

# RESEARCH HIGHLIGHTS

## ASTRONOMY

### Old bulk

*Astrophys. J.* **672**, 146–152 (2008)

Massive galaxies are common in the younger reaches of the Universe, the results of a series of recent mergers of smaller galaxies. But some massive galaxies are very old, and probably formed through the rapid gravitational collapse of enormous clouds of gas, Alan Stockton of the University of Hawaii and his colleagues conclude.

Stockton and his team analysed data from the Hubble telescope. They determined the structure of two distant, massive galaxies that seem to have formed early in the history of the Universe.

The disk-like shapes they report signal the collapse of large masses of gas, and are unlikely to have survived large galactic mergers. This implies that some massive galaxies are not merely amalgamations of smaller ones.

## CANCER BIOLOGY

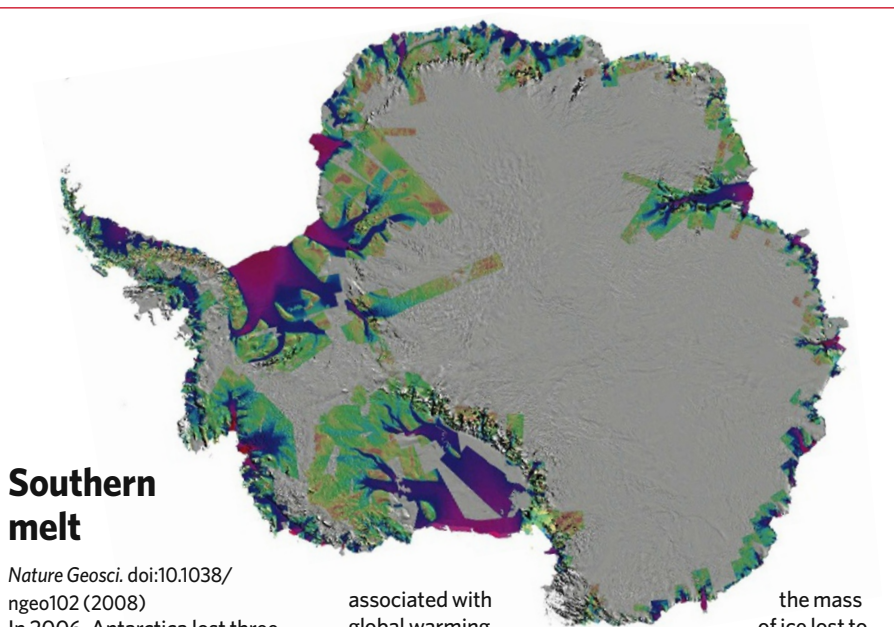
### Arrested development

*Cancer Cell* **13**, 69–80 (2008)

A molecular switch silences a neural development gene in the most common type of brain cancer, according to Howard Fine and his co-workers at the National Institutes of Health in Bethesda, Maryland.

The researchers isolated tumour-initiating stem-like cells from adults with glioblastoma. Some of the tumour cells behaved similarly to stem cells that are destined to become neurons in very young mouse embryos. Specifically, they did not produce a key protein called BMP receptor 1B, which enables cells to pick up external molecular prompts instructing them to keep developing.

Blocking the expression of BMP receptor 1B creates cells that are able to divide but not



### Southern melt

*Nature Geosci.* doi:10.1038/ngeo102 (2008)

In 2006, Antarctica lost three-quarters more ice than it did a decade earlier, researchers have found.

A comprehensive study of the continent's total ice balance concluded that, during the past 10 years, accelerating loss from melting and sliding glaciers (shown in red) greatly exceeded gains from snowfall, which increased in some regions (blue). Both effects are

associated with global warming.

Eric Rignot at the University of California, Irvine and an international team used radar interferometry data to work out glacial flow rates in 1996, 2000 and 2006 along 85% of Antarctica's coastline. The authors also modelled these glaciers' varying thicknesses, allowing them to calculate

the mass of ice lost to the ocean over time. They then subtracted this figure from the patchy accumulation of the snowpack.

Antarctica's 2006 net ice loss of almost 200 billion tonnes is comparable to Greenland's annual loss, which has been the focus of much discussion about sea-level rises.

to differentiate. Fine and his team report that cells from many of the tumours they analysed shared this molecular glitch.

## BOTANY

### Flower power

*Am. Nat.* **171**, 1–9 (2008)

Interactions with other plant species may influence the arrangement of flowers' structures, researchers have found.

Although it is well established that pollinators can shape flower evolution, the effect of neighbouring plants has remained unclear. Robin Smith and Mark Rausher of Duke University in Durham, North Carolina, investigated the relationship between two species of morning glory, *Ipomoea hederacea* (pictured left) and *I. purpurea*. Pollination of *I. hederacea* flowers with *I. purpurea* pollen yields hollow seeds that do not produce viable progeny, reducing the plant's overall fitness.

The researchers found that *I. hederacea* plants grown in contact with *I. purpurea* flowers showed considerable variation in the arrangement of the flowers' reproductive

structures. Plants with flowers in which the anthers and stigma were clustered closer together produced more seeds than those that held their reproductive parts further apart. The authors observe that this arrangement favours self-fertilization, lessening a flower's probability of being pollinated by *I. purpurea* pollen.

