Biochemistry. In the article "The TRAP220 component of a thyroid hormone receptor-associated protein (TRAP) coactivator complex interacts directly with nuclear receptors in a ligand-dependent fashion" by Chao-Xing Yuan, Mitsuhiro Ito, Joseph D. Fondell, Zheng-Yuan Fu, and Robert G. Roeder, which appeared in number 14, July 7, 1998, of *Proc. Natl. Acad. Sci. USA (***95,** 7939–7944), the authors wish to acknowledge an earlier paper that had escaped their attention. In an article entitled "Identification of RB18A, a 205 kDa new p53 regulatory protein which shares antigenic and functional properties with p53" [Drané, P., Barel, M., Balbo, M. & Frade, R. (1997) *Oncogene* **15,** 3013–3024], Drané *et al*. report the identification of a human protein, RB18A, that interacts with several anti-p53 monoclonal antibodies, shows general DNA binding properties, and stimulates p53 binding to DNA. The cDNA-derived protein sequences of RB18A and TRAP220 are nearly identical, there being minor sequence variations and an extended N terminus on TRAP220. Apart from the effect of RB18A on p53 binding to DNA, the study of Drané *et al*. did not report any additional functions of RB18A and, in contrast to the findings with TRAP220, provided no indications of its presence within a larger multiprotein coactivator complex.

Biochemistry. In the article "Molecular cloning and characterization of a cellular phosphoprotein that interacts with a conserved C-terminal domain of adenovirus E1A involved in negative modulation of oncogenic transformation" by Ute Schaeper, Janice M. Boyd, Sulekha Verma, Erik Uhlmann, T. Subramanian, and G. Chinnadurai, which appeared in number 23, November 7, 1995 of *Proc. Natl. Acad. Sci. USA* (**92,** 10467–10471), we reported the sequences for human CtBP. Reexamination of the cDNA sequences revealed certain errors. These errors have been corrected in the GenBank database (accession no. U37408).

Evolution. In the article "The role of robustness and changeability on the origin and evolution of genetic codes" by Tetsuya Maeshiro and Masayuki Kumura, which appeared in number 9, April 28, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 5088–5093), the authors wish to note the following error in Table 2 related to the initiation codons of nuclear mycoplasma. They should read: AUG, GUG, and UUG [Dybvig, K. & Voelker, L. L. (1996) *Annu. Rev. Microbiol.* **50,** 25–57]. Consequently, CMy (page 5091, last paragraph, right column) should be deleted in the text. These corrections do not change the results of the paper. A corrected Table 2 is shown below.

Table 2. Assignments of deviant codons

		Changes from SGC			
Representative genetic system	Code	Codon	Phenotype	Initiation codons	
Mitochondrial yeasts	MYe	UGA	stop ⇒ Trp	AUG	1
		AUA	Ile ⇒ Met		
		CUN	Leu ⇒ Thr		
Mitochondrial platyhelminths	MPl	UGA	stop ⇒ Trp	AUG	1
		AAA	Lys ⇒ Asn		
		AGR	Arg ⇒ Ser		
		UAA	stop ⇒ Tyr		
Mitochondrial nematoda	MNe	UGA	stop ⇒ Trp	AUN UUG GUG	6
arthropoda		AGR	Arg ⇒ Ser		
mollusca		AUA	Ile ⇒ Met		
Mitochondrial echinodermata	MEc	UGA	stop ⇒ Trp	AUG	1
		AAA	Lys ⇒ Asn		
		AGR	Arg ⇒ Ser		
Mitochondrial tunicata	MTu	UGA	stop ⇒ Trp	AUG	1
		AUA	Ile ⇒ Met		
		AGR	Arg ⇒ Gly		
Mitochondrial vertebrata	MVe	UGA	stop ⇒ Trp	AUN GUG	5
		AUA	Ile ⇒ Met		
		AGR	Arg ⇒ stop		
Mitochondrial euascomycetes	MEu	UGA	stop ⇒ Trp	AUN NUG UUA	8
Nuclear mycoplasma	CMy	UGA	stop ⇒ Trp	AUG GUG UUG	3
Nuclear euplotes	CEu	UGA	stop ⇒ Cys	AUG	1
Nuclear acetabularia	CAc	UAR	stop ⇒ Gln	AUG	1
Nuclear blepharisma	CBl	UAG	stop ⇒ Gln	AUG	1
Nuclear candida	CCa	CUG	Leu ⇒ Ser	AUG CUG	2
Nuclear bacterial	CBa	—	—	AUN NUG	7

N denotes any of A, U, G, and C, and R denotes A and G. The values in the initiation codons indicate the number of known initiation codons. The codon reassignments of each deviant code are arranged from top to bottom in the estimated order of reassignments. Compiled from http://www3.ncbi.nlm.nih.gov/htbin-post/Taxonomy/wprintgc?mode=c.

