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the condition since the 1940s stem not from how intensely autistic people feel their senses, but from how sharp their senses actually are.

Ashwin and her team tested 15 men with autism-spectrum disorders using the Freiburg Visual Acuity and Contrast Test, and found them to have, on average, 20:7 vision. This means they can see the same detail on an object 20 metres away that a person with average vision can see at 7 metres. Birds of prey have roughly 20:6 vision. What gives people with autism hawk-like vision isn't known.

PHYSICS

Black holes on the strand

Science **319**, 1367-1370 (2008)

Researchers are unlikely to travel to a black hole any time soon, but they have managed to recreate a bit of one in the lab.

Ulf Leonhardt of the University of St Andrew's, UK, and his colleagues made an artificial event horizon — the point beyond which nothing can escape — inside a fibre-optic cable. The cable was designed such that its optical properties would be altered by an ultrashort pulse of light. A beam of light on the same strand experienced the equivalent of an event horizon as it travelled near the first flash.

The authors hope that the system can be used to recreate Hawking radiation, a glow believed to surround real black holes as a result of quantum effects.

CELL BIOLOGY

Bent out of shape

Cell **132**, 807-817 (2008)

A fundamental question about how cell membranes can get dents in them was answered by Vinzenz Unger of Yale

University School of Medicine and his colleagues.

They found that proteins containing a region called an F-BAR domain form scaffolds in the peripheral cytoplasm and bring about invaginations in the cell membrane. Unger's team recreated the interactions between membranes and F-BAR proteins in a test tube, and then observed the results using electron microscopy.

F-BAR proteins, which have an elongated crescent shape, are exceptionally rigid and interact with membranes through their charged surfaces, according to the study. The proteins assemble into helical lattices and form clusters on membranes; the lattices can then bend the membranes to adopt the F-BAR protein's curved shape.

EVOLUTION

Yeast rewired

PLoS Biol. **6**, e38 (2008)

Evolution has massively rewired molecular circuits controlling gene expression in yeast, Hao Li and Alexander Johnson of the University of California, San Francisco, and their colleagues showed.

They studied how *Saccharomyces cerevisiae*, *Candida albicans* and *Kluyveromyces lactis* use the regulatory protein Mcm1, which directs the transcription of 4–12% of these three species' genes with the help of various partner

proteins. The three yeasts differ radically in the genes that are under the influence of the different Mcm1-partner pairs.

Of hundreds of Mcm1-controlled genes studied, fewer than one-fifth respond to Mcm1 in all three yeasts. The protein has picked up and lost partners as the species diverged, and in *C. albicans* has gained a new DNA-binding site that may help it thrive in human hosts.

GEOLOGY

Magma mix-up

Geology **36**, 51-54 (2008)

Basalts from the Snake River Plain (pictured left) in Yellowstone National Park in the northern United States look like they originate from deep in Earth's mantle. But they have the characteristic isotopic signature of rocks from shallower reaches — from the continental lithosphere. This curiosity has been explained by Barry Hanan of San Diego State University, California, and his colleagues.

Using mass spectrometry on samples of volcanic rock, the authors showed that deep-mantle magma can inherit the lithosphere's isotopic signature when it rises and picks up contamination.

The findings warn geologists about assuming too much from isotopic signatures.

MOLECULAR BIOLOGY

Shaping up

Science **320**, 1471-1475 (2008)

How does ubiquitin, a regulatory protein that labels other proteins for destruction, bind to so many different structures? By shuffling between arrangements until it finds the best option, according to Bert de Groot of the Max Planck Institute for Biophysical Chemistry in Göttingen, Germany, and his team.

Forty six of the arrangements were already known from X-ray crystallography of ubiquitin

recognition complexes. The researchers followed ubiquitin's structure (pictured) over pico- to microseconds in various solutions and from many angles, showing that all these conformations are likely to be adopted in living cells.

This work adds to evidence that many confirmations of the same protein often exist in dynamic equilibrium before a binding partner comes along, a model that is at odds with the 'induced fit' hypothesis.

