IN BRIEF

EVOLUTIONARY GENOMICS

Animal evolution and the molecular signature of radiations compressed in time.

Rokas, A. *et al. Science* **310**, 1933–1938 (2005)

Evolutionary relationships among metazoans have been difficult to establish using phylogenomics. Rokas *et al.* could not overcome this problem even by increasing the numbers of gene sequences from a range of metazoans. Because the phylogeny of a fungal clade of roughly the same age could be resolved using the same data, the authors conclude that this inability to resolve phylogenetic relationships in the metazoa indicates a rapid radiation of metazoan species, consistent with fossil evidence for a 'Cambrian explosion' of animal diversity.

GENETICAL GENOMICS

Combined expression trait correlations and expression quantitative trait locus mapping.

Lan, H. *et al. PLoS Genet.* 6 December 2005 (doi: 10.1371/journal.pgen.0020006.eor)

Combining linkage mapping with the identification of co-regulated genes using microarrays enables the discovery of *cis*- or *trans*-acting expression QTLs (eQTLs). However, the small regulatory contributions of *trans*-acting eQTLs makes them hard to detect. This paper describes a two-step approach to overcoming this problem. Expression traits were first mapped using samples from mice that segregated for obesity and diabetes. Regions enriched for linkage that were in *trans* to expression traits with which they share a function were then identified, providing evidence for the existence of *trans*-acting eQTLs, even when the examination of individual traits would not have yielded statistical support.

EPIGENETICS

Hyperdynamic plasticity of chromatin proteins in pluripotent embryonic stem cells.

Meshorer, E. *et al. Dev. Cell* **10**, 105–116 (2006)

As pluripotent embryonic stem (ES) cells differentiate their genome undergoes global chromatin remodelling. The authors report that although histone H1 and the linker histones are highly dynamic in mouse ES cells, they become immobilized on chromatin as cells begin to commit to a particular lineage. Experimental manipulation of the binding rate led the authors to suggest that the hyperdynamic binding is functionally important for pluripotency and maintenance of the undifferentiated state.

HUMAN DISEASE

In vitro analysis of huntingtin-mediated transcriptional repression reveals multiple transcription factor targets.

Zhai, W. *et al. Cell* **123**, 1241–1253 (2005)

Transcriptional dysregulation has emerged as a potential important candidate mechanism for Huntington disease pathogenesis. Using a specifically developed *in vitro* transcriptional assay, Zhai *et al.* showed that several components of the basal transcription machinery are directly inhibited by mutant huntingtin (HD) protein in human cells. In the case of the RAP30 subunit of GTF2F1 (general transcription factor IIF, polypeptide 1) the effects of mutant HD can be alleviated by overexpressing RAP30.