mistakable in proton-antiproton collisions.

In short, I agree with Cherfas that physicists of Fermilab know where to look for the top quark—in proton-antiproton collisions at the Tevatron!

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RU 486 Development

I read with great interest the series of articles related to the "contragestive pill" RU 486 (News & Comment, 22 Sept., p. 1319). It is not my intention to minimize the leading role of Etienne-Emile Baulieu in the clinical development and promotion in the media of this compound, as RU 486 would probably never have reached its present status without the stern determination of the INSERM biologist. However, I feel it my duty, on the grounds of simple scientific ethics, to add the following comments to the report by Jeremy Cherfas (p. 1323).

1) I was not the "chief chemist at Roussel"—this would be unfair to my colleagues; nor was I the chief of chemists, being in charge of only a small group of co-workers.

2) RU 486 was synthesized in April 1980, so it could not have been tested in 1978.

3) The story of "how" RU 486 was designed does not fit the facts as I recall them as a member of the Roussel research team, which was fully responsible for this discovery.

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I congratulate Jeremy Cherfas on his excellent article about the important work of Emile-Etienne Baulieu, who has been duly recognized for his efforts by being awarded the Lasker Prize for 1989. Baulieu points out appropriately the importance of the discovery of monohydroxytamoxifen's high binding affinity for the estrogen receptor in his own work. However, in the article that discovery is attributed to Robert Sutherland, who was a postdoctoral student in Baulieu's laboratory.

It should be noted out that the relevant papers from Baulieu's lab (*1*) both refer to earlier studies done by V. Craig Jordan (*2*). This in no way detracts from Baulieu's efforts in capitalizing on this fact to develop RU 486 and from appropriate recognition of his accomplishment.

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UCLA and Precollege Science

Bassam Shakashiri, head of the National Science Foundation's education program, appears to be saying (News & Comment, 20 Oct., p. 317) that the faculty at the University of California, Los Angeles (UCLA) are not concerned with improving precollege science. He is misinformed; the UCLA faculty have been involved with this endeavor for almost a decade. For example, Doing Chemistry (*1*), a multiyear project funded by the NSF Education Directorate, began at

UCLA in a 1983 summer workshop with Los Angeles area teachers and school districts. The dissemination phase of this project was delayed 14 months while a parade of NSF program officers were assigned to the project. More recently, UCLA faculty submitted a proposal to this directorate's solicitation for Projects to Promote the Effective Use of Technology in the Teaching of Science and Mathematics. The proposal, aimed specifically at middle and secondary school science, focused on the needs of teachers and students in urban, minority schools. The NSF Education Directorate assigned the proposal to evaluators so unfamiliar with technology that the reviewers did not appear to know the word "hardware." If Shakashiri wishes research universities to support the Education Directorate's goals, he will have to ensure efficient program management and competent peer review—long tenets of the research programs of NSF.

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Correction

After our characterization of cDNA encoding a 47-kD neutrophil cytosol oxidase factor was published (*1*), a second group published characterizations of similar cDNA clones (*2*). On the basis of an exchange of primary sequence data and resequencing, we have identified minor errors in both published sequences and have agreed on a corrected sequence. In the original numbering of our published sequence (*1*), an extra "C" should be added after base pair 900, a "GCC" should be inserted after base pair 1008, and base pairs 1013 and 1014 should be "GC." These changes alter the carboxyl terminus of the predicted protein beginning at amino acid 301 and ending at 390: RRSSIRNAHS IHQRSRKRLS QDAYRRNSVR FLQQRRRQAR PGPQSPGSPL EEERQTQRSK PQPAVPPRPS ADLILNRCSE STKRKLASAV. The new predicted protein sequence is 17 amino acids longer. The region of similarity to p21-ras-GAP is unaffected, and the carboxyl terminus remains very arginine- and serine-rich with several potential sites of phosphorylation by protein kinase C. Thus, all of the general statements made about the protein in our original paper still apply.

In addition to the three polymorphic base pair variants we reported in our original paper, four additional base pair polymorphisms have been identified, none of which affects encoded amino acids. In the original numbering (*1*), these are base pair 387 "G" or "A," base pair 825 "C" or "T," base pair 849 "A" or "G," and base pair 935 "C" or "T." These changes have been sent to GenBank and entered under accession number M25665. Readers may also request from us the complete corrected sequence.

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