Correction

In our report "Phenotypic analysis of antigen-specific T lymphocytes" by John D. Altman et al. (4 Oct. 1996, p. 94), an error appeared in the sequence of the 3' oligonucleotide that was used to create the HLA-A*0201 plasmid containing the biotinylation substrate peptide tag. In our original construct, the peptide tag was added after position 271 of HLA-A*0201, but this did not lead to efficient refolding of the protein. We then produced a new fragment by polymerase chain reaction from the original pHN1-A2 expression plasmid, using the original 5' primer and a new 3'oligonucleotide(5'-GCAGGATCCCGG-CTCCCATCTCAGGGTGAGGGGC-3'). We then subcloned this fragment into the initial A2-BSP construct using the BamHI site in the GlySer linker. Protein produced from this construct efficiently produced properly folded material. We regret any problems this may have caused.

Mark M. Davis*
Howard Hughes Medical Institute,
Department of Microbiology and
Immunology, Stanford University,
Stanford, CA 94305–5428, USA

*For coauthors John D. Altman, Paul A. H.

Moss, Philip J. R. Goulder, Dan H. Barouch, Michael G. McHeyzer-Williams, John I. Bell, and Andrew J. McMichael.

■

Duplicate Publication

We recently reported our progress toward the fully automated selection of amino acid sequences for target protein folds (1). In this communication, we described both the computational and experimental results associated with a sequence calculation that encompassed 20 of 28 residue positions in a target zinc finger fold. The success of this partial design led rapidly to a fully automated design of a new amino acid sequence for an entire protein fold (2). In our haste to report the full sequence design result, we used text and phraseology from the Journal of Molecular Biology article in the Science article. In addition, because of the closeness in time of the two publications, we did not change a reference of "unpublished results" in the Science article to a citation of the Journal of Molecular Biology communication, which clearly preceded the work reported in Science. We regret any confusion these events may have caused the editors and readers of Science and the Journal of Molecular Biology.

Stephen L. Mayo
Howard Hughes Medical Institute and
Division of Biology,
California Institute of Technology,
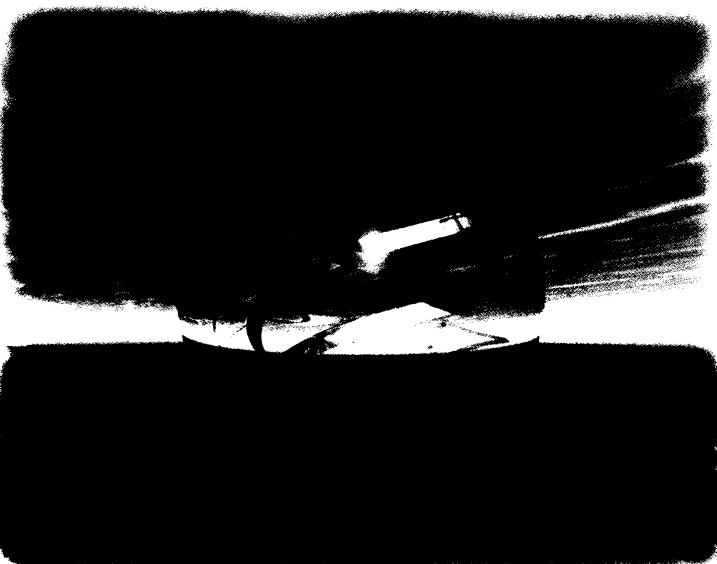Pasadena, CA 91125, USA
E-mail: steve@mayo.caltech.edu

References

1. B. I. Dahiyat, C. A. Sarisky, S. L. Mayo, J. Mol. Biol. 273, 789 (1997).
2. B. I. Dahiyat and S. L. Mayo, Science 278, 82 (1997).

Letters to the Editor

Letters may be submitted by e-mail (at science_letters@aaas.org), fax (202-789-4669), or regular mail (Science, 1200 New York Avenue, NW, Washington, DC 20005, USA). Letters are not routinely acknowledged. Full addresses, signatures, and daytime phone numbers should be included. Letters should be brief (300 words or less) and may be edited for reasons of clarity or space. They may appear in print and/or on the World Wide Web. Letter writers are not consulted before publication.