Biophysics. In the article "Folding and aggregation of designed proteins" by R. A. Broglia, G. Tiana, S. Pasquali, H. E. Roman, and E. Vigezzi, which appeared in number 22, October 27, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 12930–12933), the following correction should be noted. In Fig. 1*b*, the designed sequence of amino acids S_{36} contains a typographical error in that only 35 of its 36 monomers appear. The missing amino acid is of type R and should be located between amino acids E (sixth) and G (seventh). The correct sequence is:

S_{36} = SQKWLERGATRIADGDLPVNGTYFSCKIMENVHPLA.

Although this typographical error does not change the results presented in the paper because they were obtained with the correct number and sequence of amino acids, it constitutes a nuisance for anybody interested in reproducing our results, and we apologize for the inconvenience. We want to thank Prof. H. S. Chan, of the University of Toronto, for calling our attention to this error.

Genetics. In the article "Cluster analysis and display of genome-wide expression patterns" by Michael B. Eisen, Paul T. Spellman, Patrick O. Brown, and David Botstein, which appeared in number 25, December 8, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 14863–14868), the authors want to note that two references were inadvertently omitted. Ref. 1 refers to a precedent for coloring of data tables following cluster analysis, and ref. 2 refers to an earlier example of applying cluster analysis to gene expression data. The additional references are:

1. Weinstein, J. N., Myers, T. G., O'Connor, P. M., Friend, S. H., Fornace, A. J., Jr., Kohn, K. W., Fojo, T., Bates, S. E., Rubinstein, L. V., Anderson, N. L., *et al*. (1997) *Science* **275,** 343–349.
2. Wen, X., Fuhrman, S., Michaels, G. S., Carr, D. B., Smith, S., Barker, J. L. & Somogyi, R. (1998) *Proc. Natl. Acad. Sci. USA* **95,** 334–339.

Cell Biology. In the article "Quantitative analysis of biological membrane lipids at the low picomole level by nano-electrospray ionization tandem mass spectrometry" by B. Brügger, G. Erben, R. Sandhoff, F. T. Wieland, and W. D. Lehmann, which appeared in number 6, March 18, 1997, of *Proc. Natl. Acad. Sci. USA* (**94,** 2339–2344), Table 1 contains errors. A corrected table is reprinted below with corrections in boldface type.

Table 1. Identification of the most abundant signals in the ESI mass spectra of total lipid extract of CHO cells, as given in Fig. 1 *a* and *b*

Class of phospholipid	Ion	Total fatty acid carbon no.:no. of double bonds								
		32:1	34:2	36:2	38:4	16:0	18:0	22:0	24:1	26:0
PA	$[M-H]^-$	645	671	699	723					
PS	$[M-H]^-$	732	**758**	786	810					
PE	$[M-H]^-$	688	**714**	742	766					
Plasmenyl-PE	$[M-H]^-$	672	**698**	726	750					
PI	$[M-H]^-$	807	833	861	885					
PG	$[M-H]^-$	719	**745**	773	797					
PC	$[M+H]^+$	732	758	786	810					
	$[M+Na]^+$	754	780	808	832					
Plasmenyl-PC	$[M+H]^+$	716	742	770	794					
	$[M+Na]^+$	738	764	792	816					
PE	$[M+H]^+$	690	**716**	744	768					
Plasmenyl-PE	$[M+H]^+$	674	**700**	728	752					
PS	$[M+H]^+$	734	760	788	812					
SM	$[M+H]^+$					703	731	787	813	843
	$[M+Na]^+$					**725**	753	809	835	865

In the negative ion mode, PS and PE (with two nitrogen atoms) show signals at even-numbered m/z values, whereas PI, PG, and PA show signals at odd-numbered values. In the positive ion mode, SM signals appear at odd m/z values (2 nitrogen atoms), whereas PC, PE, and PS-signals occur at even m/z values. The m/z values are nominal monoisotopic data.

Genetics. In the article "Neurosecretory control of aging in *Caenorhabditis elegans*" by Michael Ailion, Takao Inoue, Carole I. Weaver, Robert W. Holdcraft, and James H. Thomas, which appeared in number 13, June 22, 1999, of *Proc. Natl. Acad. Sci. USA* (**96,** 7394–7397), the following corrections should be noted.

(*i*) Figs. 1 and 2 were interchanged. The figure legends are correct, but the figures were transposed. The corrected figures and their legends are shown below. (*ii*) In Table 2, line 2, the genotype of the strain should be *unc-64(e246)*, not *unc-63(e246)*. (*iii*) Table 1 originally had blank lines separating the top, middle, and bottom sections of the table. Without these spaces, it is difficult to tell what is referred to as top, middle, and bottom in the table legend. Top refers to lines 1–6, middle refers to lines 7–8, and bottom refers to lines 9–12.

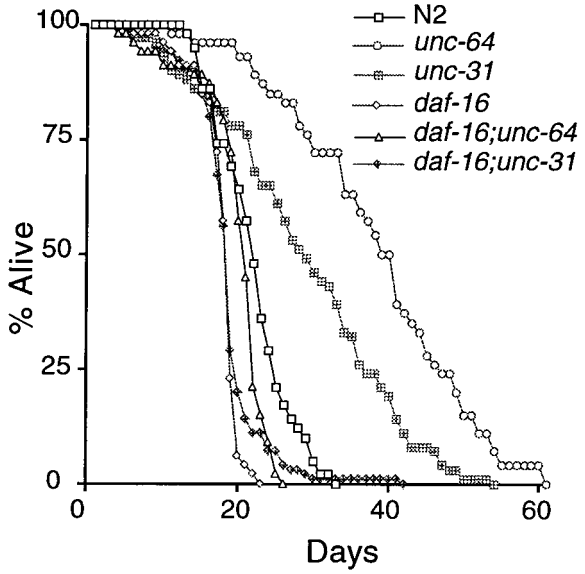

FIG. 1. *unc-64* and *unc-31* mutants have increased life spans and are suppressed by *daf-16*. Assays were performed at 20°. *unc-64* and *unc-31* have significantly longer life spans than N2 ($P < 0.0001$ for *unc-64* and $P = 0.0004$ for *unc-31*). This figure uses the same data set as Table 1.

