

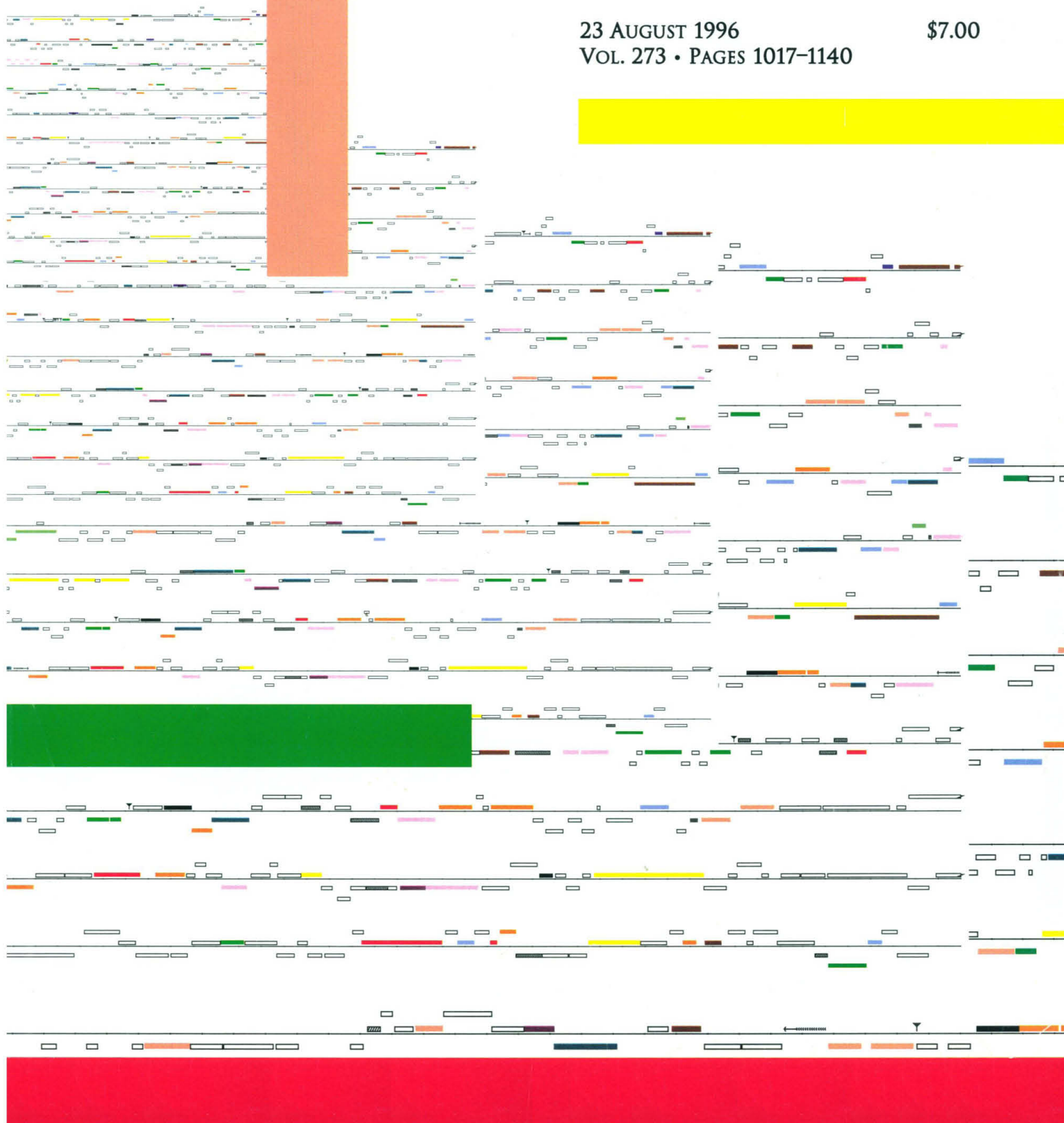


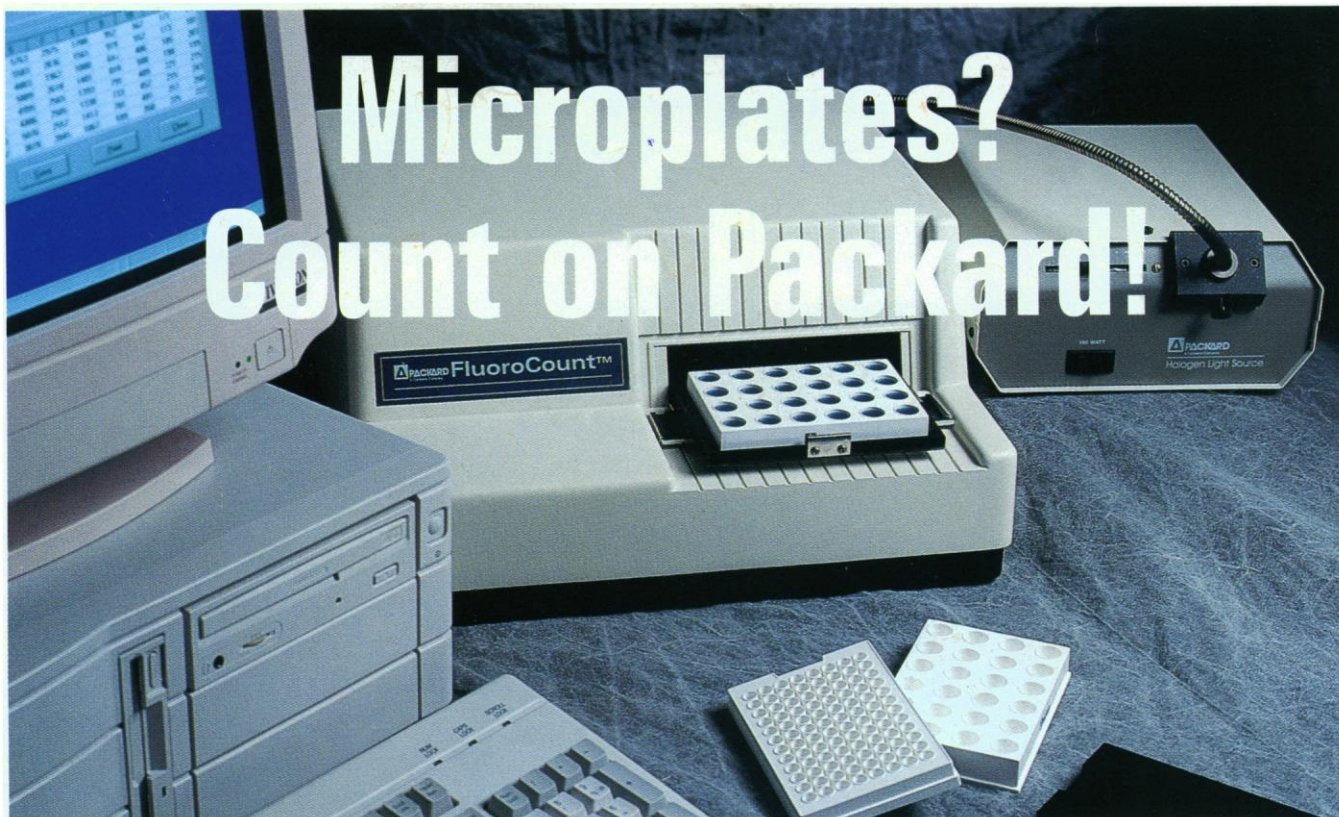
