Confirmation of the hierarchical folding of RNaseH: a protein engineering study

Tanya M. Raschke, Joan Kho and Susan Marqusee
Nature Struct. Biol. **6**, 825–831 (1999).

In Table 1, Stability of RNase H variants from urea melts and folding parameters from a global fit to a three-state, obligatory intermediate model (U↔I↔N), the entry in the first column (wt) and ninth row ($k_{ni}(H_2O)$ (s^{-1})) is 1.1×10^{-5}. The correct number should be 1.7×10^{-5}. We regret any confusion this may have caused.

Rational design of potent human transthyretin amyloid disease inhibitors

Thomas Klabunde, H. Michael Petrassi, Vibha B. Oza, Prakash Raman, Jeffery W. Kelly and James C. Sacchettini
Nature Struct. Biol. **7**, 312–321 (2000).

In the April, 2000 issue of *Nature Structural Biology*, we reported a set of six crystal structures of transthyretin bound to several different inhibitors. One of these, the structure of the transthyretin–PHENOX complex, was also described as TTR-$(4)_2$ in a recent issue of the *Journal of the American Chemical Society* (**122**, 2178–2192, 2000), without the correct citation or advanced notification given to the editors. The corresponding authors take full responsibility for this oversight and apologize to the editors, referees, and readers of these papers for any confusion this may have caused.