LHC design requires more than 1,000 high-powered superconducting magnets to accelerate protons to nearly the speed of light and bend their paths to keep them on a steady course around the ring.

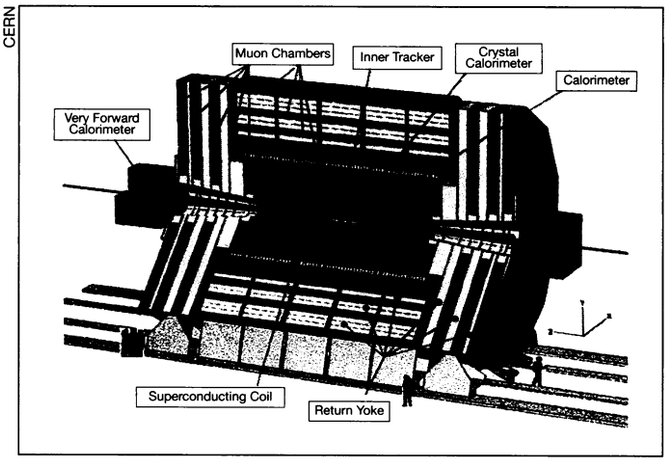
When the LHC's two adjacent proton beams, circulating in opposite directions around the ring, are brought together, protons collide at a combined energy of 14 teraelectronvolts. This energy should be high enough for researchers to detect the postulated Higgs boson. Theorists have proposed that this particle is responsible for determining the masses of other fundamental particles, but no one has detected any traces of it at the energies now accessible to particle accelerators.

The builders of both the LHC and its two main detectors face a number of formidable technical challenges. For instance, the collider's magnets must maintain larger magnetic fields than those used previously in accelerators, and they must operate at a frigid 1.9 kelvins, about 300°C below room temperature and even colder than liquid helium. Moreover, the LHC's detectors must be able to withstand intense radiation yet rapidly and precisely measure the trajectories and energies of hundreds of millions of photons, electrons, and muons per second.

Officials of DOE hope to reach a final agreement with CERN by November, before preparing the department's 1998 budget for congressional consideration.

— I. Peterson

CERN



This cutaway view of the Compact Muon Solenoid particle detector shows the instrument's layered structure. A large superconducting coil generates a uniform magnetic field of 4 teslas at its core. The detector itself measures 14.6 meters wide and 21.6 m long. Collisions between protons traveling in opposite directions spray debris into the detector's walls, where calorimeters and other devices record the arrival of the scattered particles.

Bringing bold color to chromosomes

When television executives colorize classic black-and-white films such as *Casablanca*, howls of protest from movie purists fill the air. In contrast, a report announcing the colorization of human chromosomes has raised a hue and cry of delight among geneticists—24 hues, in fact.

By attaching fluorescent markers to carefully chosen DNA sequences, investigators have learned how to paint a color-coded picture of all 24 human chromosomes (the sex chromosomes X and Y and the 22 chromosomes present in pairs).

This newly developed artistic ability should improve diagnosis of the many chromosomal abnormalities that cause cancer or other genetic diseases.

"It offers the promise of greatly improving the efficiency, as well as potentially the accuracy, of both clinical and research chromosome analysis," says Huntington F. Willard of Case Western Reserve University School of Medicine in Cleveland.

The color-coding technique is described in the April NATURE GENETICS by Michael R. Speicher, Stephen Gwyn Ballard, and David C. Ward of Yale University School of Medicine. It is "a beautiful (scientifically and literally) study," observes Michelle M. Le Beau of the University of Chicago in an accompanying commentary.

Researchers studying chromosomes traditionally stain them to reveal distinctive black-and-white banding patterns. By painstakingly analyzing the bands, a task difficult to automate, scientists can often spot chromosomal irregularities.

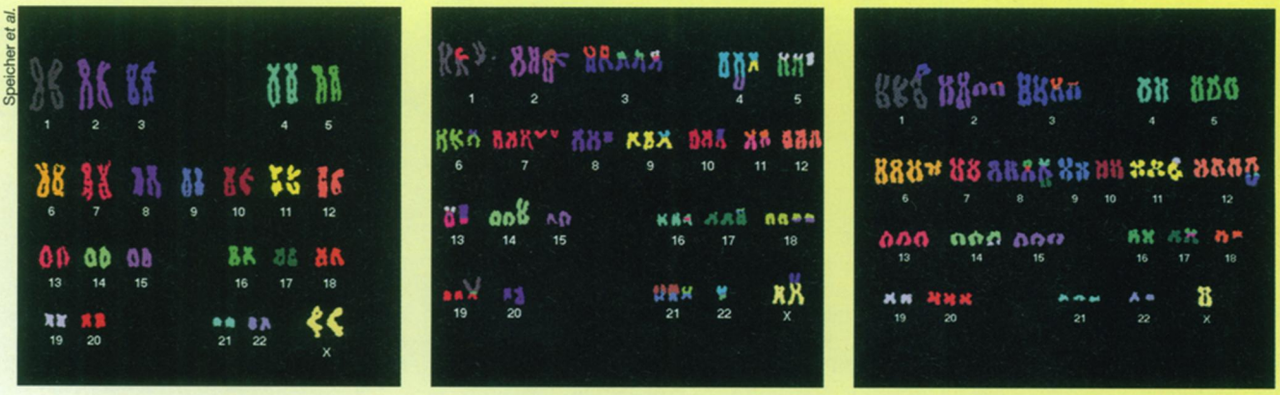
To improve the odds of finding abnormalities, and to make possible the automation of such analysis, researchers have experimented with linking fluorescent markers to known DNA sequences. These DNA-based probes attach only to specific sites within the human chromosomes.

By labeling thousands of chromosome-specific DNA sequences with five different fluorescent markers, the Yale group was able to produce unique spectral fingerprints for each of the 24 chromosomes. Using these fingerprints, they assigned a different color to the computer image of each chromosome.

This method has made it easier for researchers to detect abnormalities such as translocations, in which pieces of chromosomes exchange places with one another. "That's very important for tumor cytogenetics. Many of these rearrangements can't normally be deciphered," says Speicher.

Other research groups are working on variations of the Yale technique, ones they hope will be less costly or even easier to automate. *— J. Travis*

Speicher *et al.*



A new analytical technique colorfully shows the differences between the chromosomes in a normal cell (left) and those in cancer cells (center and right). In dividing cancer cells, parts of chromosomes inappropriately trade places and extra chromosomes persist.