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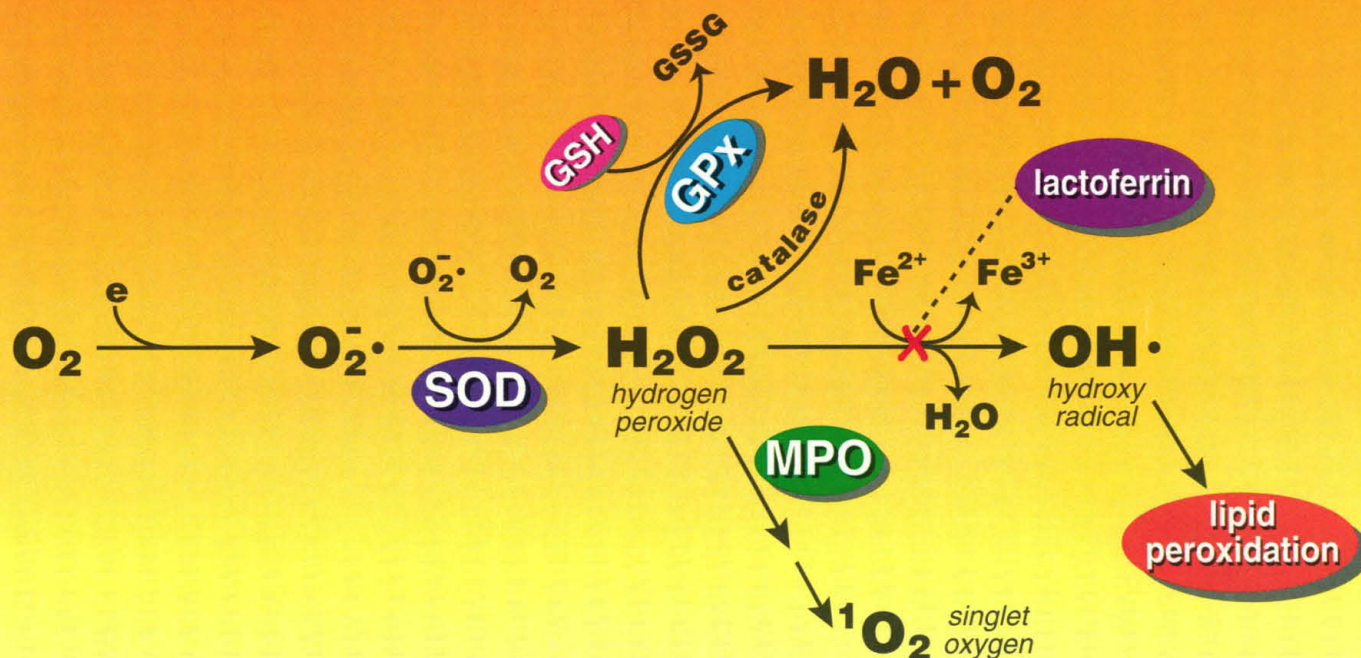


