Corrections

BIOCHEMISTRY. For the article "A universal telomerase RNA core structure includes structured motifs required for binding the telomerase reverse transcriptase protein," by Jue Lin, Hinh Ly, Arif Hussain, Mira Abraham, Sivan Pearl, Yehuda Tzfati, Tristram G. Parslow, and Elizabeth H. Blackburn, which appeared in issue 41, October 12, 2004, of *Proc. Natl. Acad. Sci. USA* (**101,** 14713–14718; first published September 15, 2004; 10.1073/pnas.0405879101), the authors note the following: "We have found an error in the *Kluyveromyces lactis* structure in Fig. 3. In CS1, a G residue was replaced with an A, and some of the sequence was inadvertently omitted. The complementary strand (CS4-ext) is correct, and the base pairing is still the same (with G:U instead of A:U). The correct sequence of CS1 and the pairing element are in the GenBank database (nucleotides 51–78 of the transcript): CTGGGGTGGTAAGGACCAGTGCCACACT. In addition, at the left side of the *K. lactis* structure a C incorrectly appeared as a G, and stem 2 should be 5′-CCAAA . . . UUUGG. Also, an A nucleotide is missing in the *Saccharomyces cerevisiae* secondary structure, and a G nucleotide was replaced by a C in human sequence." These errors do not affect the conclusions of the article. The corrected figure and its legend appear below.

