 10 years later.

This Special Anniversary Issue was commissioned to celebrate the 20 year milestone by featuring commentaries, perspectives, and reviews on a variety of topics that reflect the growing diversity within the field. In their commentary, Seth Cooper, Firas Khatib, and David Baker introduce the idea of citizen science and outline why structural biology might benefit from embracing crowdsourcing approaches (Cooper et al., 1482). Helen Berman et al. (pp. 1485) provide historical perspective on the Protein Data Bank (PDB) and how the community transformed it into its current role as a central resource and advocate for structural biology. Maya Topf and colleagues highlight recent advances in computational methods that improve the ability to interpret and integrate different structural biology techniques, leading to improved analysis of macromolecular assemblies (Thalassinos et al., 1500). Julie Forman-Kay and Tanja Mittag (pp. 1492) offer their perspective on intrinsically disordered proteins and their important contributions to complex biological functions. Allosteric conformational barcodes is the idea put forward by Ruth Nussinov and colleagues in a review that formalizes thinking about populations of protein conformational states and their functional roles (Nussinov et al., 1509). In their review, Julien Marcoux and Carol Robinson (pp. 1541) reflect on the two decades of structural biology in gas phase and use some recent examples to highlight the strengths of mass spectrometry (MS) as a tool of structural biology. Recent developments in cryoelectron tomography (cryo-ET) take center stage in the review by Jan Harapin, Matthias Eibauer and Ohad Medalia that highlights current opportunities and limitations of applying cryo-ET to vitrified cells and tissues (Harapin et al., pp. 1522). Torsten Schwede (pp. 1531) provides a review of methods for predicting 3D molecular structure and discusses how computational modeling is shifting from smaller systems to macromolecular assemblies. Finally, Wolfgang Baumeister, Friedrich Förster, and colleagues

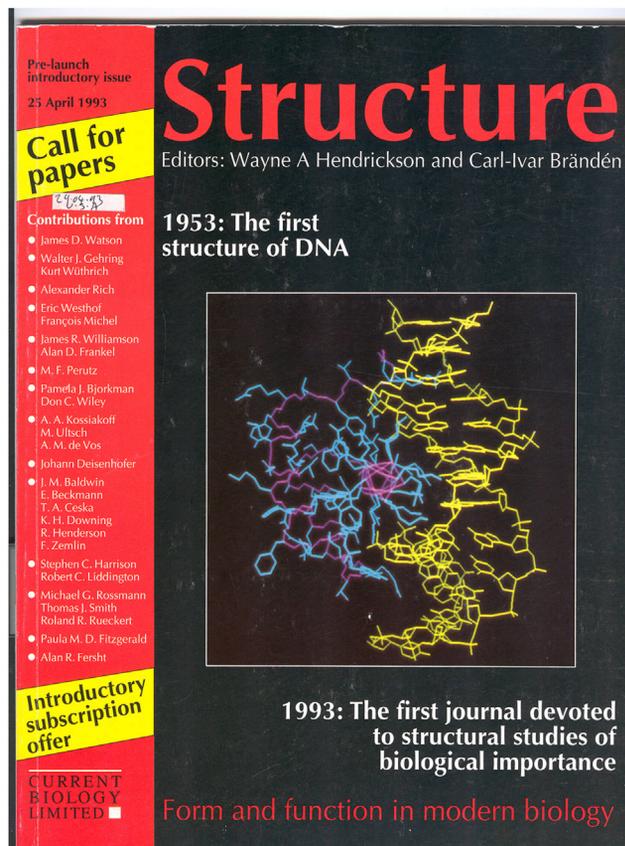


Figure 1. Cover of the Prelaunch Introductory Issue of *Structure*
The cover highlights the ongoing focus of the journal on providing a home to articles describing exciting structural insights that further understanding of modern biology. Currently, the journal has evolved to include analysis of high relevance for basic science, as well as biotechnology and translational sciences.

review exciting breakthroughs in structural studies of the 26S proteasome, a large macromolecular complex, by focusing on integrative approaches to tackle analysis of this system (Förster et al., pp. 1551).

Structure has made several changes over the last year with the aim to better serve the community. Last summer, we introduced Short Articles that focus on exciting structural observations that make a discrete point of strong general significance. We transitioned to a continuous publication model and now publish all accepted articles online ahead of print, which significantly decreased the time between acceptance and publication to 5 weeks on the average. We joined Twitter (@Structure_CP) to share information and to build a strong structural biology community in this type of social media. This summer witnessed publication of the first "The Best of *Structure*" collection, which features a selection of 2012 articles that elicited the highest attention of our readers. Access to this digital collection is free and we encourage everyone to take a look (<http://onlinedigeditions.com/publication/frame.php?i=167133&p=&pn=&ver=flex>). Finally,

looking to the future, we plan to retire Ways & Means and Technical Advances in January 2014 and replace them with a new article format, Resources, that will mirror similar formats in the other Cell Press journals. The Resource articles will highlight significant technical advances and/or major databases that are of value and interest to the broad structural biology community.

The journal and its editors remain focused on publishing exciting structural biology reports, irrespective of the method used. As structural biology has evolved over the past two decades, *Structure*, too, has evolved with the field and is now

home for a variety of reports that illuminate biology through application of X-ray crystallography, nuclear magnetic resonance (NMR) spectroscopy, electron microscopy (EM), MS, small angle scattering, computational biology, single molecule studies, and integrative structural biology, to name just a few approaches. We expect the commitment to all facets of structural biology to remain a cornerstone of the journal for years to come. We look forward to the future, fulfilling our mission to support structural biology as it continues to provide critical contributions to basic science, biotechnology, and translational sciences.

Christopher D. Lima, Editor

Andrej Sali, Editor

Milka Kostic, Senior Editor

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