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COVER

The genome of *Methanococcus jannaschii* is the first one of the Archaea domain that has been completed by whole-genome shotgun sequencing at The Institute for Genomic Research. This provides the first oppor-

tunity for large-scale comparisons of the genetic components from all principal domains—Eukaryotes, Bacteria, and Archaea. See the article on page 1058 and the News story on page 1043.



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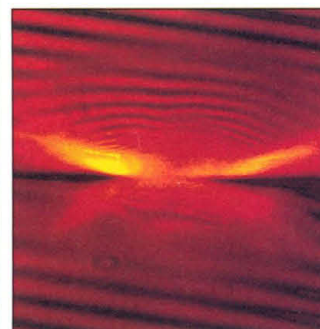
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Seeing light and dark

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THIS WEEK IN SCIENCE

edited by PHIL SZUROMI

Star quality

Spectra of hydrogen Lyman α emissions from the excess hydrogen bulge region along the magnetic equator of Jupiter have been used by Emerich *et al.* (p. 1085) to trace the structure of the jovian upper atmosphere. A model involving the equatorial collision of supersonic turbulent jets that were created in the polar auroral regions fits the spectra. Although more sophisticated modeling is necessary, a turbulent planetary atmosphere similar to a star's atmosphere may help to explain not only the hydrogen bulge but also the excess thermal energy observed in the upper atmospheres of all four outer giant planets.

Methane record

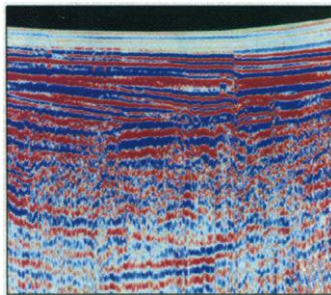
Methane is a key greenhouse gas (along with water and carbon dioxide) and has a wide range of natural sources and sinks. Brook *et al.* (p. 1087) present a record of atmospheric methane concentrations from Greenland's GISP2 ice core. This result extends an earlier, shorter record and shows that methane variations tracked both fine-scale warming and cooling events recognized in this and other ice cores and longer variations in temperature modulated by Earth's orbit.

