



nature publishing group



► **COVER:** 'Cell bars' by Patrick Morgan, inspired by the Review on p628.



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**R**ecent years have seen a shift of focus in studies of gene regulation from the characterization of individual loci to an examination of the broader regulatory context — such as the influence of remote genetic elements or the environment.

This field is continuing to expand, driven by methodological advances, as researchers try to capture the true complexity of transcriptional control.

Transcription factor–DNA interactions have long been incorporated into models of gene regulation; now these can be mapped genome-wide, as discussed in a Review by Farnham (p605). Although such studies have provided new insights, they have also thrown up new questions about how transcription factors control genes. For example, how is tissue-specific regulation achieved, and how do factors cooperate? In another Review, Cheung and Spielman (p595) take a broader look at the architecture of human gene regulation by examining what can be learnt from identifying genetic variants that influence gene expression.

However, an integrated view of gene regulation requires examination of protein output, but until recently, obtaining quantitative proteomic data was technically challenging. Now, mass spectrometry-based approaches, as discussed by Gstaiger and Aebersold (p617), are starting to provide precise proteomic data that can improve our understanding of gene regulation at the level of the protein product.

Another important facet of building complete models of regulation is the ability to measure expression dynamics under different conditions. Bennett and Hasty (p628) explain how progress in the development of microfluidic devices is now allowing the analysis of expression at the single-cell level, and they consider how this technology will contribute to improved mathematical models of the complexities of gene regulation.

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