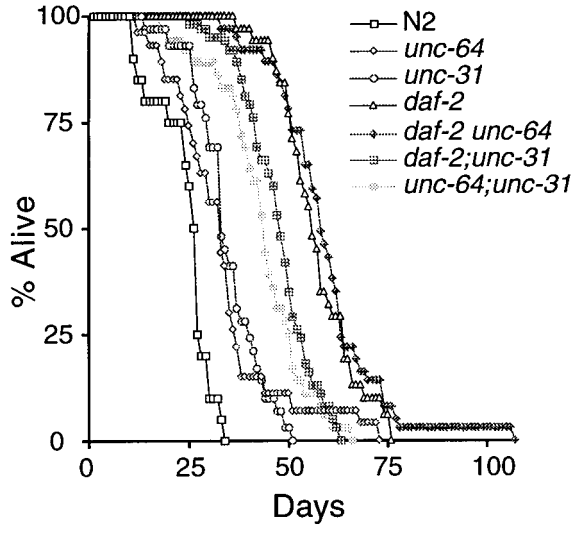

FIG. 2. Mutations in *unc-64* and *unc-31* do not enhance the longevity of *daf-2* mutants. Animals were grown at 15° to allow development past the dauer stage and then were shifted to 20°. *unc-64; unc-31* had a significantly longer life span than either *unc-64* ($P = 0.0002$) or *unc-31* ($P = 0.0005$). The *daf-2 unc-64* double mutant and *daf-2* were not significantly different ($P = 0.5139$). The maximum life span of *daf-2 unc-64* was extended to >100 days by a single animal. We have not investigated whether this has any possible significance. This figure uses the same data set as Table 2.

Medical Sciences. In the article "Osteopontin-deficient mice are resistant to ovariectomy-induced bone resorption" by Hiroyuki Yoshitake, Susan R. Rittling, David T. Denhardt, and Masaki Noda, which appeared in number 14, July, 1999, of *Proc. Natl. Acad. Sci. USA* (**96,** 8156–8160), the authors request the following correction. In the 9th line in the first paragraph and in Table 3 on page 8158, the unit in the text and the third subheading under Parameters in the table are incorrectly listed as BFR/BV, $\mu m^3/\mu m^2$/day. The correct listing is BFR/BV, %/year.

Medical Sciences. In the article "Cancer-specific chromosome alterations in the constitutive fragile region *FRA3B*" by Koshi Mimori, Teresa Druck, Hiroshi Inoue, Hansjuerg Alder, Lori Berk, Masaki Mori, Kay Huebner, and Carlo M. Croce, which appeared in number 13, June 22, 1999, of *Proc. Natl. Acad. Sci. USA* **96,** 7456–7461, the following correction should be noted. *FHIT* exon 4 was misplaced in Figs. 1 and 2. Its true placement is ≈40 kilobase pairs further centromeric at base pairs 162581 to 162673 of GenBank submission AF152363. Thus, the length of intron 4 is 284935 base pairs and the markers D3S4489 and D3S4260 and the proximal aphidicolin-induced hybrid breaks are telomeric to exon 4, i.e., in intron 4.

Microbiology. In the article "A set of independent selectable markers for transfection of the human malaria parasite *Plasmodium falciparum*" by Choukri Ben Mamoun, Ilya Y. Gluzman, Sophie Goyard, Stephen M. Beverley, and Daniel E. Goldberg, which appeared in number 15, July 20, 1999, of *Proc. Natl. Acad. Sci. USA* (**96,** 8716–8720), the authors request the following corrections. In *Experimental Procedures* (page 8717), under "*P. falciparum* Transfection and Selection of Transfectants," there was a typographical error in the concentrations of G418 used for selection. The correct concentrations are 300, 500, or 1,000 μg/ml. Under "BSD Enzyme Assay," there was a typographical error in the volume of cultured parasitized red blood cells used. The correct volume is 12 ml. In *Results* (page 8718, line 24 in column 2), the sentence should read: "Varying amounts of either gene were slotted onto the blot, corresponding to the amount of DNA that would be present per microgram of total DNA if there were 1–35 copies of the construct per cell."

Neurobiology. In the article "Bilirubin, formed by activation of heme oxygenase-2, protects neurons against oxidative stress injury" by Sylvain Doré, Masaaki Takahashi, Christopher D. Ferris, Lynda D. Hester, Daniel Guastella, and Solomon H. Snyder, which appeared in number 5, March 2, 1999, of *Proc. Natl. Acad. Sci. USA* (**96,** 2445–2450), the authors request the following correction. One of the authors, Randa Zakhary, was deleted from the final published paper. The correct author and affiliation lines are as follows:

SYLVAIN DORÉ*, MASAAKI TAKAHASHI*, CHRISTOPHER D. FERRIS*†, RANDA ZAKHARY*, LYNDA D. HESTER*, DANIEL GUASTELLA*, AND SOLOMON H. SNYDER*‡§¶

Departments of *Neuroscience, ‡Pharmacology and Molecular Sciences, †Medicine, and §Psychiatry, The Johns Hopkins University School of Medicine, 725 North Wolfe Street, Baltimore, MD 21205