Fresh fishes

Lake Victoria contains a rich diversity of endemic fish; their evolution has been debated. Johnson *et al.* (p. 1091) present seismic data and drill core evidence that Lake Victoria dried up completely in the late Pleistocene, about 12,400 carbon-14

Questions of relatedness

Archaeons are an evolutionarily separate group of single-celled organisms that include methanogens, extreme thermophiles and halophiles, and sulfur-dependent species. Our understanding of their relationship to Bacteria and Eukaryotes has generally been limited to analyses of a few genes. Bult *et al.* (p. 1058; see cover and the news story by Morell, p. 1043) have now sequenced the genome of a methanogen, *Methanococcus jannaschii*. Genes related to energy production, cell division, and metabolism resemble those of Bacteria, but those for transcription, translation, and replication resemble those of Eukaryotes. The authors conclude that, despite sharing ancient metabolic genes with Bacteria, the Archaea and Eukaryotes have a common ancestry.



years ago. The authors suggest that even small satellite lakes or ponds were unlikely to have remained. If so, then the fish diversity evolved since this time.

X-ray laser gains

Amplification occurs in x-ray lasers within an atomic plasma formed by intensely heating a metal target with an optical laser. One puzzle, however, has been that the experimentally realized gains have always been significantly less than those predicted theoretically. Cauble *et al.* (p. 1093) provide an explanation for the discrepancy. They built an x-ray laser that served as an interferometer to probe a shorter x-ray laser amplifier. What they found was that the lasing action within the plasma was highly heterogeneous, and that this inhomogeneity accounts for the loss of gain. Such results should

prove useful in developing strategies for the control of this inhomogeneity.

Delaying tactic

Sensory input challenges neuronal circuits to provide the utmost in sensitivity and discrimination. The influence of such input on the development and topographic specification of sensory neurons is well known; what is becoming clearer is the existence of active processes that occur in the mature system. Yan and Suga (p. 1100) describe the heightened tuning of auditory neurons in the Jamaican mustached bat as a result of increased activity of cortical neurons. When the echo of an emitted vocal pulse returns with a particular delay, positive feedback from the brain improves the detection of that echo in the periphery. How this modulation might reflect attention remains to be seen.

Bright and brighter

What we perceive—the brightness of one gray area as compared to another—may differ from what we see—the number of photons reflected from the

surface. Nerve cells in the primary visual cortex are known to underlie the parsing of the visual scene into borders, orientation, color, and so forth. Now Rossi *et al.* (p. 1104) show that they may be involved in the spatial integration of incident information that leads to “higher level” processes such as the representation of brightness. In an accompanying Perspective (p. 1055), Albright describes the mastery of brightness exhibited by Rembrandt.

Pili for plants

Agrobacterium, which forms tumors on plants by transferring a tumor-inducing DNA fragment into the plant cells, has found a place of honor among plant molecular biologists as a tool for transferring cloned DNA to form transgenic plants. Fullner *et al.* (p. 1107) show that pili much like those that function for bacterial conjugation form from the surface of *Agrobacterium*. It is possible that these pili function in an analogous manner but transfer DNA into the eukaryotic plant cell.

Dual role

The role of the excitatory amino acid aspartate in neurotransmission has been subject to controversy. Aspartate can act through the N-methyl-D-aspartate (NMDA) receptor in hippocampal neurons. Yuzaki *et al.* (p. 1112) present evidence that aspartate can act through a specific receptor, distinct from the NMDA receptor, in another class of neurons—the Purkinje cells. This novel receptor is predicted to have distinct properties that could be involved in synaptic plasticity.