Plant Biology. In the article "Differential expression of two isopentenyl pyrophosphate isomerases and enhanced carotenoid accumulation in a unicellular chlorophyte" by Zairen Sun, Francis X. Cunningham, Jr., and Elisabeth Gantt, which appeared in number 19, September 15, 1998, of *Proc. Natl. Acad. Sci. USA* (**95,** 11482–11488), the following correction should be noted. In Fig. 3 the lightly shaded sequences, representing amino acid identity of four of five sequences, was inadvertently lost in the electronic submission process.

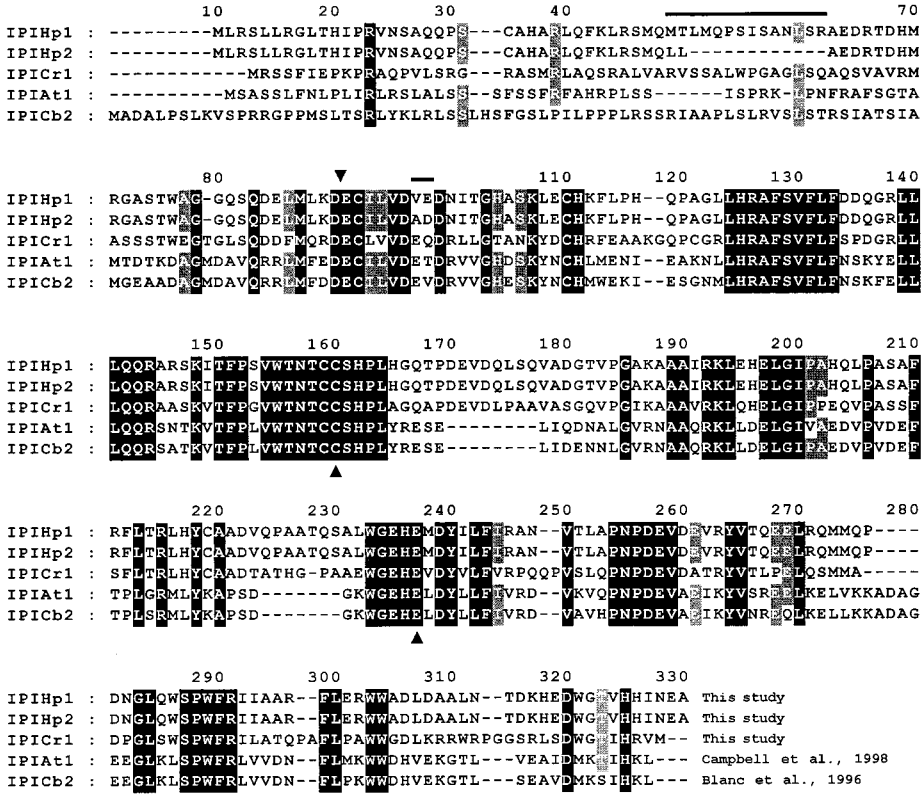

FIG. 3. Amino acid sequence alignment of IPP isomerases predicted by cDNAs of *Haematococcus pluvialis* (IPIHp1 and IPIHp2) and *Chlamydomonas reinhardtii* (IPICr1) are compared with sequences from the flowering plants *Clarkia brewerii* (IPICb2) (29) and *Arabidopsis thaliana* (IPIAt1) (30). The sequences were aligned using the program CLUSTALW (http://dot.imgen.bcm.tmc.edu:9331/multialign) and shaded using GENEDOC (http://www.concentric.net/~Ketchup/gddl.htm). The dark shading with white letters indicates amino acid identity for the aligned residue for all five proteins whereas the lightly shaded sequences represent amino acid identity for four of five sequences. The lines above the sequences indicate differences in the predicted amino acid sequences of IPIHp1 and IPIHp2. The inverted arrowhead (▼) above IPIHp1 designates the location of a truncation from the N terminus. Residues required for catalytic activity (31) are marked by upright arrowheads (▲).