IN BRIEF

GENE REGULATION

A regulatory code for neuron-specific odor receptor expression.

Ray, A., van der Goes van Naters, W. & Carlson, J. R. *PLoS Biol.* **6**, e125 (2008)

Comparative genomics and experimental manipulation were used to detect the control regions that target the expression of specific combinations of olfactory receptors to different neurons in *Drosophila*. Conserved regions close to the receptor genes were detected by comparing sequences across 12 fly genomes; transgenic experiments identified both positive and negative control elements, the combination of which not only define the unique address of each receptor but, by influencing axon guidance, might even control the design of the nervous system.

HUMAN DISEASE

XPD helicase structures and activities: insights into the cancer and aging phenotypes from XPD mutations.

Fan, L. & Fuss, J. O. *et al. Cell* **133**, 789–800 (2008)

Structure of the DNA repair helicase XPD.

Liu, H. & Rudolf, J. *et al. Cell* **133**, 801–812 (2008)

The structural and enzymatic study of the archaeal homologue of the human xeroderma pigmentosa protein (XPD) explains how point mutations in this helicase cause three distinct human disorders. XP-causing mutations disable the DNA-repair function, leaving individuals prone to cancer; the two ageing disorders Cockayne syndrome and trichothiodystrophy arise when the enzyme is, respectively, defective in protein–protein interactions, causing defects in transcription and repair, or locked in position so that DNA is repaired rather than transcribed.

COMPLEX TRAITS

Genome-wide analysis reveals a complex pattern of genomic imprinting in mice.

Wolf, J. B., Cheverud, J. M., Roseman, C. & Hager, R. *PLoS Genet.* **4**, e1000091 (2008)

Although we understand several well-documented cases of imprinting at individual loci, we know little about the contribution of imprinting to quantitative traits. The authors carried out a genome-wide scan for imprinting QTLs (iQTLs) for body weight and growth in mice and identified 10 loci, 5 of which were significant at the genome level. Some of these loci had patterns of imprinting effects that were more complex than simple maternal or paternal dominance.

EPIGENETICS

Genome-wide analysis reveals MOF as a key regulator of dosage compensation and gene expression in *Drosophila*.

Kind, J. *et al. Cell* **133**, 813–828 (2008)

Dosage compensation in *Drosophila* involves upregulation of the genes on the single X chromosome in males, and this is known to be associated with hyperacetylation of histones. The authors carried out chromatin immunoprecipitation and microarray analyses for the position and the effects of binding of the conserved histone acetyltransferase MOF, and found that it binds differentially to male and female X chromosomes. This is likely to be an important step in establishing differential gene expression.