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► **COVER:** 'Heart's content' by Patrick Morgan. Adapted from the image of a corrosion cast of the vasculature of a newborn mouse, provided by Jonathan Epstein, University of Pennsylvania, Philadelphia, USA (also see the Review on p49).



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The concept of a histone code has influenced many who work in the fields of chromatin and epigenetics. The basic idea is that different combinations of the chemical marks that decorate histone tails are read out by interacting proteins, which ultimately determines the expression status of the underlying DNA.

However, as highlighted in the Review by Steven Henikoff on page 15, a body of evidence has built up that requires us to consider a different view of chromatin's influence on eukaryotic gene expression. Here, chromatin is not considered as a static template that varies only in the marks added or removed from histone tails. Instead, nucleosome destabilization and histone turnover are essential ingredients for propagating active chromatin states. In particular, Henikoff points to a key role for the dynamic replacement of 'standard' histone H3 with the variant H3.3 in the epigenetic memory of gene-expression states. This theme crops up again in a Research Highlight on page 2. The topic here is recent work in *Xenopus laevis* showing that replacement with H3.3 is essential for cells to remember their previous gene-expression states as they commit to developmental fates.

In the context of this dynamic view of the role of chromatin in gene expression, the influence of histone modifications needs to be considered in terms of their effects on nucleosome stability. And as well as the roles of histone variants, other aspects of chromatin biology — such as the functions of histone chaperones and chromatin-remodelling enzymes — can be reconsidered in terms of their role in gene expression through histone turnover.

As we begin 2008, the editors would like to thank the authors of our 2007 articles, and all those who provided valued input through peer review, for their contributions to *Nature Reviews Genetics* over the past year.

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