EDITED BY GILBERT CHIN AND JAKE YESTON

GEOLOGY

Fighting for Exposure

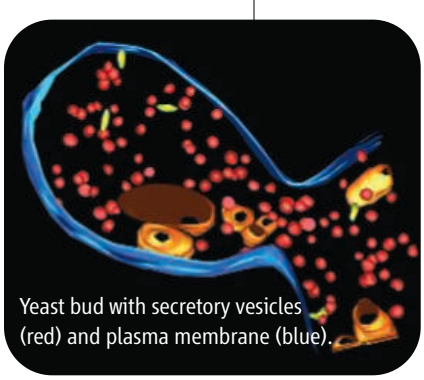
Geologic maps provide information on the distribution of rocks and deposits currently exposed on Earth's surface. It has been recognized for some time that fewer older rocks are exposed than younger ones; only a few outcrops remain from Earth's earliest history, more than 3.5 billion years ago. Wilkinson *et al.* separate out rocks deposited at the surface (volcanic and sedimentary rocks) from those that form in the crust (metamorphic and intrusive rocks representing chilled magma bodies) and show how the exposures today of rocks of different ages and origination depth reflect geologic history and processes. On average, about 6.5% of continental land is covered by new sediments or volcanic deposits every million years. Young metamorphic and plutonic rocks are rare; the average age of metamorphic rocks (nearly 1 billion years) is older than that of intrusive rocks (about 200 million years), reflecting the greater difficulty in exposing deeper rocks. Together, the data imply that long-term rates of burial and uplift are about equal at roughly 0.5 km per million years, in reasonable agreement with rates measured by other techniques in many specific orogenic belts. — BH

Geol. Soc. Am. Bull. **121**, 760 (2009).

CELL BIOLOGY

Sorting Out Rafts

During membrane trafficking within eukaryotic cells, lipids and membrane-bound proteins are sorted and transported to their intracellular destinations, generating organelles with distinctive compositions of proteins and lipids. One major trafficking nexus is the trans-Golgi network (TGN), where proteins that have traversed the early stages of the secretory pathway are collected before transport to the plasma membrane. The plasma membrane is enriched in sphingolipids and sterols in comparison to internal membranes; how this sorting of lipid components occurs remains poorly understood, although lipid rafts—organized microdomains that include sterols, sphingolipids, saturated glycerophospholipids, and proteins—have been proposed to play a role.



Yeast bud with secretory vesicles (red) and plasma membrane (blue).

Klemm *et al.* recovered post-Golgi secretory vesicles from yeast cells that had been modified so as to accumulate these vesicles in the bud. These vesicles were then subjected to a shotgun lipidomics procedure, which confirmed that the vesicles were enriched in ergosterol and sphingolipids. Thus, the TGN, in addition to acting as a sorting station for proteins, can indeed sort lipids. The vesicles also exhibited a more ordered lipid structure than the Golgi membrane, consistent with the idea that lipid rafts contribute to lipid sorting. — SMH

J. Cell Biol. **185**, 601 (2009).

APPLIED PHYSICS

Cloud Gazing

For persons deep in thought, or perhaps simply wishing to pass time peacefully, looking up at the clouds has been an idle pursuit practiced for millennia. To those in the communication business, though, cloud gazing and characterization are serious issues. There is an increasing demand for higher data transfer rates between Earth-based communication stations and space-based satellites. Optical signals provide the fastest possible route of communication between two points. However, Earth-to-space optical links can be hampered by signal attenuation or obstruction from cloud cover. Nugent *et al.* have developed a thermal infrared cloud imaging system that can characterize and classify clouds above a communication station. With this established ability to determine the optical depth of particular clouds, they can apply their technique toward keeping the communication channels open even when there is partial or thin cloud cover. — ISO

Opt. Express **17**, 7862 (2009).

BIOTECHNOLOGY

A Bright Idea

The identification of single-nucleotide polymorphisms (SNPs) across individuals can contribute to characterizing underlying genetic variation in humans, DNA damage, and potential biomarkers of disease. However, it is currently challenging to detect SNPs in real time at room temperature and without the addition of a battalion of exogenous reagents.

