

# nature Structural biology

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*molecular form & function*

## Recalling and foretelling

The editors of *Nature Structural Biology* spent the last half of 1999 actively seeking to broaden the content of the journal. This was a fitting goodbye to a century (and a millennium) that saw the extraordinary accumulation of scientific knowledge, resulting at first in the establishment of numerous subfields of biological research (such as molecular biology, structural biology, cellular biology, and biochemistry) and eventually in the blurring of the lines between these disciplines. Our specific goal for *Nature Structural Biology* has been to attract more biochemical, molecular, and cellular biology studies into the journal, to increase the variety of research presented, making the content more representative of the types of research that yield structural information, both directly and indirectly<sup>1,2</sup>.

Reaching this goal depends on many factors, including spreading the word of the journal's expanding scope, attracting high quality submissions, maintaining or increasing standards for publication, and continuing a strong commitment to our core content of high resolution structures and protein folding. Have we begun to see results from our efforts? The answer is an unqualified yes. To be able to mark the beginnings of success after only six months of focused activity underscores the growing importance of structural research to a wider audience, a trend that is also illustrated by the rising impact factor of *Nature Structural Biology*<sup>3</sup>.

### Looking back: spreading the word and initial results

*Nature Structural Biology* — along with the field of structural biology itself — has been evolving. Scientists interested in structural questions are now routinely using a battery of diverse techniques, not just X-ray crystallography and NMR spectroscopy, to address a wide range of biological problems. This change in the research environment is a logical progression and clearly reflects the interests of readers and authors of papers in the journal. Approximately six months ago, our efforts to inform the community of the broad editorial scope of *Nature Structural Biology* increased significantly<sup>2</sup>. We began to actively encourage the submission of research studies that use biochemistry and molecular biology either to pose interesting structural questions or to address important issues raised by available structures. Our efforts included posting 'call for papers in biochemistry and molecular biology' notices, maintaining a special section of the web site to explain the journal's evolution ([http://structbio.nature.com/nsb\\_evolution/](http://structbio.nature.com/nsb_evolution/)), and communicating our intentions person to person. As a result, the number of molecular, biochemical, cellular, and biophysical studies submitted to *Nature Structural Biology*, and reaching the printed pages of the journal, has certainly increased. At the same time, we have continued to welcome a healthy stream of high quality structural determinations and protein folding studies.

Importantly, all of the work appearing in *Nature Structural Biology* has fallen, and will continue to fall, under the umbrella term 'structural biology' — interpreted as research on the molecular form and function of biomolecules. In the last six months of 1999, we published high quality papers with structural relevance in every key area of our scope (high-resolution structural determinations, molecular and biochemical research into cellular processes, and protein folding studies) and saw several fields grow in prominence. High-resolution X-ray crystal and NMR studies included structures of the cricket paralysis virus<sup>4</sup>, plant chalcone synthase<sup>5</sup>, human heme oxygenase<sup>6</sup>, a DNA Holliday junction<sup>7</sup>, pyruvate formate-lyase<sup>8</sup>, a single strand break repair protein<sup>9</sup>, and the ribosomal L30-RNA complex<sup>10</sup>. In addition, molec-

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ular biology and biochemical studies provided indirect structural insight into many biological processes, including regulation of Src<sup>11</sup>, autoprocessing of HIV-1 protease<sup>12</sup>, selection of HIV-1 cell entry inhibitors<sup>13</sup>, *in vitro* evolution of allosteric ribozymes<sup>14</sup>, atomic force microscopy studies of protein folding<sup>15</sup>, structure-function analysis of potassium channels<sup>16</sup>, and the import of proteins into mitochondria<sup>17</sup>. Protein folding research has also continued to be a major editorial focus; the journal presented results on co-translational folding of proteins<sup>18</sup>, investigations of the role of topology in folding<sup>19–21</sup>, analysis of the effect of GroEL on the folding of hen lysozyme<sup>22</sup>, and description of the energetics of T4 lysozyme folding<sup>23</sup>. Finally, enhanced research activity in several areas, such as cryo-electron microscopy and structural dynamics, has led to an increase in coverage of these topics in the journal. It is likely that all of these areas will continue to be well represented in *Nature Structural Biology*.

While the editors of *Nature Structural Biology* have encouraged submission of a wide variety of research, we have not lowered our standards for any type of paper. It goes without saying that to be accepted, the quality of the science must be excellent. Additionally, we require a high degree of biological insight as well as widespread interest in the subject matter. Perhaps not surprisingly, our standards have increased in many areas; for example, in some cases we have requested that functional data accompany a structural determination, when certain speculative interpretations could be easily addressed by such work. Our policies have allowed us to choose (and help to improve) the best papers for review and publication. This has resulted in a strong mix of science in the journal, of which ~25% in recent issues has been biochemistry and molecular biology research. We hope readers and potential submitters have noticed and welcomed our efforts and the ensuing heightened variety of research in the journal. To help promote an understanding of the scope of *Nature Structural Biology*, examples of some of the papers from the last half of 1999 (listed above) can be accessed — free of charge — in pdf form on the *Nature Structural Biology* web site ([http://structbio.nature.com/nsb\\_evolution/](http://structbio.nature.com/nsb_evolution/)), along with examples of papers posted previously.

#### This issue: exceptional example of variety

The January, 2000 issue of *Nature Structural Biology* clearly reflects the eclectic range of science covered by the journal. The topics of the papers and methods utilized are quite varied: molecular dynamics studies of the protein ‘glass’ transition (page 34), three different methods for examining protein folding pathways (pages 58, 62, and 78), investigation of the side chain dynamics in a protein–ligand complex (page 72), single particle cryo-electron microscopy studies (pages 44 and 48), high resolution structural determinations (pages 23, 38, and 53), and *in vitro* evolution of a tRNA synthetase-like ribozyme (page 28). This variety is also evident in the News and Views section of this issue, where experts place into a broader context some of the work mentioned above (pages 3, 5, 7, and 11) as well as molecular biology studies of mRNA splicing (page 14) and structural results on an anti-cancer, anti-HIV protein (page 17).

#### Looking ahead: review commissions and manuscript submissions

Undoubtedly, the readership of *Nature Structural Biology* will broaden along with the content and the growing impact of structural research. Thus, we plan to include more review material in the journal to help make the content more accessible to a wider audience. In addition to the popular News and Views reports, we are commissioning more comprehensive reviews that will pull together results from biochemistry, molecular biology, and high-resolution structural experiments in specific fields. Suggestions from our readers for specific review topics, or areas suitable for special focus issues of the journal, are welcome.

The staff of *Nature Structural Biology* will continue to encourage submission of a diverse range of material, always with a strong emphasis on structural interpretation. We will also maintain high standards for publication. We would appreciate feedback from our readers on our plans and on the content of the journal. Furthermore, we encourage researchers to contact us about possible submissions.

Although we have only just begun to make these long-term changes to the journal, we are pleased that we can already see results from our efforts. All of us at *Nature Structural Biology* look forward to improving the journal further in the coming year.

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