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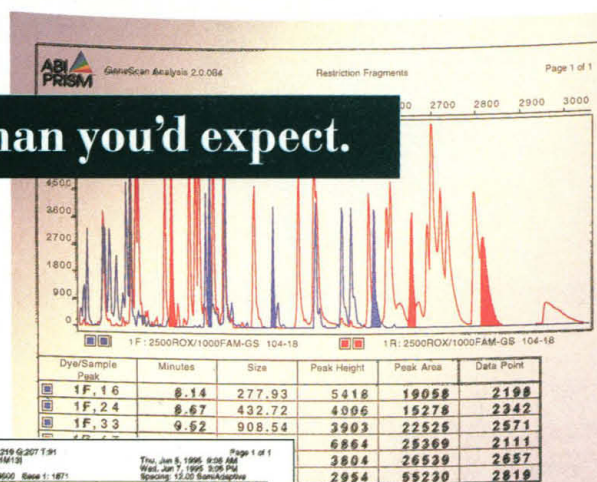
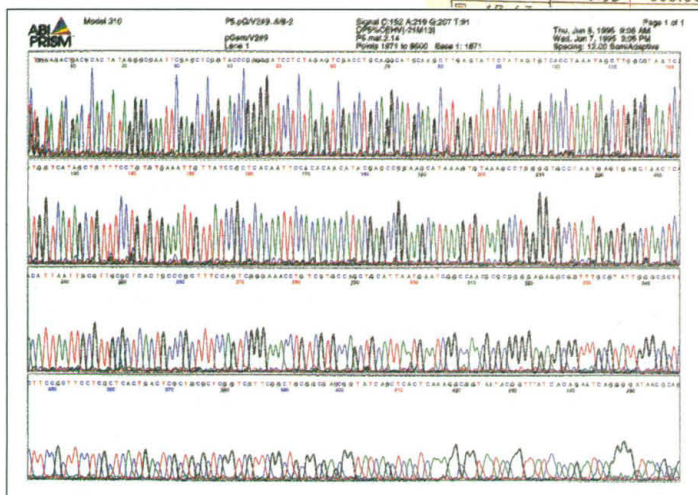


