## nature structural & molecular biology

## Getting resourceful

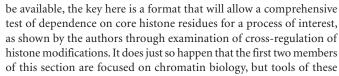
A new section in *Nature Structural & Molecular Biology* will house articles that serve primarily as Resources and also lead to novel molecular insights, adding a new flavor to our pages.

ur focus at *Nature Structural & Molecular Biology* is on the underpinnings of biological processes at the molecular level. However, in this era of large-scale, high-throughput experimentation, recent years have seen an increasing number of submissions that describe mammoth data sets and the tools that

facilitate their analysis. These data sets and resources, and their subsequent analyses, are no doubt of interest and use to our readership, and it is with this in mind that we now introduce our Resource section.

A Resource is an analysis of a new data set, as described in the content types section of our Guide to Authors (http://www.nature.com/nsmb/authors/index.html). While such analyses may describe large data sets, they should also lead to novel and arresting conclusions. This section of the journal will be broad in its scope. In an era of burgeoning and ever-expanding technological advances, the approaches and findings that characterize this section, as for any

area of the journal, will undoubtedly change over time. Our Guide to Authors, however, gives examples of the types of study one might expect to find in this section, and our August issue provides two examples. On page 873, Winston and colleagues carry out a broad analysis of the SWI/SNF-type ATP-dependent chromatin remodelers in *Schizosaccharomyces pombe*, examining the composition, function and effect on gene expression of these complexes, and thus providing not only new insights, but also a comprehensive backdrop for the study of chromatin remodeling in a previously little-tapped species that is an important model organism for many other cellular processes. Meanwhile, on page 881, work from Shilatifard and colleagues describes an entirely different type of resource in the form of a toolkit: a complete library of alanine scanning mutants across the core histones and an illustration of its utility. Although alanine mutations have been made in histones before and the reagents from any research article should



kinds could just as easily come from the study of any biological process.

Additional examples of Resources might ultimately include databases and new genome-wide analyses with conclusions of broad interest. In addition, although the above papers arise from single laboratories, Resources could also serve as a home for conclusions made through coordinated analyses by multiple laboratories that might arise, for example, from the increasing number of consortium grants.

So what makes a Resource suitable for our pages in particular? *Nature Structural & Molecular Biology*, and *Nature Structural Biology* before it, has long been a home for insights into molecular mechanism and will

continue to be. So although the data in these sections are likely to be large-scale in approach, findings at the molecular level, into mechanism, function and interaction, will still characterize this section. Both Resources in this issue emphasize the utility of the described systems to gain insights into regulation and function of the complexes focused on. Darwin rather famously once pointed out the importance of going beyond the purely observational, saying that otherwise one "might as well go into a gravel-pit and count the pebbles and describe the colours." Similarly, the insights obtained through Resources should, as in any section of the journal, go beyond the descriptive and penetrate into the mechanistic.

We look forward to receiving your contributions to this new section. And we especially want to hear back from the communities that the Resources are intended to benefit, to know whether they are serving their purpose.

