

Self-assembling organic nanotubes based on a cyclic peptide architecture

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IN this Letter important references to earlier works were inadvertently left out. De Santis *et al.*, in the context of a theoretical conformational analysis of linear regular L,D polypeptides, suggested formation of parallel and antiparallel cylindrical structures through interannular association of β -type rings¹. Synthesis of some cyclic oligopeptides with S_{2n} symmetry, with the construction of tubular structures as the stated goal, was first reported by Tomasic and Lorenzi², when the possibility of tubular aggregate formation was tentatively assigned based on the solubility profiles and infrared analysis². We thank G. P. Lorenzi for kindly bringing these references to our attention. □

1. De Santis, P., Morosetti, S. & Rizzo, R. *Macromolecules* **7**, 52–58 (1974).
2. Tomasic, L. & Lorenzi, G. P. *Helv. chim. Acta* **70**, 1012–1016 (1987).

A deep earthquake aftershock sequence and implications for the rupture mechanism of deep earthquakes

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Nature 372, 540–543 (1994).

THE numbers on the depth scale in Fig. 3a and b in this Letter were incorrect, making the total width of the aftershock zone look as though it was 25 km, rather than 50 km as correctly reported in the text. The numbers on the y-axis of Fig. 3a should

read 555, 575 and 595 km (not 565, 575 and 585 km as published); on the y-axis of Fig. 3b they should be 545, 565, 585 and 605 km (instead of 560, 570, 580 and 590 km). □

A TCP1-related molecular chaperone from plants refolds phytochrome to its photoreversible form

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THE following correction concerns only the contribution to this paper of E.M., R.G. and E. Schäfer. We purified a protein of M_r 60,000 (60K) from oat seedlings that possesses an oligomeric structure of 600K and is partially similar to the cytosolic TCP1 proteins from certain eukaryotes. Specific oligonucleotides were generated following internal peptide sequencing and were used to screen a cDNA library from oats. Ten clones were characterized by sequencing, all of them containing the TCP1-related internal sequenced published before our paper. The clones belong to two subclasses which mainly differ in the deduced amino-terminal sequence of the mature proteins: ALESA for one and ELESF for the other class.

All clones are very similar to β -glucosidase from *Zea mays* and glucosidases and galactosidases from other organisms¹, but show no overall homology to TCP1 genes. The purified 60K protein has β -glucosidase and β -galactosidase activity, which was recently confirmed by Rüdiger and co-workers².

To test the putative chaperone activity of the 60K protein, we purified it in high amounts using a purification procedure slightly different from that published in our paper. In contrast to the data published in our paper, this purified fraction is not able to refold phytochrome to its photoreversible form. On the other hand, it can prevent the aggregation of denatured citrate synthase in a light-scattering assay. Because the purified fraction contains traces of an 800K protein strongly crossreacting with antibodies raised against chloroplast cpn60 or against *E. coli* GroEL, we cannot definitely exclude that the apparent chaperone activity is caused by the contaminating proteins and not by the 60K β -glucosidase. □

1. Brzobohaty, B. *et al. Science* **262**, 1051–1054 (1993).
2. Gus-Mayer, S. *et al. FEBS Lett.* **347**, 51–54 (1994).