libraries. As a leading supplier of these tools, we would like to offer a possible explanation for the reported contamination of the CCRF-CEM cDNA used by the Généthon group mentioned in the article.

Since the initial complaint was reported to us, we have discontinued the sale of this library. We have deduced that the yeast sequences might have been introduced through a low-level contamination of yeast genomic DNA in yeast tRNA (purchased from a respected supplier of research-grade biochemicals) that was used as a co-precipitant of cDNA during cDNA synthesis. Until recently, this method was a common, generally accepted step in cDNA synthesis. It does not affect the quality or functionality of the library when it is used for the purpose for which it was intended (screening with a specific DNA probe). Ambiguity may arise when screening is done with a probe of significant homology to yeast sequences. Unfortunately, we had not anticipated early on that our libraries would be used for massive direct-sequencing purposes, as was done by the Généthon group. Nevertheless, as of November 1992, we stopped using tRNA in the preparation of our libraries.

To further understand the implications of the reported contamination, we also screened 20 libraries, which had been constructed using tRNA, with yeast-specific PCR primers. Eighteen (90%) produced faint positive bands, suggesting a frequency estimated to be less than 0.5%. Probing the same libraries with a 2-kilobase human β-actin cDNA probe revealed 0.15 to 0.9% positive signals, suggesting a normal representation of β-actin sequences. The same 2-kilobase β-actin probe did not produce positive signals when it was used to probe a yeast genomic library.

We agree with the major thrust of Anderson's article—that closer monitoring of the veracity of published sequences is critical. And while we sincerely regret the unfortunate experience of Généthon, we believe the extent of the contamination may not be as great as we initially thought and may represent an extreme case. The libraries we have studied thus far indicate that specific clones can be isolated if specific probes are used. This is further supported by the hundreds of genes isolated and published with Clontech libraries. As preventive measures, in addition to discontinuing the use of tRNA during library construction, we have implemented additional quality control parameters to estimate sequence representation of β-actin sequences in all libraries. We are also developing more rigorous procedures with which to eliminate incidental contamination.

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Sequencing the Human Genome

The article "NIH to appeal patent decision" by Christopher Anderson (News & Comment, 15 Jan., p. 302) incorrectly quotes me as saying that Incyte Pharmaceuticals "will have sequenced the entire human cDNA [complementary DNA] library of 50,000 to 100,000 gene sequences by 1995." We do indeed project that most human genes will be identified by 1995, but not by Incyte alone, as was stated in the article. Rather, we predict such a short time frame on the basis of the efforts of numerous independent groups, both in industry and academia, who, like Incyte, are rapidly expanding their large-scale cDNA sequencing capabilities.

Much of the public debate about the merits of cDNA sequencing is focused on the filing of patents on fragments of genes. We believe that gene fragments are of value and are thus worth patenting. Nevertheless, because of the rapid identification of new genes by many different groups worldwide, we believe that use patents may ultimately be more important than DNA patents to the future of the biotechnology industry. We plan to pursue the biological function of interesting new molecules we discover in our program accordingly.

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Converting Weapons to Fuel

Of the many new problems introduced by the end of the Cold War, none presents a greater threat than the fate of weapons-grade nuclear materials in several countries of the Commonwealth of Independent States (CIS). Denaturing stockpiles of weapons-grade uranium could be accomplished quickly by reversing the separation process used to make it. Enriched uranium could be mixed with depleted material to create isotopic compositions that would not be weapons-grade but would be useful as fuel for nuclear power reactors. This process is cheap and would require no research, development, or investment in infrastructure. Recent indications that the United States may purchase weapons-grade uranium from Russia (*1*) are heartening. Such a purchase could be preceded or followed by denaturing.

Unfortunately, denaturing weapons-grade plutonium is not feasible, as it can be reversed by widely known chemical processes. However, plutonium could be consumed in the intense neutron fields of nuclear reactors. The technology and infrastructure necessary to produce mixed oxide fuel, composed of natural or depleted uranium and a small percentage of plutonium, are available in several nations. If all of the power reactors in the United States were fueled with mixed oxides, the time required to effectively eliminate a weapons-grade plutonium stockpile of 200 tons (a common estimate of the total stocks in the United States and the CIS) would be about 2 years.

It took four decades to build up today's stockpiles of weapons-grade uranium and plutonium; they could be eliminated in a few years. Furthermore, they could provide a benefit to mankind in the form of electric power, which would partly compensate for the terror they have engendered.

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1. "Economic stimulus and investment package fact sheet" (U.S. Department of Energy, Washington, DC, 1993).

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The G-Word

I enjoyed very much "Heavenly name dropping" (ScienceScope, 29 Jan., p. 587), which gently pokes fun at my co-author Leon Lederman for calling his new book *The God Particle*. I must say that I've gotten a giggle out of the mental picture of Lederman crisscrossing the country over the past 6 weeks, eating bad airline food, breathing the rancid air in television green rooms, developing repetitive motion disorder