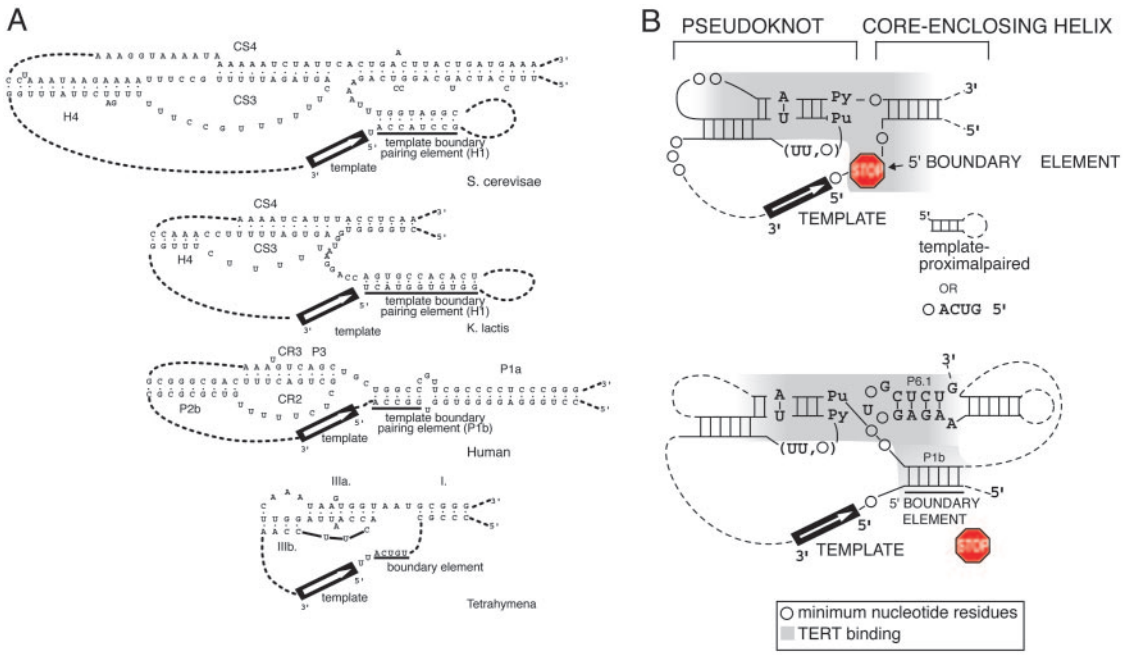

Fig. 3. Proposed unified model for the common secondary structure core for TER RNA. (*A*) Comparison of the common core and TERT-binding regions in representative species of eukaryotes: the budding yeasts *S. cerevisiae*, *K. lactis*, human (vertebrate), and *Tetrahymena thermophila* (ciliate) TER RNAs. (*B*) Proposed unified model for the common secondary structure core for all TER RNAs. The model (see text) is based on data from the present article combined with published data from ciliates, mammals, and yeasts (*Kluyveromyces* and *Saccharomyces* groups). Nucleotides or structures important for binding of TERT (Est2p in *S. cerevisiae*) are indicated by gray shading. The barrier function of the TER RNA is achieved in different ways in different phylogenetic groups (*Upper*). In the budding yeasts only the secondary structure of the 5′ boundary element (helix 1) is important, with no requirement for a given sequence. Helix 1 begins one to four TER RNA residues upstream from the last nucleotide of the maximal putative template (15, 16). In contrast, in ciliate TERs, the 5′ boundary element is a conserved primary sequence ACUG 5′, located two residues upstream from the last template residue copied (26) (*Lower*). In vertebrate TERs, the P1b helix provides template 5′ boundary function (32). Like the yeast helix 1, the barrier function of vertebrate P1b helix requires only its paired structure, but not its sequence, and the P1b helix can be located four or more residues upstream of the 5′ boundary of the template used *in vitro*. However, in mouse, rat, and hamster TER RNAs, the 5′ end of the whole TER molecule is only 2 bases up from the 5′ boundary of the templating domain. Thus, it has been surmised that run-off copying occurs in those species, and then the extra bases are trimmed off by the inherent endonuclease activity of the TER ribonucleoprotein (32, 38, 39).

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BIOCHEMISTRY. For the article "Docosahexaenoic acid: A positive modulator of Akt signaling in neuronal survival," by Mohammed Akbar, Frances Calderon, Zhiming Wen, and Hee-Yong Kim, which appeared in issue 31, August 2, 2005, of *Proc. Natl. Acad. Sci. USA* (**102,** 10858–10863; first published July 22, 2005; 10.1073/pnas.0502903102), the authors note that the labels "+Serine" and "−Serine" in Fig. 1*C* are reversed. The corrected figure and its legend appear below.

