

## IN BRIEF

**TRANSCRIPTION**

## Transcriptional mutagenesis induced by 8-oxoguanine in mammalian cells

Brégeon, D., Peignon, P.-A. & Sarasin, A. *PLoS Genet.* **5**, e1000577 (2009)

DNA-damaging agents are known to have mutagenic consequences, but little is known about how they affect transcription. These authors used a luciferase-based reporter system to show that 8-oxoguanine (8OG) lesions are efficiently bypassed by RNA polymerase II in mammalian cells. However, the lesions were not repaired by the transcription-coupled repair machinery, leading to transcriptional errors, the magnitudes of which were dependent on the sequence context surrounding the 8OG. The 8OG-containing reporter genes produced mutant luciferase proteins, which suggests that DNA lesions might lead to long-term phenotypic changes.

**EVOLUTION**

## Positive selection of tyrosine loss in metazoan evolution

Tan, C. S. *et al. Science* 9 Jul 2009 (doi:10.1126/science.1174301)

This paper suggests that evolutionary changes at a genome-wide scale occur to accommodate the evolution of increasingly complex cell signalling systems. Looking at a set of metazoan species, the authors found a negative correlation between the number of tyrosine kinases and the number of tyrosine residues encoded in the genome. They propose and provide evidence for a model in which, as the number of enzymes that catalyse tyrosine phosphorylation increases, there is positive selection for tyrosine loss to avoid the detrimental effects of this modification.

**GENOME ORGANIZATION**

## Protein occupancy landscape of a bacterial genome

Vora, T., Hottes, A. K. & Tavazoie, S. *Mol. Cell* **35**, 247–253 (2009)

This paper describes a new method of mapping global protein occupancy across a complete prokaryotic genome at high resolution. The *in vitro* protein occupancy domain (IPOD) method, which involves crosslinking proteins to DNA and quantifying protein-bound DNA fragments using high-density tiling arrays, revealed extensive (1 kb) domains of protein occupancy across the *Escherichia coli* genome. Although some of these domains are associated with transcription, many are in silent regions and could be involved in chromosomal domain organization. IPOD also holds promise for exploring the dynamics of transcriptional networks.

**GENE REGULATION**A transposon-based chromosomal engineering method to survey a large *cis*-regulatory landscape in mice

Kokubu, C. *et al. Nature Genet.* **41**, 946–952 (2009)

Large *cis*-regulatory regions are important for transcriptional control in mammals, but their characterization has been hampered by the limited availability of tools for manipulating large regions of mammalian genomes. These authors describe a novel approach to meet this challenge. They engineered a cassette containing the *Sleeping Beauty* transposon and an enhancer-detecting reporter into the mouse *Pax1* transcription factor gene locus. The 'local hopping' capability of the transposon moved the cassette around the locus, revealing where regulatory sequences were located.