Genetics. In the article "Down syndrome phenotypes: The consequences of chromosomal imbalance" by J. R. Korenberg, X.-N. Chen, R. Schipper, Z. Sun, R. Gonsky, S. Gerwehr, N. Carpenter, C. Daumer, P. Dignan, C. Disteche, J. M. Graham, Jr., L. Hugdins, B. McGillivray, K. Miyazaki, N. Ogasawara, J. P. Park, R. Pagon, S. Pueschel, G. Sack, B. Say, S. Schuffenhauer, S. Soukup, and T. Yamanaka, which appeared in number 11, May 24, 1994, of *Proc. Natl. Acad. Sci. USA* (**91**, 4997–5001), the authors request that the following correction be noted. The name of an author, L. Hudgins, was misspelled. The title and authors should read as follows:

Down syndrome phenotypes: The consequences of chromosomal imbalance

J. R. KORENBERG, X.-N. CHEN, R. SCHIPPER, Z. SUN, R. GONSKY, S. GERWEHR, N. CARPENTER, C. DAUMER, P. DIGNAN, C. DISTECHE, J. M. GRAHAM, JR., L. HUDGINS, B. MCGILLIVRAY, K. MIYAZAKI, N. OGASAWARA, J. P. PARK, R. PAGON, S. PUESCHEL, G. SACK, B. SAY, S. SCHUFFENHAUER, S. SOUKUP, AND T. YAMANAKA

Biochemistry. In the article "An arcane role of DNA in transcription activation" by Sangryeol Ryu, Susan Garges, and Sankar Adhya, which appeared in number 18, August 30, 1994, of *Proc. Natl. Acad. Sci. USA* (**91**, 8582–8586), a printer's error resulted in the omission of the title and edited column heads from Table 1. The corrected table is shown here.

Table 1. Effect of increased distance and single-strand interruptions in the spacer on *lac* transcription

	Insertion	Single-strand interruption	Spacer sequence	Cooperative RNAP binding	% *lac* transcription
1.	—	—	–53 CATTAGTTAACCCAGG –38 GTAATCAATTGGGTCC	+	100
2.	—	Nick	–53 CATTAGTTAACCCAGG –38 GTAATCAA↑TTGGGTCC	+	78.5 ± 3.5
3.	—	1-base	–53 CATTAGGCCCTCCAGG –38 GTAATCC GGAGGTCC	+	53.6 ± 8.2
4.	—	2-base	–53 CATTAGGCACCTCAGG –38 GTAATCC GGAGTCC	+	17.0 ± 17.4
5.	—	4-base	–57 CATTAGGCACCCCTGG –38 GTAATCC GGACC	+	0
6.	10 bp	—	–63 CATTAGTTTCGAATTCGAAACCCAGG –38 GTAATCAAAGCTTAAGCTTTGGGTCC	NT	51.0 ± 1.0
7.	10 bp	6-base	–63 CATTAGTTTCGAATTCGAAACCCAGG –38 GTAATCAAAGC TTTGGGTCC	NT	0

DNA templates carried the shown variations in the spacer region. The amount of transcription of each template interrupted in the bottom strand was normalized as percentage of the transcription obtained for the corresponding isogenic intact double-stranded linear template. The last column shows the average of several experiments, including the standard deviations, obtained from independent preparations of DNA. Results shown in each line were obtained with DNA templates which were mixtures with nicks or gaps at the indicated position(s) of one or the other strand. Results were the same as shown in the last column when homogeneous single-stranded DNA circles with interruption in the bottom (as shown in column 4) or the top strand made by a bacteriophage f1 replication-packaging system were used as templates. +, RNAP binding to wild-type DNA templates in the presence of CRP; NT, not tested.

Biochemistry. In the article "Roles of heme iron-coordinating histidine residues of human hemopexin expressed in baculovirus-infected insect cells" by Tomoko Satoh, Hiroyuki Satoh, Shin-ichiro Iwahara, Zbynek Hrkal, David H. Peyton, and Ursula Muller-Eberhard, which appeared in number 18, August 30, 1994, of *Proc. Natl. Acad. Sci. USA* (**91**, 8423–8427), the arrow was missing from Fig. 3 due to a printer's error. The corrected figure and legend are shown here.

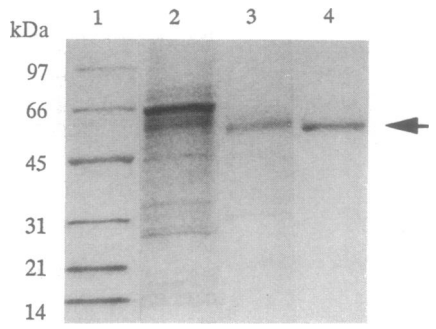

FIG. 3. SDS/PAGE of recombinant wild-type Hx after each purification step. Aliquots (5 μg) were analyzed by SDS/4–20% gradient PAGE and stained with Coomassie brilliant blue R-250. Lanes: 1, molecular size markers; 2, conditioned medium 48 hr postinfection; 3, following Con A-agarose chromatography; 4, eluate from SP-Sepharose chromatography. Arrow indicates the recombinant Hx at 55 kDa.