once the station is ready," says Baldwin.

One pressing problem is how to maintain interest in a program with few research opportunities until the space station is ready to do science in 2005. "We're at a very critical stage in building the space station," says Gaffney, "and not to do good science once it is ready would be an absolute tragedy."

–ANDREW LAWLER

HUMAN GENOME PROJECT

Chromosome 21 Done, Phase Two Begun

Chalk up two achievements—one public relations, the other scientific—for the international consortium in the race to sequence the human genome. This week, on the eve of an annual genome meeting at Cold Spring Harbor Laboratory in New York—and, perhaps, to preempt an expected statement from rival Celera Genomics of Rockville, Maryland—the international consortium announced on 8 May that it has completed (almost) "phase one" of the project, the rough draft of the human genome. (85% of the promised 90% of the draft sequence is now available in GenBank, says the consortium.) On 9 May, the consortium entered "phase two" and turned its collective sequencing firepower to "finishing" the human genome—that is, producing a 99.99% accurate sequence. Celera

Gold standard. The highly accurate sequence of chromosome 21 should help illuminate Down syndrome.

CREDIT: (RIGHT) RCSB

head J. Craig Venter dismissed the announcement as an "artificial" milestone and "science by press release"—a tactic he has used himself.

But Venter lauded the consortium's other announcement: the complete sequence of chromosome 21, only the second chromosome to be finished. Already, this chromosome, published electronically this week and in print in the 18 May issue of *Nature*, has reached the gold standard for which the consortium is striving for the entire genome, says Yoshiyuki Sakaki, who directs the human genome sequencing effort at the Institute of Physical and Chemical Research (RIKEN) outside Tokyo and whose team did half the sequencing.

Together, the 62 scientists from 13 labs have determined the identities of 33.5 million bases of the long arm and another 280,000 bases of the short arm of chromosome 21. Just three clone gaps remain—stretches, each about 30,000 bases long, that could not be determined with current technology. By contrast, chromosome 22, which is roughly the same size and was completed last December, has 10 such gaps (*Nature*, 2 December 1999). In another technical tour de force, the chromosome 21 team can also claim the longest contiguous stretch of DNA ever sequenced, at 25.5 million bases, says Sakaki.

Sequencing proceeded so quickly in part because several groups interested in Down syndrome had begun mapping chromosome 21 in the 1980s, before the Human Genome Project even existed. In Down syndrome, an extra copy of chromosome 21 results in mental retardation, heart problems, and other abnormalities. Now the task of figuring out just what goes wrong in this devastating disease will be far easier. Instead of finding the expected 800 to 1000 genes, gene prediction programs came up with just 225. "We now have a real definition of who the [genetic] players are," says Roger Reeves, a geneticist at Johns Hopkins University School of Medicine.

The paucity of genes on chromosome 21—one 7-million-base stretch contains just one gene—may have broader implications as well: If the gene prediction programs prove correct, then the entire human genome could have less than the 100,000 genes previously estimated.

As sequencers enter the home stretch, competing claims of genome accomplishments should be coming fast and furious. But, says Reeves, it will be quite a while before any sequence beats the accuracy and completeness of chromosome 21.

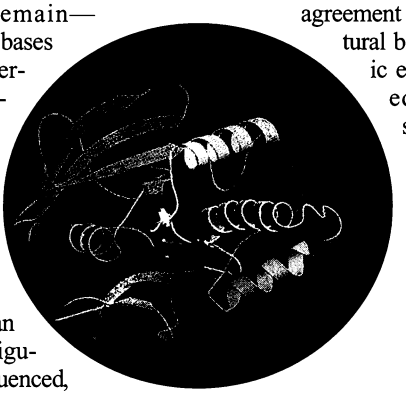
–ELIZABETH PENNISI

With reporting by Leslie Roberts.

STRUCTURAL GENOMICS

Protein Data Justice for All

Scientists who crack protein structures and colleagues who want to decipher what these proteins do are on the verge of a watershed agreement that would usher structural biology into the genomic era. The carefully crafted guidelines are designed to help coordinate international financing of publicly funded protein structure efforts and ensure prompt release of structure data so that no team has an unfair advantage in working out the functions of unknown proteins.



Fast and fair. New guidelines urge teams to quickly submit structures to repositories such as the Protein Data Bank, which last week released this image of human protein tyrosine phosphatase–1B.

The guidelines, being finalized as *Science* went to press, come at a time when robotics and computer automation promise to transform structural biology into a high-speed effort, dubbed "structural genomics," in which researchers will churn out thousands of protein structures in the next 5 years. Nurturing this souped-up approach, the National Institutes of Health (NIH) this fall plans to fund up to six structural genomics pilot centers to establish and test techniques for high-throughput x-ray crystallography and nuclear magnetic resonance (NMR) spectroscopy, the workhorse technologies of structural biology. Similar approaches are being adopted or considered in Japan, the United Kingdom, France, Brazil, and Germany (*Science*, 17 March, p. 1954).

To help coordinate these efforts, officials at NIH and Britain's Wellcome Trust last month brought some 50 leading protein specialists to the Wellcome Trust Genome Campus in Cambridge, U.K., for a brainstorming session on how to release data quickly and fairly. They had a gulf to bridge.

"Bioinformatics experts want fast access" so they can run follow-up experiments, says John Norvell, who heads the structural genomics program at the National Institute of General Medical Sciences in Bethesda, Maryland. But "experimentalists want time to check the data."

