Cell Biology. In the article "Cloned mammalian neutral sphingomyelinase: Functions in sphingolipid signaling?" by Stefan Tomiuk, Kay Hofmann, Michael Nix, Markus Zumbansen, and Wilhelm Stoffel, which appeared in number 7, March 31, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 3638–3643), two typographical errors occurred: (*i*) the two C-terminal lysine residues (**KK**) of the mouse sequence in Fig. 1 on page 3640 should be omitted. The protein contains 419 amino acid residues ending on alanine as stated on page 3639 and (*ii*) also on page 3640 (left column, line 13) the text should read: phosphatidylcholine was found to be cleaved by approximately 3% efficiency not 30%.

Cell Biology. In the article "Segregation of viral plasmids depends on tethering to chromosomes and is regulated by phosphorylation" by Chris W. Lehman and Michael R. Botchan, which appeared in number 8, April 14, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 4338–4343), the following correction should be noted. On page 4341, the numbering of the amino acid positions of two mutations was inadvertently reversed in Table 1 and Fig. 4*B* and *C*. The numbers 108 and 237 should be reversed. Specifically, where the mutant F108L is mentioned, it should be replaced with F237L, and when the mutant K237E/H357Q is mentioned, it should be replaced with K108E/H357Q.

Genetics. In the article "Separation of killing and tumorigenic effects of an alkylating agent in mice defective in two of the DNA repair genes" by Hisaya Kawate, Kunihiko Sakumi, Teruhisa Tsuzuki, Yoko Nakatsuru, Takatoshi Ishikawa, Seiichi Takahashi, Hiroshi Takano, Tetsuo Noda, and Mutsuo Sekiguchi, which appeared in number 9, April 28, 1998, of *Proc. Natl. Acad. Sci. USA* (**95**, 5116–5120), the authors request the following correction. On page 5118, in the legend of Fig. 3, line 3, "8 weeks after this administration" should be "7 days after this administration."

Microbiology. In the article "DNA strand separation during activation of a developmental promoter by the *Bacillus subtilis* response regulator Spo0A" by Dean A. Rowe-Magnus and George B. Spiegelman, which appeared in number 9, April 28, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 5305–5310), the following correction should be noted. In Fig. 2, the DNA sequences shown for MB8NT and MB8T templates are incorrect. The sequence of the bottom strand of the MB8NT template should be 3′-AACGAATATACTTAACTTCGTTCTTC-5′, and the sequence of the top strand of the MB8T template should be 5′-TTGCTTATATGAATTGAAGCAAGAAG-3′ (the sequences that are incorrect in the figure are underlined).

Neurobiology. In the article "Zebrafish ultraviolet visual pigment: Absorption spectrum, sequence and localization" by Judith Robinson, Ellen A. Schmitt, Ferenc I. Harosi, Richard J. Reece, and John E. Dowling, which appeared in number 13, July 1, 1993, of *Proc. Natl. Acad. Sci. USA* (**90,** 6009–6012), the authors request the following correction. The proposed structure for the ultraviolet-sensitive visual pigment opsin (Fig. 3) is not correct. The proposed opsin structure was based on a DNA sequence, termed ZF02, that was identified as the ultraviolet-sensitive opsin gene based on messenger RNA *in situ* hybrid-ization studies that showed staining of the short-single cones, the ultraviolet-sensitive cones, in zebrafish. Subsequent *in situ* hybridization studies with the RNA probe generated from the ZF02 sequence have consistently shown staining of rods and no staining of the short-single cones in zebrafish [see Raymond, P. A., Barthel, L. K. & Stenkamp, D. L. (1996) *Invest. Ophthal. Vis. Sci.* **37** (5), 948–950 and Schmitt, E. A., Fadool, J. M. & Dowling, J. E. (1996) *Invest. Ophthal. Vis. Sci.* **37** (5), 695]. The original localization of the ZF02 riboprobe to the short-single cones may have resulted from diffusion. We have notified GenBank that the ZF02 sequence (accession no. L11014) is not that of an ultraviolet opsin gene, and their description of the sequence notes this fact. The other results reported in the paper, including the wavelength sensitivities of the various types of cones in zebrafish, the *in situ* absorption spectrum of the zebrafish ultraviolet visual pigment, and the structure of the zebrafish retinal mosaic are correct to the best of our knowledge.

Population Biology. In the article "Concordance of gene genealogies reveals reproductive isolation in the pathogenic fungus *Coccidioides immitis"* by Vassiliki Koufopanou, Austin Burt, and John W. Taylor, which appeared in number 10, May 13, 1997, of *Proc. Natl. Acad. Sci. USA* (**94,** 5478–5482), the authors wish to point out that further molecular analysis has revealed the following errors in three of the published sequences. For the dioxygenase locus, the genotypes of isolates CA3 and CA5 should read as TTATC instead of CCGCT, and for the orotidine decarboxylase locus the genotype of TX1 isolate should read as CAAGCCAA instead of CAGGTTAG (Table 1). These corrections do *not* change the main results and conclusion of the paper, that *Coccidioides immitis* is subdivided into two reproductively isolated taxa, one of which is centered in California. Indeed, they indicate greater divergence between the two taxa, as follows. All gene genealogies now include a branch separating the Californian from the non-Californian isolates, indicating a more complete sorting of alleles between the two groups than previously apparent, though the genealogies are no longer significantly different by the partition homogeneity test ($P = 0.38$; PAUP*4.0d61). The partition between Californian and non-Californian isolates is still highly significant ($P = 0.002$), and the two groups are separated by 17 instead of 8 fixed differences, distributed among all 5 loci. Significance tests from randomizations of the corrected data set with and without the partition are as before (see Fig. 3), still consistent with panmixia within each of the two taxa. The average pairwise divergence of isolates within the Californian and non-Californian groups is $d_C = 1.26 \times 10^{-3}$ (2.32×10^{-3}) and $d_{NC} = 1.80 \times 10^{-3}$ (3.05×10^{-3}), respectively (coding regions only; values in parentheses based on third-base positions only); the average pairwise divergence between groups is $d_{C\text{-}NC} = 10.75 \times 10^{-3}$ (25.09×10^{-3}), 10-fold larger than the within-group values, and the estimated time the two taxa have been reproductively isolated is 11 Myr instead of 8 Myr. The authors wish to thank Mathew Fisher (University of California, Berkeley) for pointing out the errors and supplying the correct sequences.