

reaction technique alone has won a Nobel prize. There are Nobel prizes for those who work for freedom of peoples as well. With a tube of blood, we can match DNA with a reasonably low chance of error. We can also test blood for genes, viruses, drugs, alcohol, medications, and more substances every day. Blood analysis can be a more precise tool than a strip search. It can become a tool that can be used to improperly invade the privacy of mass populations of innocent individuals.

Someone in early pregnancy, on the birth control pill, just out of a pub in Cardiff, or carrying any number of viruses could be singled out and embarrassed by such tests. We should be aware of their potential for stigmatizing these innocent individuals.

Thomas E. Goffman
1650 Jonquil Street, NW,
Washington, DC 20012, USA

Corrections and Clarifications

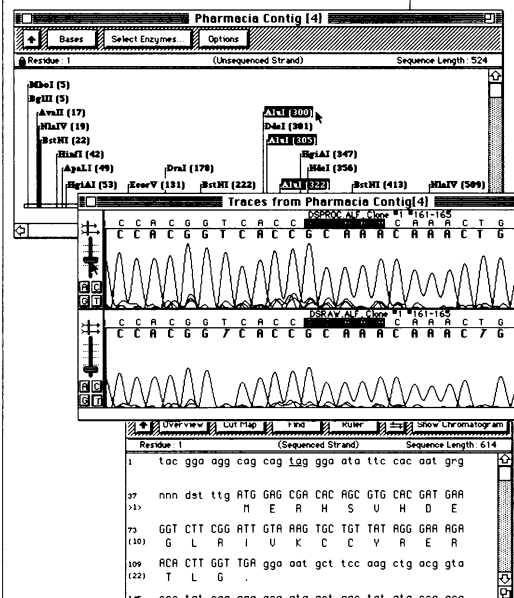
Discrepancies appeared between the Perspective "Springs for wings" by R. M. Alexander (7 Apr., p. 50) and the report "Muscle efficiency and elastic storage in the flight motor of *Drosophila*" by M. H. Dickinson and J. R. B. Lighton (7 Apr., p. 87). Substantial

changes were made in the report after its submission: the original calculations of inertial power overestimated elastic storage and so precluded direct calculation of muscle efficiency. Revised calculations of inertial power resulted in greatly reduced estimates of minimum elastic storage and a direct calculation of muscle efficiency. Because of an oversight, these changes were not communicated to Alexander, who based his Perspective on the original manuscript. *Science* regrets the error.

In figure 3A (p. 1961) of the Research Article "Architectures of class-defining and specific domains of glutamyl-tRNA synthetase" by O. Nureki *et al.* (31 Mar., p. 1958), the labels for the ribbon diagrams showing the folding of *Thermus thermophilus* glutamyl-tRNA synthetase (GluRS) and glutaminyl-tRNA synthetase (GlnRS) were inadvertently interchanged. The diagram for GluRS appeared at the top, and that for GlnRS appeared at the bottom.

In table 1 (p. 1124) of the article "Prehistoric extinction of Pacific island birds: Biodiversity meets zooarchaeology," by David W. Steadman (24 Feb., p. 1123), the column headings for modern and fossil record were reversed; under each island name, the letters "F M" should have appeared.

New! Sequencher 3.0 accelerated for Power Macintosh...



Sequencher™

*"After demos of all of them...
Sequencher is the best.
Nothing else came close."*

Paul Morrison, Director
Molecular Biology Core
Dana-Farber Cancer Institute

If you manage or use a core sequencing facility, consider Sequencher's special benefits:

- Entire sequencing projects, including raw data, are stored in a single file.
- The huge chromatogram files are compressed up to 80%.
- The scientist-friendly interface is so intuitive that clients use the program with little or no training.
- Easy to use editing tools find data conflicts in a keystroke.
- Network licensing lets you work from any Mac.

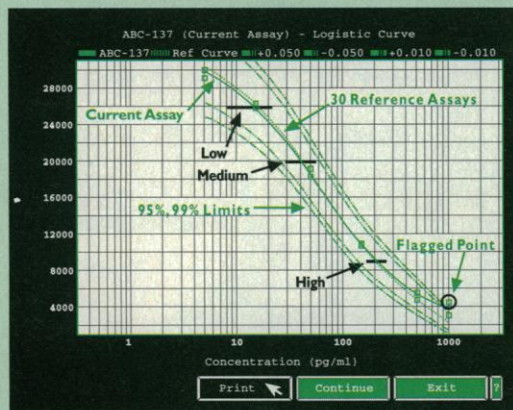
Seeing is believing! Call 800-497-4939 for a free Sequencher 3.0 demo disk.

**T C A G E N E
A G T C O D E S**

Gene Codes Corporation
2901 Hubbard, Ann Arbor, MI 48105
Phone: 313-769-7249 Fax: 313-769-7074

Bad Antibody?

StatLIA® immunoassay software immediately tells you if your antibody is bad. Really. Along with your tracer, buffer, incubation conditions ... or any of the 9 components.



StatLIA's unique standard curve lets you review an assay's reliability quickly, by graphing confidence limits, a reference curve, and the current assay's replicate data points.

Call 1-800-824-8842 for a free demo disk.

StatLIA®
from **Brendan** True Scientific Reliability
See us at ASM Booth #419

Plus, with StatLIA you can:

- Immediately pinpoint the cause of a flagged assay without repeating it
- Detect fluctuations in standard curves and their causes
- Maintain data consistency for long-term research

Find out why StatLIA is now used by major research, pharmaceutical, clinical and government laboratories throughout North America.