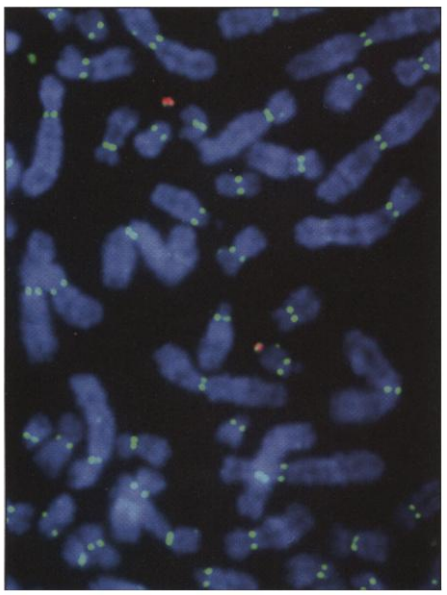
INTRODUCTION

Unlocking the Genome

Yes, there is life after the announcement of the sequencing of the human genome. Back in February, we all spoke about the new doors to research that the sequence would open. Not even a year later, the truth of that prediction is abundantly clear.

This issue is a potpourri of new ideas, projects, and scientific advances. Avise (p. 86) starts us off with a look at how metaphors of the genome are evolving, ranging from beads on a string to a social collective. Two essays explore how genomic information can benefit society or, if misused, legitimize discrimination and evil acts. Singer and Daar (p. 87) describe how genomics and biotechnology can improve health in developing countries. In a Science and Society essay, Allen (p. 59) reviews the history of the eugenics movement and the danger of a sequel.

Moving from the two-dimensional genome sequence to the three-dimensional structure of proteins will require high-throughput protein analysis. Stevens *et al.* (p. 89) discuss international efforts to forge collaborations and develop such technology, whereas Baker and Sali (p. 93) provide an in-depth perspective on the state of the art of protein modeling.



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The genome still harbors mysteries, including how genomic material is replicated. Gilbert (p. 96) reviews data indicating that a specific origin sequence is not always a requisite in eukaryotes and how these findings can shed light on selective pressures operating on the regulation of DNA replication. Rhaguraman *et al.* (p. 115) describe a genome-wide analysis of replication patterns in yeast, using high-density oligonucleotide arrays.

Although the centromere is crucial for chromosome segregation during cell division, it has been difficult to study because of its high content of repetitive DNA. Schueler *et al.* (p. 109) have used a variety of approaches to pinpoint the region of the centromere that is crucial for its function and to study its evolution. Further commentary can be found on *Science*'s Functional Genomics Web site* and in a News of the Week story by Pennisi.

One of the most significant applications of sequence information is to localize disease-associated genes. Pennacchio *et al.* (p. 169) combine comparative genomics, overexpression and knockout studies in mice, and population studies of polymorphisms in humans to identify a new member of the apolipoprotein family associated with control of triglyceride levels in the blood (see News of the Week story by Seydel).

Special features related to genomics can also be found on the Signal Transduction Knowledge Environment (STKE) Web site.† The potential of advances in genome analysis to affect studies of aging are discussed in the Editorial by Martin (p. 13), which describes the launch of the Science of Aging (SAGE) Knowledge Environment.‡ In the News section, Pennisi and Normile (p. 82) explore the decisions ahead for funding agencies, which must now choose among a plethora of riches, from comparative genomics to proteomics—and the ongoing debates over which deserve top priority.

Although prediction is risky (and we do not want to leak the surprises of future issues), we are sure that scientific bounty from the genome will only increase.

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* www.sciencegenomics.org † stke.sciencemag.org ‡ sageke.sciencemag.org

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See also Editorial on p. 13, Science and Society Essay on p. 59, Book Review on p. 62, Research Articles on pp. 109 and 115, and Report on p. 169.

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