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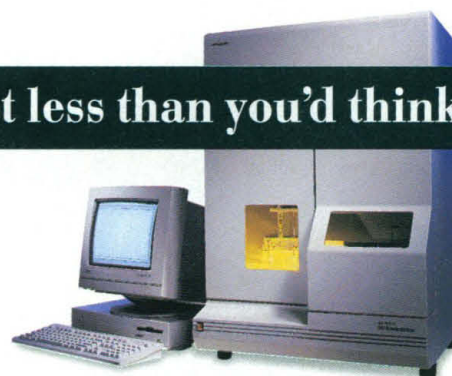
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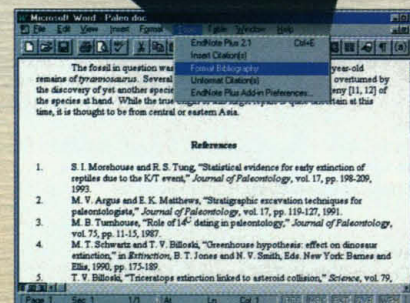
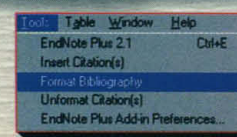
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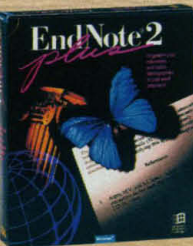
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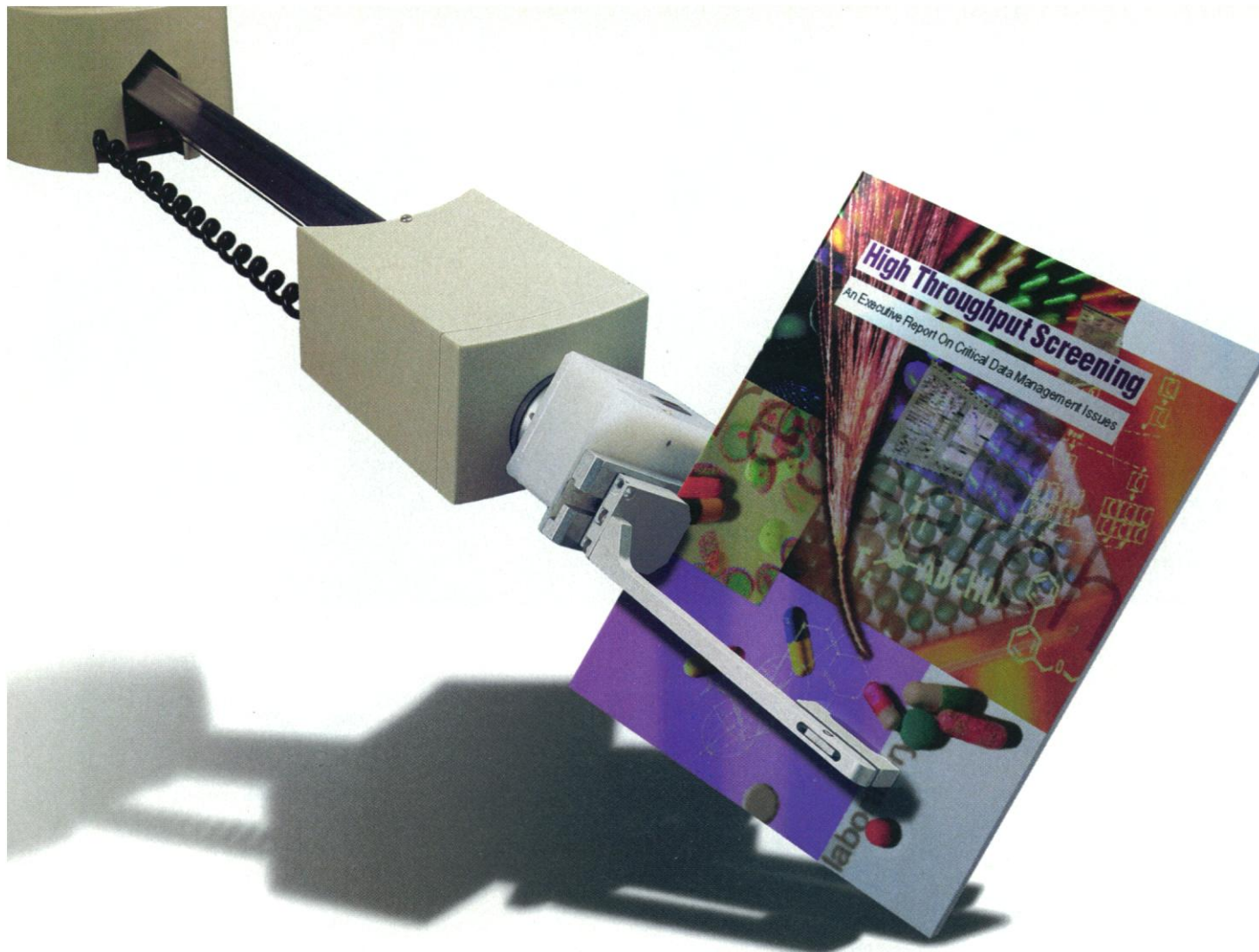
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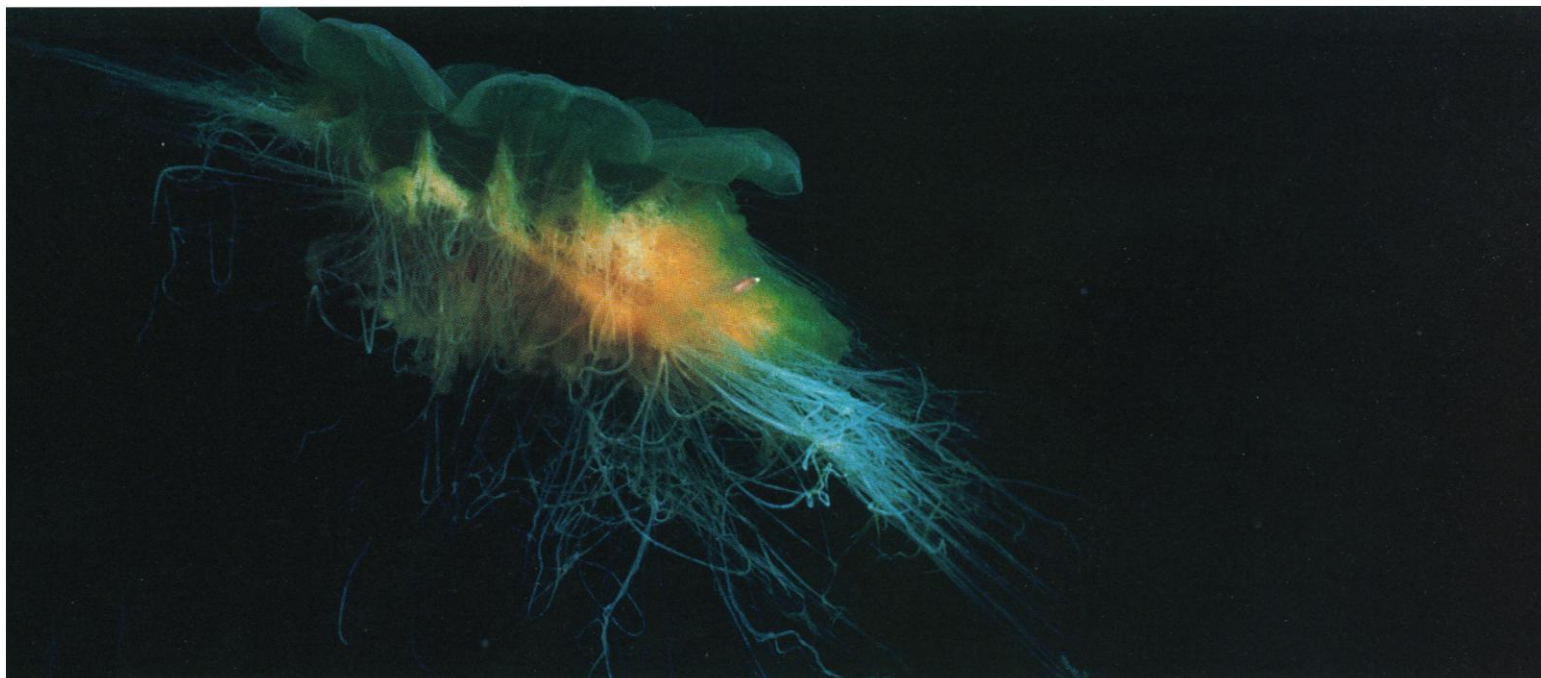
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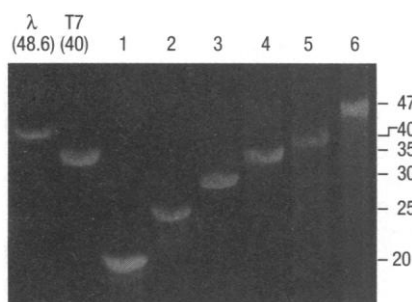