## SELF-ASSEMBLY

### Snakeskin nanobelts

*Nano Lett.* doi: 10.1021/nl0722830 (2007)

Nanoscale algorithmic self-assembly, in which the molecular components of structures are programmed to stick together according to simple rules, could eventually lead to new forms of molecular computing.

Satoshi Murata of the Tokyo Institute of Technology and his colleagues have created DNA 'tiles' that spontaneously clip together in solution, producing ribbons with constant widths of about 100 nanometres.

The self-assembly is defined by sequences of single-stranded DNA on the tiles' edges. When complementary DNA strands match,



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the tiles stick together, and the widths of Murata's ribbons are kept in check by special 'boundary' tiles.

The researchers have also programmed the tile-matching rules so that they embody computational cellular-automaton models. The arrangements that result resemble snakeskin belts under the microscope.

#### IMAGING TECHNIQUES

### Heliomicroscopy

*J. Microsc.* **229**, 1-9 (2008)

Electrons are commonly used to image materials at high resolution, but their negative charge and high energies can damage fragile samples. To get around this, a group of physicists used helium atoms instead, and successfully photographed a hexagonal copper mesh.

Bodil Holst at Graz University of Technology in Austria and her colleagues propelled helium through a nozzle and used a device known as a Fresnel zone plate to focus the beam onto the copper. This created an image with 2-micrometre resolution.

The experiment demonstrates that helium atoms can generate a picture even when fired at a sample much more slowly than would be required for electrons to produce an image. Holst says the technique might one day be used to image proteins and weak polymers.

#### MOLECULAR BIOLOGY

### How to host HIV

*Science* doi: 10.1126/science.1152725 (2008)

To be able to infect human cells, HIV requires more than 250 host proteins, say researchers at Harvard Medical School in Boston, Massachusetts. Only 13% of these proteins have previously been implicated in HIV infection, and the collection could yield potential drug targets for anti-HIV therapies.

Stephen Elledge and his colleagues turned down the expression of more than 21,000 genes in human cell cultures. Each gene was silenced individually in a separate cell line, and all the lines were then tested for their ability to support HIV infection.

The proteins not previously known to have a role in HIV infectivity include some that transport vesicles between organelles, and components of a protein complex called Mediator, which regulates gene expression.

#### EVOLUTIONARY BIOLOGY

### A twist in the tale

*Biol. Lett.* doi:10.1098/rsbl.2007.0602 (2008)

A snail with a shell that coils in four directions has been discovered in Malaysia. Reuben Clements of the conservation group WWF-Malaysia in Selangor and his team have described 38 examples of the gastropod — all with curves in similar positions — found in soil from a single limestone site. The creature came as a surprise because the majority of land snails' shells twist around one or two axes. Most species in the genus *Opisthostoma*, in which the new specimens fall, have three coiling axes.

*Opisthostoma vermiculum*, or 'little worm', as the authors have named the curvy creature (pictured below left), is the first of two species with bizarrely arranged coils that the team found.



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#### GENETICS

### Lethal matings

*Science* doi:10.1126/science.1151107 (2008)

When two strains of *Caenorhabditis elegans* mate, one-quarter of their grandchildren die during early development because of a weird genetic incompatibility that is maintained by natural selection.

Hannah Seidel,

Matthew Rockman and Leonid Kruglyak at Princeton University in New Jersey,

who discovered the incompatibility, crossed worms of the 'Bristol' strain with individuals from the 'Hawaiian' strain, then allowed the offspring to self-fertilize. Those embryos that lacked a gene called *zeel-1* — a deletion characteristic of the Hawaiian strain that is passed on in mendelian ratios — were sensitive to the product of another gene that is carried in sperm. A version of the latter gene from the Bristol strain arrested the development of such embryos.

Because Hawaiian and Bristol worms live together all over the world, the team propose that the incompatibility is not an example of incipient speciation. The genes involved probably confer some unknown benefit to counteract the reproductive cost, they add.

## JOURNAL CLUB

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### A geneticist reflects on DNA sequence variants that influence gene expression and disease risk.

Most people are familiar with the Human Genome Project and the HapMap, which catalogued the millions of DNA-sequence differences among humans. But which of these differences influence our risk of developing diseases remains unclear. This is particularly true for disorders such as heart disease that involve not only many genes but also the interactions among them. In addition, the effects of variations in DNA sequence are often subtle, such as altered levels of gene expression. Identifying those DNA sequences that determine levels of expression across individuals could have great medical potential.

One paper that illustrates this point looks at the two major contractile proteins of the human heart, the  $\alpha$ - and  $\beta$ -forms of the myosin heavy chain (E. van Rooij *et al. Science* **316**, 575-579; 2007). Here, Eric Olson and his team at the University of Texas in Dallas identify a microRNA, called miR-208, that regulates how much of the  $\beta$ -form heart cells produce.

A healthy heart requires a particular ratio of  $\alpha$ - and  $\beta$ -heavy chains for its cells to function normally. When stressed, heart cells tend to make too much of the  $\beta$ -form, causing the organ to enlarge, replete with fibrous connective tissue, and less able to contract. This often happens in people with heart disease.

In finding miR-208, the researchers have determined a key component in the molecular basis of heart failure. The next step might be to look for sequence variants of miR-208 and of other gene-expression regulators that could explain why some people are more susceptible to heart disease than others. In this way, whole biological networks could be pieced together and common medical problems more fully understood.

Discuss this paper at <http://blogs.nature.com/nature/journalclub>