Insect population control by homing endonuclease-based gene drive: An evaluation in *Drosophila melanogaster*, pp. 33–44
Yuk-Sang Chan, Daniel A. Naujoks, David S. Huen and Steven Russell
Homing endonuclease genes (HEGs) mediate their own spread to homologous target sites throughout populations by co-opting homologous recombination. It has been suggested that HEGs could be engineered to target genes essential for viability or fecundity of a host and, by harnessing their ability to spread, could be used to control insect populations. But HEGs have never been found in metazoans, so will this work? This article shows that a model HEG, I-SceI, can achieve transmission in *Drosophila melanogaster*.

Prion-forming ability of Ure2 of yeasts is not evolutionarily conserved, pp. 81–90
Herman K. Edskes, Abbi Engel, Lindsay M. McCann, Andreas Brachmann, Huei-Fung Tsai and Reed B. Wickner
Prion formation cannot be taken for granted. Although the Ure2 protein forms prions in *Saccharomyces cerevisiae*, these investigators find that Ure2 of *Candida albicans* but not Ure2 of *C. glabrata* can form a prion in *S. cerevisiae*, even though *C. albicans’* Ure2 is less similar to *S. cerevisiae’s* Ure2 than is Ure2 of *C. glabrata*. Thus, prion formation is not evolutionarily conserved.

Heat avoidance is regulated by transient receptor potential (TRP) channels and a neuropeptide signaling pathway in *Caenorhabditis elegans*, pp. 91–103
Dominique A. Glaser, Will C. Chen, Rebecca Agin, Bronwyn L. MacInnis, Andrew B. Hellman, Paul A. Garrity, Man-Wah Tan and Minam B. Goodman
Like humans, nematodes do not like extreme heat. These investigators identify two independent pathways that mediate heat avoidance in *Caenorhabditis elegans*. One relies on two orthologs of mammalian heat-sensing ion channels that are expressed in sensory neurons. The second pathway depends on an interneuron and involves a neuropeptide and its G-protein-coupled receptor. This article offers additional avenues for drug discovery in pain management.

Quantitative epigenetics through epigenomic perturbation of isogenic lines, pp. 215–227
Frank Johannes and Maria Colomé-Tatché
Variation in chromatin state often results in gene expression changes that are transmitted across generations and therefore contribute to heritable phenotypic variation. These investigators developed a general experimental approach for mammalian and plant species to incorporate these non-Mendelian features into quantitative genetic models. Their approach illustrates a fundamental continuity between genetic and epigenetic inheritance and demonstrates the importance of epigenetic changes in phenotype inheritance.

Rhabdoviruses in two species of *Drosophila*: Vertical transmission and a recent sweep, pp. 141–150
Ben Longdon, Lena Wilfert, Darren J. Obbard and Francis M. Jiggins
This article reports a remarkably rapid spread of two recently discovered viruses in *Drosophila* populations. The authors estimate that one of these viruses swept through the fly population in the United Kingdom within the past ~11 years to infect 39% of flies, during which time the viral population doubled approximately every 9 months. The viruses are transmitted vertically by both males and females, and this biparental mode of transmission is probably responsible for the rapid spread of the parasite through the host population.

Sustained and rapid chromosome movements are critical for chromosome pairing and meiotic progression in budding yeast, pp. 21–32
Megan Sonntag Brown, Sarah Zanders and Eric Alani
How do homologous chromosomes find each other during meiosis? Several roles have been proposed for the telomere-led chromosome movements that are a conserved feature of Meiosis I prophase, including promoting homolog pairing and removing inappropriate chromosomal interactions. This article describes evidence that rapid chromosome movements are important for homolog pairing and recombination in budding yeast and that they promote efficient meiotic progression.

An optimal weighted aggregated association test for identification of rare variants involved in common diseases, pp. 181–188
Jae Hoon Sul, Buhm Han, Dan He and Eleazar Eskin
Because of their low occurrence, it is difficult to identify a single rare variant involved in disease. To overcome this challenge, groups of rare variants in each gene are examined to detect whether they are involved in disease. These authors propose a grouping method that is more accurate in detecting associations between groups of rare variants and a disease than previous methods. They also show that their method can detect an association in real data.

Genome rearrangements in maize induced by alternative transposition of reversed *Ac/Ds* termini, pp. 59–67
Chuanhe Yu, Janbo Zhang and Thomas Peterson
Double trouble: A lone DNA transposon usually moves without causing other genome changes, but two members of the maize *Ac/Ds* family situated near each other can cause big trouble in the form of chromosome breaks and rearrangements. Here the authors characterize rearrangements caused by paired *Ac/Ds* elements and find a surprisingly high frequency of deletion of the sequence between the transposons. These deletions seem to be produced when transposition occurs during DNA replication, with the transposon ends inserting into a newly-replicated sister chromatid. These results provide new insight into the secret lives of transposons.