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SCIENCE

The Genome of *Methanococcus jannaschii*

Fig. 3. The gene map of the *M. jannaschii* genome. Genes positioned above the line are transcribed in the forward direction; genes below the line are transcribed in the reverse direction. Each line represents approximately 150,000 bp of genome sequence. Coding regions are color-coded according to puta-

tive role as described in the key. Additional features, such as ribosomal operons, tRNAs, and repetitive elements, are also indicated in the key. Gene identification numbers correspond to those in Table 1.

Table 1. Summary of genes from *M. jannaschii* having putative identifications. Gene numbers correspond to those in Fig. 3. Each identified gene has been assigned a putative cellular role category adapted from Riley (34). The putative gene identification and percent amino acid identity are given. An expanded version of this table, with additional match information, can be viewed on the World Wide Web at <http://www.tigr.org/tdb/mdb/mjdb/mjdb.html>. Abbreviations: biosyn, biosynthesis; dep, dependent; dinucl, dinucleotide; diP, diphosphate; fam, family; form, forming; mop, molybdopterin; prot, protein; put, putative; rel, related; sub, subunit; term, termination; triP, triphosphate;

ATase, aminotransferase; BP, binding protein; Co, coenzyme; CoA, coenzyme A; CoM, coenzyme M; DAPA ATase, 7,8-diaminopelargonic acid aminotransferase; DCase, decarboxylase; DHase, dehydrogenase; DTase, dehydratase; G3PDHase, glyceraldehyde-3-phosphate dehydrogenase; GlcNAc, *N*-acetylglucosamine; H4MPT, tetrahydromethanopterin; LPS, lipopolysaccharide; MFR, methanofuran; MTase, methyltransferase; MVR, methylviologen-reducing; PRAC, phosphoribosylformiminoimidazole carboxamide; PRAD, phosphoribosylaminoimidazole; PRTase, phosphoribosyltransferase; RDase, reductase; Sase, synthase-synthetase; Tase, transferase.

Fig. 3.

