or were left untreated (**Fig. 1**). They concluded that the passage through mitotic phase and the formation of metaphase chromosomes were essential to increase replication speed, and next investigated the mechanism behind this rapid replication.

By performing DNA combing, a technique that allows the measurement of DNA length between origins of replication, the Méchali team found that somatic nuclei contained more replication origins when the nuclei had undergone mitosis. This explained the increase in DNA replication speed, because a cell that simultaneously uses more origins of replications will duplicate its genetic material faster. The researchers also found that the increase in replication sites went hand in hand with a remodeling of chromatin that increased the number of DNA attachment sites to the nuclear membrane, typical for sperm nuclei or the nuclei of early embryos.

These experiments suggested to Méchali that the formation of mitotic chromosomes is important for genetic reprogramming of somatic nuclei used in nuclear transfer because it resets the organization of replication origins and thus ensures that the nuclei can keep up with the frantic pace of DNA replication needed in the first cell divisions of early embryonic development. It will be interesting to see if the success rate of nuclear transfer is indeed increased if the somatic nucleus can be induced to form metaphase chromosomes before its transfer. If this is the case, researchers can then focus on the next challenges in therapeutic cloning, for example, obtaining stem cells from the cloned embryos, or generating specific tissue—potential highlights for another day.

Nicole Rusk

RESEARCH PAPERS

Lemaitre, J.M. *et al.* Mitotic remodeling of the replicon and chromosome structure. *Cell* **123**, 787–801 (2005).

surprising to some, as Robinson explains, "When we first started looking at complexes with mass spectrometry, many people thought that the overall conformation of the gas phase complex would be completely different to that in solution. The fact that we have now shown that the collision cross-section is very similar to that calculated for the native state would argue against a large structural change as complexes go from solution to gas phase."

This technique will allow investigation of quaternary structure under a variety of conditions, as well as transient or reversible associations that do not lend themselves to detection by other methods. Indeed, Robinson explains that a major reason for selecting TRAP for the validation of the new technique was that the forces holding the complex together are fairly weak. But perhaps most strikingly, unlike other structural probes such as crystallography or nuclear magnetic resonance spectroscopy, this mass spectrometry–based method will allow researchers to be able to individually examine quaternary oligomeric states. "Heterogeneity is a real problem in structural biology, especially for large protein assemblies," says Robinson. She and her colleagues are optimistic that structural biology will reap the benefits of this newly discovered powerful capability of mass spectrometry.

Allison Doerr

RESEARCH PAPERS

Ruotolo, B.T. *et al.* Evidence for macromolecular protein rings in the absence of bulk water. *Science* **310**, 1658–1661 (2005).

NEWS IN BRIEF

GENOMICS

A mouse atlas of gene expression: large-scale digital gene-expression profiles from precisely defined developing C57BL/6J mouse tissues and cells

Working with tags from 72 different LongSAGE libraries, Siddiqui *et al.* have undertaken the detailed analysis of tissue- and developmental stage–specific mouse gene expression at an unprecedented scale. This examination of 8.55 million different tags yields a wealth of data—now publicly available—on a majority of known genes, as well as thousands of previously unidentified loci.

Siddiqui, A.S. *et al. Proc. Natl. Acad. Sci. USA* **102**, 18485–18490 (2005).

MICROFLUIDICS

Multistep synthesis of a radiolabeled imaging probe using integrated microfluidics

The isotopes used in PET imaging can be difficult to work with, as their very short half-lives require rapid (and expensive) processing. Lee *et al.* describe an innovative microfluidics-based reactor system for fast and potentially scalable probe production and suggest that such systems could provide a faster and cheaper approach for other, similar synthetic chemical processes.

Lee, C.-C. *et al. Science* **310**, 1793–1796 (2005).

PROTEIN BIOCHEMISTRY

Extracellular accumulation of recombinant proteins fused to the carrier protein YebF in *Escherichia coli*

YebF, an *E. coli* protein of unknown function, acts as an efficient carrier for the secretion of fused proteins, and Zhang *et al.* demonstrate that bacteria expressing YebF fused to hydrophobic and hydrophilic proteins from a broad range of sizes will rapidly translocate the fusion proteins intact to the surrounding medium, offering a potentially valuable tool for protein production.

Zhang, G. *et al. Nat. Biotechnol.* **24**, 100–104 (2006).

MICROARRAYS

Lipid microarrays identify key mediators of autoimmune brain inflammation

The pathological foundation of multiple sclerosis (MS) is the autoimmune destruction of the myelin sheaths that insulate nerves. The lipids in the sheath are thought to be a key target in this process, and Kanter *et al.* have developed a system for generating lipid microarrays, which they use to identify lipids recognized by MS antibodies from among 50 potential targets.

Kanter, J.L. *et al. Nat. Med.* **12**, 138–143 (2006).

IMAGING AND VISUALIZATION

Quantum dot–based multiplexed fluorescence resonance energy transfer

The unique chemical and fluorescent properties of quantum dots make them excellent candidates for studies using fluorescence energy resonance transfer (FRET). Clapp *et al.* take advantage of the narrow fluorescence spectra of quantum dots to perform multiplexed FRET experiments in which up to four potential molecular interactions can be monitored simultaneously.

Clapp, A.R. *et al. J. Am. Chem. Soc.* **127**, 18212–18221 (2005).