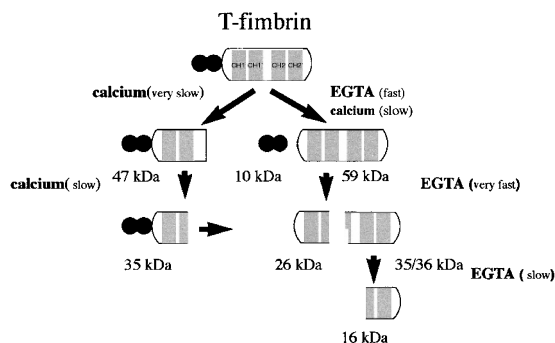


errata

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. 4c 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. 4c 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 Molscript¹, Setor², O³ and Grasp⁴. Sequence alignments were produced using Alscript⁵.

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-independent three-dimensional solid model representations of macromolecules. *J. Mol. Graphics* **11**, 134–138 (1993).
 3. Jones, T.A., Taylor, J.Y., Cowan, D. & Kjeldgaard, M. Improved methods for building protein models in electron density maps and the location of errors in the model. *J. Mol. Biol.* **127**, 315–332 (1987).
 4. Nicholls, A., Sharp, K. & Honig, B. Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons. *Protein Struct. Funct. Genet.* **11**, 281–296 (1991).
 5. Barton, G.I. ALSCRIPT: a tool to format multiple sequence alignments. *Protein Engng.* **6**, 37–40 (1993).