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Metalloregulatory proteins, here superimposed on the periodic table, act as metal-specific sensors that translate changes in metal ion concentration into changes in gene expression; elevations are proportional to the logarithm of the elemental abundances in the universe.

Most of these proteins mediate metal-responsive transcription by RNA polymerase (top left). See page 715. A special section on bioinorganic chemistry begins on page 701; see also the Perspective on page 699. [Image: Bryson Biomedical Illustrations]

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Indicates accompanying feature



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THIS WEEK IN SCIENCE

edited by PHIL SZUROMI

Cytochrome P450 structure

Cytochrome P450 enzymes are monooxygenases that participate in steroid biosynthesis and detoxification. Ravishandran et al. (p. 731) have determined the x-ray crystal structure of the hemoprotein domain of P450BM-3 from Bacillus megaterium that catalyzes the monooxygenation of fatty acids. The P450 enzymes fall into two classes that differ in their redox partners. Comparison of the structure of P450BM-3, a class II P450 that resides in the endoplasmic reticulum, with that of P450cam, a class I mitochondrial enzyme, reveal differences in the regions for substrate and redox-partner binding.

Metal insulators

Quasicrystals lie somewhere between perfect crystals and purely amorphous materials, and much effort has gone into learning what effect their quasiperiodicity has on condensed matter properties. Pierce et al. (p. 737) find that high-quality bulk icosahedral alloys of aluminum, palladium, and rhenium exhibit low-temperature resistivities that are orders of magnitude higher than those of disordered metals or metallic glasses. Although these materials have the high electron density characteristic of metals, they behave as insulators at low temperature. The authors interpret this as evidence of electron localization and band-gap formation that result from the quasiperiodic structure of these alloys.

Gathered in garnet

Uranium-thorium isotopic data on basalts can provide information on the origin and mecha-

Assorted ices on Pluto and Triton

Both Pluto and Triton, Neptune's largest moon, have thick surface layers of mainly nitrogen ice mixed with ices of other simple molecules such as carbon monoxide, carbon dioxide, and methane. Ground-based infrared spectroscopy reveals similarities and differences in the mixture of ices on each body (Owen *et al.*, p. 745, and Cruikshank *et al.*, p. 742). Seasonal temperature variations on Triton are such that nitrogen ice cycles on a 700-year time scale between cubic and hexagonal crystal structures. Duxbury and Brown (p. 748) argue that the repeated phase transitions fragment the ice to produce a more reflective surface. Tryka *et al.* (p. 751) show how the two phases may be distinguished observationally through subtle differences in their infrared spectra. In a Perspective, Lunine (p. 697) sets these new observations and inferences in the context of the chemical evolution and dynamical development of the outer solar system.

nisms of magmatism at midocean ridges and elsewhere, provided that the distribution of these elements in minerals and melts in the mantle is known. Many oceanic basalts are enriched in thorium-230 compared to uranium-238; residual minerals in the source region thus apparently retain uranium in preference to thorium. In a series of experiments, LaTourette et al. (p. 739) show that garnet is the only major phase in the mantle that could account for such fractionation. The data imply that melting begins in the garnet stability field, at depths below 70 kilometers, and that melts ascend fast enough from this great depth that a significant fraction of radiogenic thorium-230 is preserved upon eruption.

Blocking a defense buildup

Salicylic acid, a useful human analgesic, was originally isolated from plants, where it appears to act as a signal in systemic acquired resistance, the ability of the plant to resist reinfection by pathogens at sites far away from the initial infection. Gaffney *et al.* (p. 754) blocked salicylic acid accumulation in tobacco plants by transforming them with a gene for a *Pseudomonas* enzyme that converts salicylic acid to catechol. When these transgenic plants were infected with tobacco mosaic virus, the effects of primary infection were more severe and systemic acquired resistance was not induced.

Alkali ion binding and enzymes

Many proteins that bind the alkaline earth metals calcium or magnesium have been described. Much less is known about proteins that bind the alkali cations sodium and potassium. Toney et al. (p. 756) provide the crystal structure of dialkylglycine decarboxylase, an enzyme that is positively regulated by potassium and negatively regulated by sodium. The geometry of the ligands at the alkali metal binding site changes with the identity of the ion, and these changes connect to movements of amino acid residues located at the active site. This enzyme also is unusual because it catalyzes both a decarboxylation and a transamination with the aid of a pyridoxal phosphate cofactor.

Uneven start

Most eukaryotic promoters have a TATA box sequence located approximately 30 nucleotides upstream of the transcription start site, and DNA melting associated with transcription from such promoters occurs approximately 20 nucleotides downstream of the TATA box. In yeast, the distance between the TATA box and the transcription start site varies greatly; TATA lies between 30 and 120 nucleotides upstream of transcription start site. Giardina and Lis (p. 759) show that DNA melting in yeast begins about 20 bases downstream of TATA, and that distance to the transcription start site may vary from about 10 to 90 nucleotides.

TAP dance

Peptide antigens can activate T cell responses only if they are bound to a major histocompatibility complex (MHC) molecule. For class I MHC molecules, these peptides are generated in the cytosol and must be translocated into the lumen of the endoplasmic reticulum (ER). Neefjes et al. (p. 769) present direct evidence that two putative protein transporters, TAP1 and TAP2, are required for MHC class I assembly in a process dependent on adenosine triphosphate. A radiolabeled peptide was introduced into the cytosol; addition of an N-linked glycan to the peptide indicated that it had been translocated into the ER. Both TAP-1 and TAP-2 had to be expressed in a TAP-deficient cell line in order to see translocation.

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