They then used the STM to define numbers of atoms on a (STM) to build gold chains with... tunneling microscopy. Conductivity spectra taken at 30 points along a 20-atom chain... of the underlying substrate enhances their mobility. Larger clusters form a stable hexagonal honeycomb structure that is commensurate with the underlying surface.

An Overly Simple Seesaw

A popular paradigm for understanding global oceanic heat budgets is that of a “bipolar seesaw,” wherein a heat gain in one hemisphere is balanced by a loss in the other. This concept has been invoked to explain the apparently alternating periods of... in the shallow crust. Hector Mine earthquake in southern California. They model the displacements as an elastic response to the large event and find that the fault zones are compliant in the shallow crust.

Reducing Stress in California

The buildup of stress and strain between and within fault zones is poorly understood but important for assessing seismic hazards. Fialko et al. (p. 1858) measured small surface displacements on nearby fault zones related to the 1999 magnitude 7.1 Hector Mine earthquake in southern California. They model the displacements as an elastic response to the large event and find that the fault zones are compliant in the shallow crust.

Old Gold Deposits

Gold deposits in the Kaapvaal Craton of South Africa represent about 40% of the gold production on Earth, yet the origin of this large concentration remains controversial. Kirk et al. (p. 1856; see the Perspective by Frimmel) used the rhenium-osmium isotopic system to derive an age of formation for the gold and pyrite aggregates. The gold and pyrite is older than the conglomerate rock that hosts them. Thus, the gold was derived from detritus from older source rocks and not hydrothermal in origin. The age of the gold mineralization coincides with the age of stabilization of the Kaapvaal craton (about 3 billion years ago) and indicates that the gold was probably derived from hot and fertile mantle sources.

Controlling Chromatin Through RNA Interference

The link between RNA and the epigenetic regulation of gene expression are well known from studies of X-chromosome dosage compensation, where the noncoding RNAs Xist and Tsix play a critical role in silencing genes on the X-chromosome. RNA interference (RNAi) also silences gene expression at the posttranscriptional level by destroying cognate RNAs and is thought to defend the genome against invasion of “foreign” nucleic acids. Volpe et al. (p. 1833; see the Perspective by Allshire) now show that the RNAi machinery regulates the formation of centromeric heterochromatin in fission yeast. At least one component of the RNAi machinery, Rdp1, is bound to centromeric sequences. RNA transcripts identified as originating from these centromeric repeats are the likely targets of RNAi.

On the Mend

The breast cancer susceptibility gene BRCA2 is necessary for the repair of double-stranded DNA breaks through homologous recombination, in which the intact member of a chromosome pair is used as a template to mend the damaged partner. Yang et al. (p. 1837; see...
the cover and the Perspective by Wilson and Elledge) present the structure of the carboxyl-terminal domain of BRCA2 in complex with a second protein DSS1 and with single-stranded DNA. The binding of BRCA2 directly to DNA may enable it to serve as a scaffold for assembling the components that undertake the restoration of chromosome integrity.

**Ribosome Regulation by Protein Products**

The leader peptide regulation of the *Escherichia coli* tryptophanase operon, tnaC, has a stop codon at position 25 that yields a 24 residue peptide in the absence of inducer. However, in the presence of tryptophan, the leader peptide stays attached to the stalled ribosome as a peptidyl tRNA and termination is blocked. By altering codons and spacing between codons in the leader peptide, Cong and Yanofsky (p. 1864; see the Perspective by Sachs and Geballe) show that the sequence of the nascent peptide can regulate the translating ribosome, perhaps by creating a ribosome binding site for free tryptophan. Hence, peptides are not only products of translation but they can also control ribosome movement during translation.

**Caught in the Act**

The process of membrane fusion is key to many cellular events in membrane trafficking, virus entry, and cell division. However, the mechanism of fusion itself, and a detailed structural understanding of how two lipid bilayers can fuse in a nonleaky fashion, have been difficult to nail down. Yang et al. (p. 1877; see the Perspective by Gruner) have now visualized a structure that seems to represent a lipid bilayer fusion intermediate consisting of a kind of stalk structure formed by the opposed lipid monolayers.

**Dendritic Cells Show Self-Control**

Dendritic cells (DCs) are increasingly being recognized for their ability to shut down some types of immune response and for contributing to the state of immune tolerance. Elucidation of putative tolerogenic DC subsets is under way, although the mechanisms by which these cells might modulate immunity have yet to be established. Munn et al. (p. 1867) now describe a subset of human DCs that can inhibit T cell responses, at least in vitro, to alloantigens through the catabolism of tryptophan by the enzyme indoleamine 2,3-dioxygenase (IDO). It is known that IDO can prevent antigen-specific responses of T cells in vivo, as well as in vitro. The present demonstration that a subset of human DCs can inhibit T cell responses via IDO in vitro makes it plausible that these cells might use the same mechanism in vivo. Whether DCs actually regulate immune responses to self-antigens, transplants, and tumors by this mechanism remains to be established.

**Type-Setting Methylation Marks in Chromatin**

Histone methylation, which is involved in the formation of heterochromatin, can also control DNA methylation and hence gene expression. The role of chromatin-remodeling factors in this pathway has been ill-defined, although it is known that the SWI/SNF-like protein DDM1 in *Arabidopsis* is required for the DNA methylation of centromeric and heterochromatic repeats. Gendrel et al. (p. 1871) analyze the methylation state of histone H3 and show that DDM1 is required for the maintenance of H3 methylation patterns in interstitial heterochromatin, but is not required to maintain the overall level of histone methylation. The authors speculate that DDM1 functions to “type-set” these epigenetic methylation marks.

**Light-Activated Fluorescence**

In order to study a cohort of proteins in a living cell, Patterson et al. (p. 1873) developed a fluorescent tagging method that can be photoactivated. Proteins were engineered to express a variant of green fluorescent protein that has low fluorescence until specifically photoactivated under a microscope. The dynamics of nuclear transport and lysosomal membrane exchange in living cells are described.