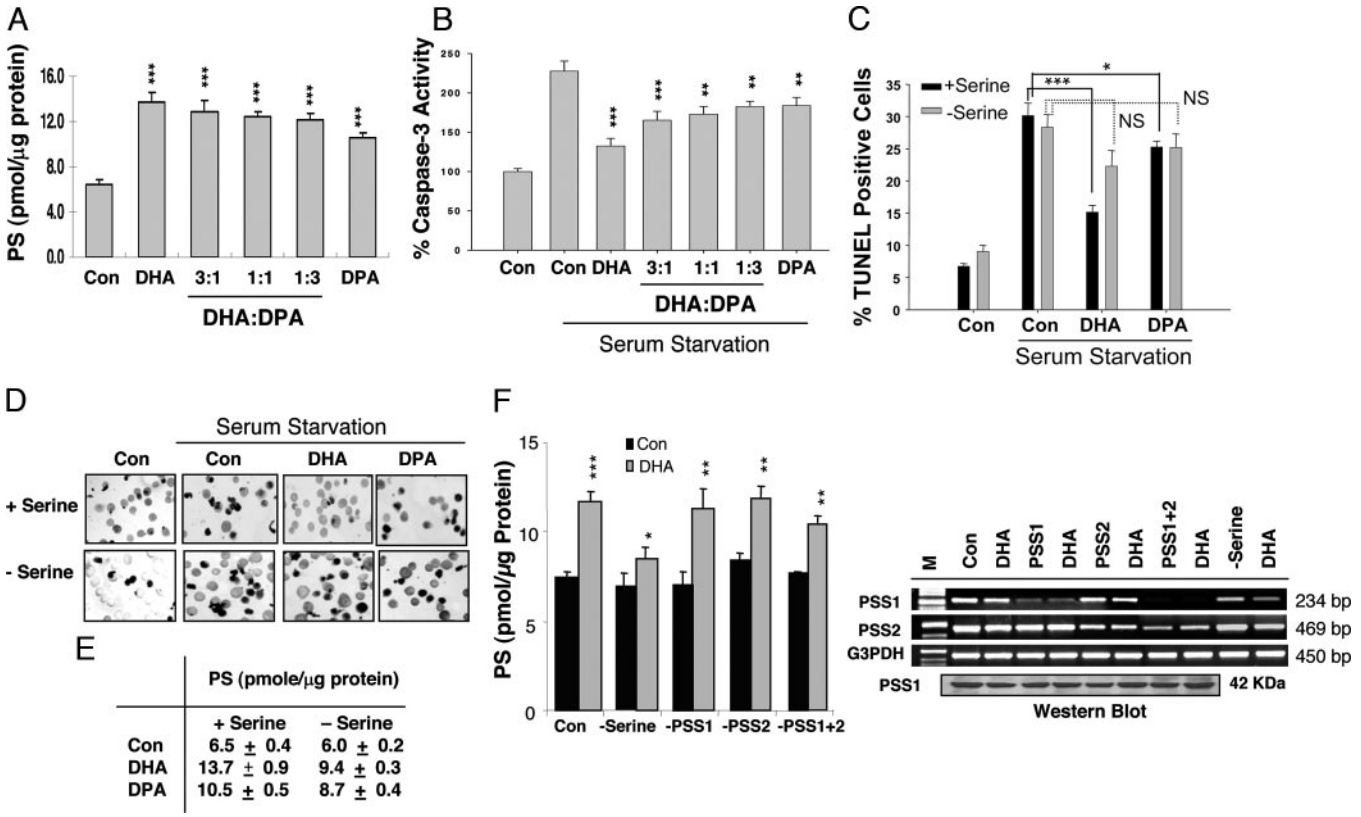

Fig. 1. Effect of DHA on PS accumulation and apoptotic cell death. (*A* and *B*) Differential effects of DHA and DPA on PS accumulation (*A*) and caspase-3 activity induced by serum starvation (*B*). (*C–E*) PS-dependent inhibition of apoptosis evidenced by TUNEL positive cells (*C*) and representative micrographs (*D*), with respect to PS accumulation altered by polyunsaturated fatty acids and serine depletion (*E*). (*F*) Effect of *pss1* and *pss2* gene silencing on DHA-induced PS accumulation. Caspase-3 activity was expressed as the percentage to the basal value from the nonenriched control. Statistical significance was tested against nonenriched (*A* and *F*) or nonenriched serum-free control (*B* and *C*). ***, $P < 0.001$; **, $P < 0.01$; *, $P < 0.05$; NS, not significant.

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MEDICAL SCIENCES. For the article "Phenotypic knockout of VEGF-R2 and Tie-2 with an intradiabody reduces tumor growth and angiogenesis *in vivo*," by Nina Jendreyko, Mikhail Popkov, Christoph Rader, and Carlos F. Barbas III, which appeared in issue 23, June 7, 2005, of *Proc. Natl. Acad. Sci. USA* (**102,** 8293–8298; first published May 31, 2005; 10.1073/pnas.0503168102), the authors should have noted that Fig. 3*A Upper Left* and *Upper Right* were published previously. The figure legend should have included the following credit statement: "Reprinted with permission from ref. 17 (Copyright 2003, American Society for Biochemistry and Molecular Biology)."

17. Jendreyko, N., Popkov, M., Beerli, R. R., Chung, J., McGavern, D. B., Rader, C. & Barbas, C. F., III (2003) *J. Biol. Chem.* **278,** 47812–47819.

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