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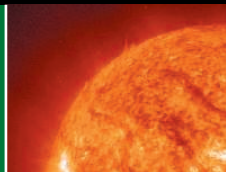
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LETTERS

edited by Jennifer Sills

Keeping an Eye on the Prize

I WAS VERY DISAPPOINTED TO FIND OUT (“Fame inflation,” *Newsmakers*, 1 February, p. 553) that I, like Steven Running, am not a Nobel laureate. According to the “Dear colleagues” letter I received from Ogunlade Davidson and Bert Metz on behalf of the IPCC, I am indeed a Nobel laureate, albeit perhaps along with many, many others. The letter says, “You no doubt have heard about the award of the Nobel Peace Prize to the IPCC, jointly with Al Gore of the USA. This makes all of you a Nobel laureate and we, as co-chairs, want to congratulate you wholeheartedly with this exceptional recognition.” Additionally, a beautiful Nobel Peace Prize certificate with my name on it now adorns my wall. Although the financial remuneration has not yet arrived, I have enjoyed the celebrity status associated with the honor. **ROGER A. SEDJO**

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Epigenomics: A Roadmap, But to Where?

RECENTLY, THE DIRECTOR OF THE NATIONAL Institutes of Health (NIH) allocated \$190 million for an “Epigenomics” Roadmap initiative (*1*). As investigators in this area, we endorse the idea that chromatin biology is an appropriate, if not essential, area for the NIH to support, not only for its fundamental biological significance but also its relevance to human disease. Nonetheless, we believe that this initiative, at least in its current form, will not yield significant benefits. If the use of the term “epigenome” is intended to equate the value of this Roadmap initiative with the Human Genome Project, it fails on several grounds.

First, it does not consider our current understanding of the roles of sequence-

specific DNA recognition events and transcriptional networks in controlling epigenetic changes. A multifaceted effort that elucidates transcriptional circuits that tell us where and when signal-responsive, sequence-specific regulators function would be more useful for understanding cell type programming.

Second, merely cataloging modification patterns offers comparatively little new or useful information. We already know that most genes are associated with one of a few patterns of chromatin modifications and that the patterns themselves do not tell us how that gene is regulated or how its expression state is inher-

