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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