**1972** Peter Mazur and Stanley Leibo pioneered cryopreservation of mammalian embryos. At Oak Ridge they succeeded in freezing, thawing, and implanting mouse embryos, thus spurring a revolution in the livestock industry.

**1973** Bruce Ames at the University of California, Berkeley, devised a screening test, now known as the Ames test, for identifying potential cancer-causing chemicals and pharmaceuticals.

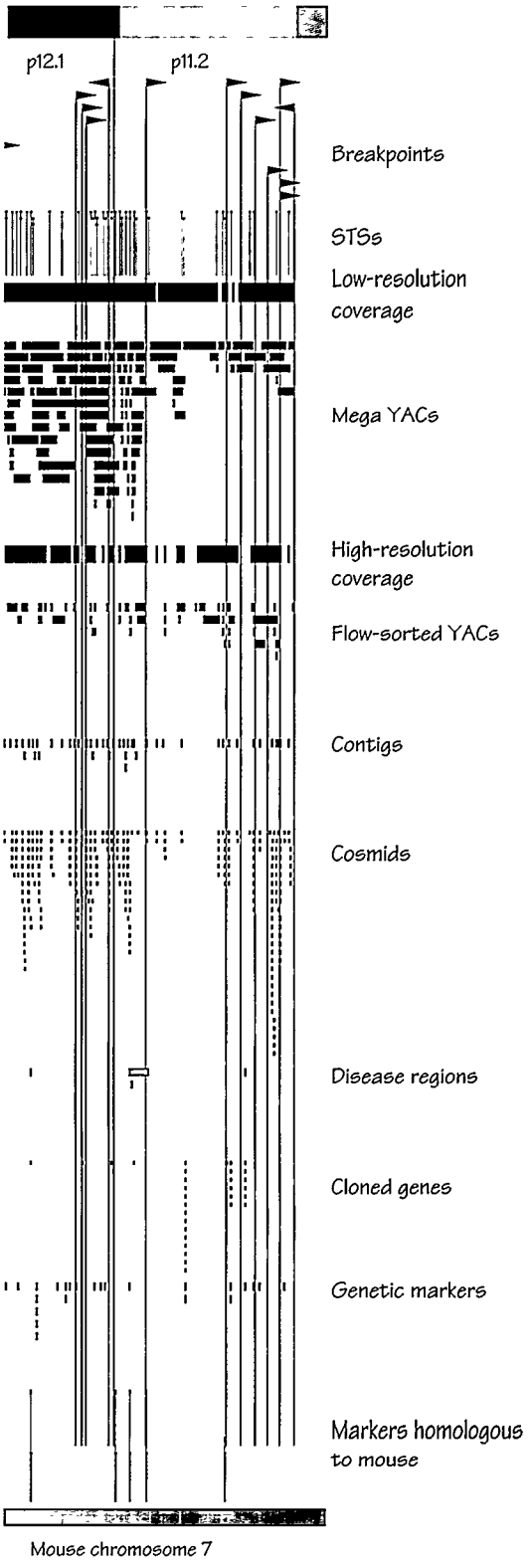
**1974** Brookhaven biologists demonstrated that ultraviolet-produced pyrimidine dimers in cells induce the formation of tumors. They would later succeed for the first time in using UV light to transform normal human cells in culture to premalignant cells.

ents' exposure to radiation. Indeed, the Radiation Effects Research Foundation maintains a precious resource of frozen white-blood cells from almost a thousand families of survivors and children, awaiting the day when their DNA can be analyzed for telltale mutations. But that day awaits new tools for genetic analysis and a far more detailed knowledge of the human genetic makeup. Thus the tie to the genome project.

In 1986 the DOE boldly announced its Human Genome Initiative, both to develop these needed tools and, far more broadly, to provide a comprehensive picture of the human genetic script. For the genome project is no less than this, to read in detail the sequence of three billion letters (or *base pairs*) that makes up the genetic recipe of our species. The ultimate payoffs stretch the imagination: Molecular medicine will turn from treating symptoms to addressing the deepest causes of disease; new pharmaceuticals will attack diseases at their molecular foundations. More sensitive diagnostic tests will uncover ailments in their earliest stages. New preventive therapies targeting individuals with genetic susceptibilities—either to heritable disease or to environmental carcinogens—will thwart some diseases altogether. Even gene therapy will become possible, actually "fixing" genetic errors.

By the mid-eighties, the foundations for this formidable project were already firmly established. GenBank, a DNA sequence repository, was in place at Los Alamos, backed up by DOE computer and data-management expertise. Chromosome-sorting capabilities, essential to the genome initiative, existed at both Livermore and Los Alamos. And these same labs had recently launched the National Laboratory Gene Library Project. Nonetheless, the idea of sequencing the entire genome was greeted at first by skepticism. Today, though, the DOE's prescient initiative has been embraced nationally and internationally, and the genome project is making steady progress toward reaching its goal in the year 2005.

Together with investigators supported by the National Institutes of Health, DOE-funded laboratories and university scien-




**MAPPING THE TERRAIN** A much-simplified map covering some 20 million base pairs of chromosome 16 hints at the complexity of chromosomal mapping. Most of the different symbols indicate a different kind of well-characterized chromosomal fragment or marker; collectively, these genomic signposts provide a sound basis for detailed sequencing efforts.