

Evolution. In the article "Evolution of parasitism: Kinetoplastid protozoan history reconstructed from mitochondrial rRNA gene sequences" by James A. Lake, Vidal F. de la Cruz, Paulo C. G. Ferreira, Carlos Morel, and Larry Simpson, which appeared in number 13, July 1988, of *Proc. Natl. Acad. Sci. USA* (85, 4779–4783), the authors request that

A	TTAATTTAAT 301	AAAATTATAA 580	AATAATCCTA 690
B	...T.....A..CT.T...
C	...T.....A.....T...
D	...T.....A.....T..-
A	ATTGTTTTTA 44	TGATGCTATA 147	TAAATAACAT 203
B	.AA.....	.AG.....T....
C	.AA.....	.A.....A..
D	.A.....	.A.....T.A..
E	.AA.....	.AG.....T.T..
A	A--TAAATTA 211	ATTTAGTCA 306	
B	TAT.T.C.A.	
C	---...C...	
D	---...TC..AC..	
E	---.T.CA..	.C.....CA.	

the following corrections be made to the aligned sequences in Fig. 1. The authors indicate that these nucleotide substitutions occurred during editing of the sequences for the Figure and that the trees were constructed using the correct data set. The corrected nucleotides are indicated in boldface type.

Genetics. In the article "Host genes that influence transposition in yeast: The abundance of a rare tRNA regulates Ty1 transposition frequency" by Hua Xu and Jef D. Boeke, which appeared in number 21, November 1990, of *Proc. Natl. Acad. Sci. USA* (87, 8360–8364), an important reference, number 28, was inadvertently omitted. The authors request that the following citation be noted in the *Discussion*, in the sentence beginning 14 lines from the bottom of column 2 on p. 8363. "According to this model, when translating ribosomes encounter the codons CUU-AGG (encoding Leu-Arg) near the end of the *TYA* ORF (where it overlaps with *TYB*), tRNA^{Leu}_{UAG}, which can translate all six leucine codons (28), recognizes the CUU codon and is then transferred to the ribosomal peptidyl (P) site."

28. Weissenbach, J., Dirheimer, G., Falcoff, R., Sanceau, J. & Falcoff, E. (1977) *FEBS Lett.* 82, 71–76.

Medical Sciences. In the article "*N*-(Fluorenyl-9-methoxycarbonyl) amino acids, a class of antiinflammatory agents with a different mechanism of action" by Ronald M. Burch, Moshe Weitzberg, Natalie Blok, Richard Muhlhauser, David Martin, Stephen G. Farmer, Jenny M. Bator, Jane R. Connor, Chiew Ko, Wendy Kuhn, Barbara A. McMillan, Maureen Raynor, Barry G. Shearer, Carol Tiffany, and Deidre E. Wilkins, which appeared in number 2, January 1991, of *Proc. Natl. Acad. Sci. USA* (88, 355–359), the authors request that the following corrections be noted. Author lines should be read as follows: RONALD M. BURCH, MOSHE WEITZBERG, NATALIE BLOK, RICHARD MUHLHAUSER, DAVID MARTIN, STEPHEN G. FARMER, JENNY M. BATOR, JANE R. CONNOR, MARK GREEN, CHIEW KO, WENDY KUHN, BARBARA A. McMILLAN, MAUREEN RAYNOR, BARRY G. SHEARER, CAROL TIFFANY, AND DEIDRE E. WILKINS.

Further, a typographical error in the manuscript (p. 359, near top of first column) indicated the study duration to be 28 days, instead of the correct duration, 14 days.

Biochemistry. In the article "Molecular cloning and characterization of interferon α/β response element binding factors of the murine (2'-5')oligoadenylate synthetase ME-12 gene" by Cong Yan and Igor Tamm, which appeared in number 1, January 1991, of *Proc. Natl. Acad. Sci. USA* (88, 144–148), the authors request that the following correction be noted. Ref. 3 should read as follows:

3. Yan, C., Sehgal, P. B. & Tamm, I. (1989) *Proc. Natl. Acad. Sci. USA* 86, 2243–2247.

Genetics. In the article "Increased expression of a 58-kDa protein kinase leads to changes in the CHO cell cycle" by Bruce A. Bunnell, Lucie S. Heath, Donald E. Adams, Jill M. Lahti, and Vincent J. Kidd, which appeared in number 19, October 1990, of *Proc. Natl. Acad. Sci. USA* (87, 7467–7471), the authors request that the following be noted. Due to DNA sequence compression between nucleotides 123 and 207, two additional amino acids should be added to the sequence and a corresponding change in the predicted amino acids, corresponding to amino acids 41–70, of the cDNA sequence should be noted. This change results in an open reading frame of 436 amino acids instead of 434. However, the remainder of the predicted amino acid sequence of the protein as well as all of the remaining data in the paper are unaffected by this change. The new human cDNA sequence agrees with the predicted amino acid sequence and size of the murine p58 protein kinase homologue (1). The revised human p58 cDNA and protein sequence is on file with the GenBank data base under accession no. M37712.

1. Kidd, V. J., Luo, W., Xiang, J., Tu, F., McCune, S. & Snead, M. L. (1991) *Cell Growth Differ.*, in press.