Xiao *et al.* have engineered a detection system consisting of a single strand of DNA, which folds into a discontinuous double helix composed of three seven–base pair stems and incorporates both a fluorescent moiety and a quencher. When this molecule finds a perfectly complementary piece of DNA, it forms a detector-target hybrid, disrupting the proximity of

CREDITS (TOP TO BOTTOM): MICHAEL MISCHENKO (NASA/GISS); KLEMM *ET AL.*, *J. CELL BIOL.* **185**, 601 (2009)

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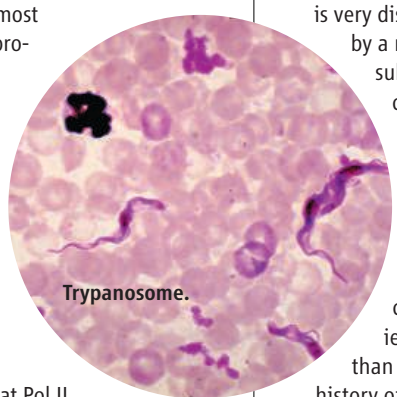
the fluorophore and quencher, and yielding a fluorescent burst. It can discriminate between targets differing by only a single nucleotide, and hybridization to the target occurs within 30 min at room temperature and in the presence of a 64-fold excess of a singly mismatched competitor. — LMZ

Angew. Chem. Int. Ed. **48**, 10.1002/anie.200900369 (2009).

MOLECULAR BIOLOGY

Start and Stop Signals

Human sleeping sickness is caused by the parasitic protozoan *Trypanosoma brucei*, which is transmitted when the tsetse fly bites. As in prokaryotes, the genes in this microorganism are arrayed in large polycistronic transcription units. Despite this unusual organization relative to what is seen in most other eukaryotes, the promoter elements where RNA polymerase II and its associated transcription factors bind have largely eluded identification.



Trypanosome.

Using the ChIP-seq method, which involves DNA sequencing of chromatin immunoprecipitations, Siegel *et al.* suggest that Pol II transcription factors look for histone modifications and histone variants. Levels of acetylated histone H4 (H4K10ac) are higher at Pol II transcription start sites. In addition, histone variants H2BV and H2AZ, as well as the bromodomain protein BDF3, colocalize with H4K10ac. The authors also show that decoration with these histone variants correlates with less stable nucleosomes, which would allow for their displacement by transcription initiation complexes. A third feature defined by histone variants, in this instance H3V and H4V, is the transcription termination regions. Finally, G-rich stretches in the sense strand upstream of H4K10ac sites may serve as directional signposts for transcription. Hence, *Trypanosoma* appears to use nucleotide sequence and chromatin structure to mark starts and stops. — BAP

Genes Dev. **23**, 1063 (2009).

ASTRONOMY

Signs of Old Age

Researchers believe that most of the stars we see today were formed during short but very vigorous bursts in early dusty galaxies. Although the starlight emanating from these galaxies is concealed by dust, bright submillimeter emission, which traces dust heated by the ultraviolet light from newly formed stars, can be detected at great distances. Using data from a new submillimeter survey combined with radio, infrared, and optical observations, Coppin *et al.* found the most distant submillimeter galaxy yet detected: Its redshift of 4.76 suggests that intense star formation occurred in galaxies within 1 billion years of the Big Bang. In a different study, Cowie *et al.* used a submillimeter interferometer to determine an accurate position for HDF 850.1, a submillimeter galaxy discovered in 1998. Their data are not consistent with any previous optical identifications; no counterpart can be found even in the Hubble Deep Field, one of the deepest optical images available. Combined with information at other wavelengths, this result implies that HDF 850.1 is very distant, most probably characterized by a redshift greater than 4. Very few submillimeter galaxies have been confirmed at these high redshifts, but their absence could simply be the result of the observational difficulties involved in determining their positions. Both groups of authors suggest that galaxy formation models could be challenged if such galaxies proved to be more common than anticipated at early times in the history of the universe. — MJC

Mon. Not. R. Astron. Soc. **395**, 1905 (2009); *Astrophys. J.* **697**, L122 (2009).

MICROBIOLOGY

Surely Something Is Missing

Cell division in the parasitic protozoan *Entamoeba histolytica* is an olio of polyploidy, multiple nuclei, and failed cell division. In the latest of a series of studies, Mukherjee *et al.* show that multiple genome complements arise because the amoeba lacks the regulatory components present in higher eukaryotes that not only control the structure of the microtubule organizing centers but also couple cytokinesis with nuclear division. The result in *Entamoeba* is the formation of multipolar spindles, which segregate multiple copies of the chromosomes simultaneously into unequal daughter cells. This phenomenon can be observed both in vitro and within the intestine, and there does not appear to be strong selective pressure to constrain genomic exuberance, possibly because having such lax controls is an advantage for a parasite that may encounter sudden shifts in its environment. — CA

PLoS Negl. Trop. Dis. **3**, 3409 (2009).

CREDIT: DR. MAE MELVIN/CDC

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