with each other directly. In fact, in all cases the sense–antisense pairs are distant from one another and clearly do not form any structure resulting from their 'complementarity'.

To take a specific example, the antisense homology box in guanylate kinase (1GKY) is formed by residues 3–12 (PIVISGPSGT) and 75–84 (GNYYGSTVAS). Both peptides are fragments of β-sheets buried inside the protein core and are separated by another β-strand (residues 93–100). The minimum distance between peptides forming the AHB is about 8 Å between the side chains of residues Val 5 and Ser 80. Clearly, there is no complementary interaction between the two AHB-forming fragments. The fact that both fragments were buried inside the protein also excludes the possibility that they can play any role in intermolecular recognition.

Inspection of the other nine AHBs, using molecular graphics showed that they also occurred in different secondary structures, both inside and on the surface of proteins, and again, one could not observe any shape complementarity between peptides belonging to AHBs, which are, in all cases, completely separated one from the other.

We conclude that whatever successes or failures the Molecular Recognition Theory has in explaining peptide-receptor interactions on the biochemical level it is clearly not applicable to protein folding. We can therefore answer the question put by Blalock at the end of his article: "Wouldn't it be truly ironic if Nature coded shape on one DNA strand and complementary shape on the other?" It would be ironic, but Nature does not use this opportunity in coding protein structures.

ANDREZJ KIERZEK,
DANUTA PLOCHOCKA &
PIOTR ZIELENKIEWICZ
Institute of Biochemistry and Biophysics
Polish Academy of Sciences
Pawinskiego 5a
02-106 Warsaw, Poland

Blalock replies — Although I applaud the efforts of Kierzek *et al.* to answer the question posed at the end of my News & Views article, it seems premature to conclude from their rather limited evaluation that Nature does not use AHB or complementary peptide sequences in protein folding. First, it is difficult if not impossible to evaluate whether they analysed the sequences in the same way as Baranyi *et al.* Considering the sequence degeneracy that is a component of the Baranyi *et al.* system and the number of AHBs per protein that these authors found in their evaluation, it is surprising that Kierzek and colleagues identified so few AHBs per protein. This suggests that the sequence analyses used by each group may not have been the same. Alternatively, the differences in the number of AHBs in the two systems could result from Baranyi *et al.* evaluating integral membrane proteins while Kierzek *et al.* obviously did not since such three-dimensional structures have yet to be determined. It is possible that AHBs or complementary peptide sequences play a greater role in the configuration of membrane-associated proteins. A second and perhaps more important concern is the 'static' nature of known protein structures. It is conceivable that AHBs are involved as temporary docking sites during the folding process itself and would be seen in certain transitional states for a particular polypeptide chain. If so, these sites may not be evident after the establishment of disulphide bonds, salt bridges and so on in the completely folded protein. These are obviously issues that need to be addressed before conclusions are reached about the role of AHB in protein folding and structure. In the meantime, as elegantly demonstrated by Ruiz-Opazo *et al.*[5] in the October issue of *Nature Medicine*, it is clear that in certain instances the Molecular Recognition Theory can explain peptide/receptor interactions and their evolution. With this in mind, it would be surprising if Nature completely excluded this tactic when folding proteins.

J. EDWIN BLALOCK
Department of Physiology and Biophysics
University of Alabama at Birmingham
Birmingham, Alabama 35294, USA

1. Blalock, J.E. Genetic origins of protein shape and interaction rules. *Nature Med.* 1, 876–878 (1995).
2. Baranyi, L. *et al.* The antisense homology box: A new motif within proteins that encodes biological active peptides. *Nature Med.* 1, 894–901 (1995).
3. Ruf, J. *et al.* Immunopurification and characterization of thyroid autoantibodies with dual specificity for thyroglobulin and thyroperoxidase. *Autoimmunity* **11**, 179–188 (1992).
4. Bernstein, F.C. *et al.* The Protein Data Bank: A computer-based archival file for macromolecular structures. *J. molec. Biol.* **112**, 535–542 (1977).
5. Ruiz-Opazo, N., Akimoto, K. & Herrera, V.L.M. Identification of a novel dual angiotensin II/vasopressin receptor on the basis of molecular recognition theory. *Nature Med.* 1, 1074–1081 (1995).

Sterilizing dental equipment

To the editor — In the September issue of *Nature Medicine*, Lewis and Arens presented data concerning the resistance of microorganisms to disinfection[1]. A number of points call for a reassessment of their conclusions that heat sterilization is required to render dental equipment free from contaminating microorganisms.

First, in discussing sterilization procedures for reusable dental equipment the authors do not consider the importance of cleaning equipment before disinfecting and sterilization. Without a doubt, thorough cleaning is the most important reprocessing step[2], and any study that assesses the efficacy of a biocidal agent must include cleaning in its methodology. For example, it has been shown[3] that flexible endoscopes contaminated with the human immunodeficiency virus (HIV) require only a two-minute soak in 2% (alkaline) glutaraldehyde after thorough cleaning in order to yield endoscopes 100% free of HIV. Lewis and Arens, however, ignored the significance and benefits of cleaning. Briefly, their study immersed dirty cluster plates, containing a lubricant contaminated with HIV, into an aqueous solution of glutaraldehyde at room temperature for two hours and found this exposure time to be insufficient to inactivate HIV.

Under these test conditions, the inability of a liquid germicide to completely inactivate the HIV organism, however, is not surprising; in fact, it is expected. Failure to remove organic debris, bioburden, and lubricants from the surfaces of dirty medical instruments prior to chemical immersion is likely to render any disinfection or sterilization process ineffective (see, for example, refs 4 and 5). For example, 'sterilization' processes that use ethylene oxide gas[5] and liquid chemical sterilants[6–8] are likely to fail if cleaning is inadequate. Even pressurized steam, which is the most reliable sterilization process, may be ineffective if the instrument is not first thoroughly cleaned[9].