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lider LEP of CERN started producing results showing precisely that type of deviation.

The CDF results also can be interpreted as measuring an α_s larger than predicted by PT within the Standard Model. While this effect could conceivably signal "new physics," it agrees qualitatively with our prediction. In fact, we speculated (1) that perhaps the running of α_s might be obtained from the PT formula by replacing the so-called QCD scale Λ by the energy dependent quantity $\sqrt{\Lambda^2 + (\gamma Q)^2}$ (corresponding to mean field critical behavior). We choose Λ and γ so that α_s agrees with the measured values at 5 and 91 gigaelectron volts; then the modified formula for the running of α_s leads to a cross section at the highest CDF energies that is more than 40% higher than the PT prediction, in general agreement with the experimental results.

Our scenario would have dramatic implications, requiring a reevaluation of many predictions made in the past three decades in particle and condensed matter physics. The theories affected would range from "strings" to thin magnetic films.

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2. ———, "Expected deviations from perturbative QCD at 1 TeV or less" (preprints MPI-Ph/92-18 and AZPH-TH-92-06, Max-Planck-Institute für Physik, Munich, Germany, and Department of Physics, University of Arizona, Tucson, AZ, January 1992), in: *Rencontre de Physique de la Vallée d'Aoste*, M. Greco, Ed. (Edition Frontières, Gif-sur-Yvette, France, 1992), pp. 125–131.

Antihydrogen

Physicists at Fermilab, under the leadership of Rosanna Cester, have already synthesized antihydrogen, albeit unwittingly (A. Watson, *Research News*, "Physicists produce first antiatom," 12 Jan., p. 147). Cester's group planned in the late 1980s an experiment, codenamed E760, to study charmonium states produced by intercepting an intense beam of antiprotons with a hydrogen gas jet target (<http://fn760b.fnal.gov>). Charles Munger and his colleagues recognized this serendipitous antihydrogen production and are finishing the construction of a suitable detector at Fermilab in order to confirm the phenomenon (<http://fnal.fnal.gov/e862>). Munger's group, in addition, is planning to measure one of anti-

hydrogen's fundamental spectroscopic transitions, the Lamb shift. Antihydrogen atom production with this technique is rare; the cross section is estimated to be a few picobarns. This corresponds to the production of a few antihydrogen atoms per week for a beam of 10^{13} antiprotons, crossing a dense gas target of 10^{13} atoms per square centimeter a million times a second. Fermilab's Antiproton Accumulator is scheduled to get a new feeder accelerator, the Main Injector, by 1999 and ambitious plans are under way for the addition of a permanent magnet antiproton storage ring. These upgrades at Fermilab will guarantee a copious source of antiprotons in the United States.

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Dominance in Crayfish

I am an 8th-grade student at Westland Middle School in Bethesda, Maryland. I read with interest the article "Neurobiology: Social status sculpt activity of crayfish neurons" by Marcia Barinaga (*Research News*, 19 Jan., p. 290), which discussed the report "The effect of social experience on serotonergic modulation of the escape circuit of crayfish" by Shih-Rung Yeh *et al.* in the same issue (p. 366).

A statement in Barinaga's article says that male crayfish display dominance behavior toward other males. My 1995 school science fair project was on the subject of fighting and dominance behavior in crayfish. I paired crayfish, videotaped their encounters, and noted the resulting dominance behavior. I carefully noted the sex of the crayfish. I discovered that not only males fight males, but females fight males and females fight other females. In general, one cannot predict which animal will finally be dominant. That is, females or males can show dominance in a mixed fight. I also observed that relative size or the absence of a claw were not predictors of dominance.

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Amide Cleavage by a Ribozyme: Correction

Pertaining to our report "Cleavage of an amide bond by a ribozyme" (13 Jan. 1995, p. 237) (1), we recently obtained data

demonstrating a second reaction pathway superimposed on the amide cleavage reaction. The second pathway involves two successive phosphoester transfer reactions: first, miscleavage by the ribozyme at a DNA phosphoester adjacent to the amide linkage (1, figure 2); second, attack by the 3' hydroxyl of the miscleavage product at a phosphate immediately preceding a non-encoded nucleotide that is present at the 3' terminus of a small proportion of ribozyme molecules that are produced by in vitro transcription. The resulting ribonucleoside-terminated product has nearly identical electrophoretic mobility compared with the amide-terminated product of the amide cleavage reaction when analyzed in a denaturing polyacrylamide gel at pH 8.3. The two products can be separated by polyacrylamide gel electrophoresis at pH 6.5, revealing that the second pathway dominates over amide bond cleavage. The rate of RNA-catalyzed amide cleavage is about 50-fold slower than we reported, thus representing only about a 10^2 -fold rate acceleration when compared with the uncatalyzed reaction. The amide- and ribonucleoside-terminated products are derivatized with sulfosuccinimidyl-6-(biotin-amido) hexanoate at approximately the same rate when incubated at pH 8.5 (1,

figure 3). The amine-, but not the ribonucleoside-terminated product is reactive with ninhydrin and can be derivatized with dansyl chloride, in accordance with the behavior of the authentic amine-terminated compound. The ribonucleoside-terminated product can be converted to an all-deoxynucleotide molecule, one residue shorter in length, by oxidation of the 2',3'-diol to a dialdehyde and subsequent β -elimination.

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Corrections and Clarifications

During editing, an error was introduced in the caption of the figure accompanying Barry Ci-

pra's article "A proof to please Pythagoras" (Research News, 22 Mar., p. 1669). The equation in line 2 should have read, " $y^2 = x^3 - 36x$."

In figure 5A (p. 781) of the article "Intercalation, DNA kinking, and the control of transcription" by M. H. Werner *et al.* (9 Feb., p. 778), a methyl group was inadvertently placed at the C5 position of the cytosine base and omitted from the thymine base (that is, the A·T base pair was depicted as an A·U base pair and the G·C base pair as a G·5-methylC base pair). Thus, the C base should have a proton at the C5 position and the T base a methyl group at the C5 position. The hydrogen bonding depicted for the two base pairs was correct.

Letters to the Editor

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