The issue boils down to how protein structures are gleaned and checked before release, says Wayne Hendrickson, a structural biologist at Columbia University. Computer programs, fed data from x-ray crystallography and NMR experiments, generate the likeliest set of three-dimensional coordinates for all of a protein's atoms. Bioinformatics experts initially wanted guidelines that mandate the release of those computer predictions the instant they are produced. Such a policy would be similar to the way sequence data from the publicly funded human genome project are posted daily on the Web.

"That did not fly," says Tom Terwilliger, an x-ray crystallographer at Los Alamos National Laboratory in New Mexico. Experimentalists maintain that protein structure analysis is more complex than spitting out raw genome sequence data. Each modeling prediction must be vetted, Hendrickson says. Several participants, he says, felt there's "no need to abandon the current standards of investigators making the decision" on when data are ripe for release.

But although structural biologists will still make the call on when data are solid, they won't be allowed to withhold a structure for the sake of determining its function. That means changing the status quo. When a protein structure is submitted to a journal today, Hendrickson says, it's almost always accompanied by findings—from experiments that alter key amino acids in the protein, for instance—that allow scientists to make educated guesses about how the protein works. But with a high-speed approach to solving protein structures, says Norvell, "publishing will have to be done in a different way."

NIH and other agencies that plan to pour money into the structural genomics centers don't want to freeze out biologists not associated with the centers. According to Hendrickson, "everyone agreed that the concept should not give those groups a privileged status."

As a compromise, researchers will be asked to publish their results—most likely in electronic format or as a brief summary in a specialist journal—within 2 to 4 weeks of finishing a structure, says Stephen Burley, a structural biologist at The Rockefeller University in New York City. "The moment the paper is posted on the Web," he says, "the coordinates would be placed in the Protein Data Bank," which is freely available to all researchers. The burden will be primarily on funders to enforce the timelines. They're accustomed to that, Burley says: Agencies regularly use their leverage over purse strings to ensure that structural biologists submit coordinates to the Protein Data Bank as soon as findings are published.

As an additional prod, structural biologists plan to add a little peer pressure. Hendrickson and others say the new guidelines call on each structural genomics center to keep a log on the Web of which structures they are attempting to solve. They would chart milestones such as cloning, isolating, and purifying a protein, and coaxing it to form a crystal. This will not only help to prevent several groups from working on the same projects, says Hendrickson, but "it will put internal pressure on the groups that they wouldn't be able to hold something forever."

–ROBERT F. SERVICE

With reporting by Michael Hagmann in Cambridge, U.K.

GLOBAL WARMING

Some Coral Bouncing Back From El Niño

Coral reefs in the Indian and Pacific oceans seem to be recovering more quickly than expected from a recent devastating "bleaching" caused by high ocean temperatures. New research suggests that the nascent recoveries may be partly due to the unexpected survival of juvenile coral that somehow avoided the brunt of the environmental assault. "It may indicate that reefs are more resilient than we had thought," says Terry Done, a senior research scientist at the Australian Institute of Marine Science in Cape Ferguson who studies reefs in the Indian Ocean. However, the coral would not be able to mature and recover from the repeated bleaching forecast to accompany projected global warming, he adds.

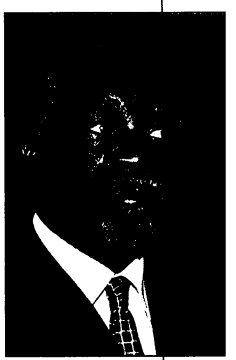
Resilient reefs. There may be hope for some areas hard hit by extensive coral bleaching after 1997–98 El Niño event.

Coral stressed by heat or disease expel zooxanthellae, the symbiotic algae that give the white

CREDITS: (TOP TO BOTTOM) MICHEL EULER/AP; PROVIDED BY GREOGOR HODGSON

ScienceScope

Unconventional Committee South African President Thabo Mbeki's controversial AIDS advisory panel found little common ground this week and ended up establishing a four-person committee to devise tests of fringe ideas about what causes the disease. Mbeki outraged many mainstream AIDS researchers last month when he questioned whether HIV causes AIDS and named leading skeptic Peter Duesberg of the University of California, Berkeley, to a deeply divided 33-member panel that will recommend ways South Africa should fight the disease (*Science*, 28 April, p. 590).



The panel, which met on 6 and 7 May in Pretoria, appointed two researchers from each camp to work on formulating experiments that could test theories about HIV's role in AIDS, which threatens more than 10% of South Africa's 42 million people. The four—Duesberg, William Makgoba of South Africa's Medical Research Council, Helene Gayle of the Centers for Disease Control and Prevention in the United States, and Harvey Baily, a Mexico-based AIDS researcher—plan to confer by Internet over the next 6 weeks. They will return to South Africa to present their ideas before the 7 July opening of the 13th World Conference on AIDS.

Critics call the exercise a waste of time and money. But Mbeki told the panel he is keeping an open mind: "You can't respond to a catastrophe merely by saying 'I will do what is routine.' "

Eyes on the Finnish Searching for new ways to battle type I diabetes, the Juvenile Diabetes Foundation (JDF) is turning to the country with the world's highest incidence of the disease. Last week, JDF signed off on two 5-year contracts, together worth over $4 million, to support Finnish researchers.

A joint venture with the Academy of Finland and the Sigrid Juselius Foundation will focus on new treatments, such as using stem cells to replace lost pancreas cells. The other program, run by Turku University since 1995, aims to test 20% of Finnish newborns for genetic susceptibility, then follow at-risk children in a bid to pinpoint what triggers the disease. Says JDF chief science officer Bob Goldstein: "It's a fabulous chance to do long-term epidemiology."