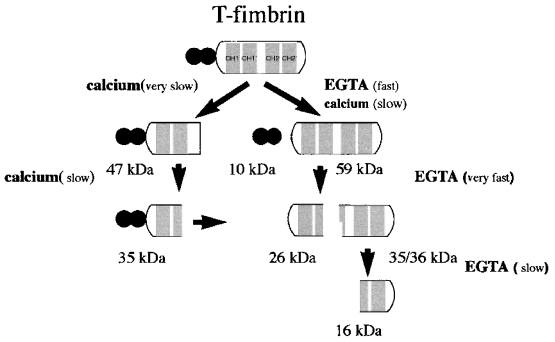
errata

An atomic model of fimbrin binding to F-actin and its implications for filament crosslinking and regulation

Dorit Hanein, Niels Volkmann, Sharon Goldsmith, Anne-Marie Michon, William Lehman, Roger Craig, David DeRosier, Steve Almo and Paul Matsudaira *Nature Struct. Biol.* **5**, 787–792 (1998).

Due to a printer's error, Fig. 4*c* was misprinted. The correct version is shown below.



correction

Structure of the ATP-dependent oligomerization domain of N-ethylmaleimide sensitive factor complexed with ATP

Richard C. Yu, Phyllis I. Hanson, Reinhard Jahn and Axel T. Brünger *Nature Struct. Biol.* **5**, 803–811 (1998).

In this paper, Fig. 4*c* was mistakenly printed upside down.

A protein disulfide oxidoreductase from the archaeon *Pyrococcus furiosus* contains two thioredoxin fold units

Bin Ren, Gudrun Tibbelin, Donatella de Pascale, Mosè Rossi, Simonetta Bartolucci and Rudolf Ladenstein *Nature Struct. Biol.* **5**, 602–611 (1998).

The authors would like to note that the structural figures were generated using the programs Molscript[1], Setor[2], O[3] and Grasp[4]. Sequence alignments were produced using Alscript[5].

1. Kraulis, P.J. MOLSCRIPT: a program to produce both detailed and schematic plots of protein structures. J. Appl. Crystallogr. **24**, 946–950 (1991).
2. Evans S.V. SETOR: hardware-lighted three-dimensional solid model representations of macromolecules. J. Mol. Graphics **11**, 134–138 (1993).
3. Jones, T.A., Zou, J.Y., Cowan, S.W. & Kjeldgaard, M. Improved methods for building protein models in electron density maps and the location of errors in the model. Acta Crystallogr. A **47**, 110–119 (1991).
4. Nicholls, A. Sharp, K. & Honig, B. Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. Proteins Struct. Funct. Genet. **11**, 281–296 (1991).
5. Barton, G.J. ALSCRIPT: a tool to format multiple sequence alignments. Protein Engng. **6**, 37–40 (1993).