issue of patents on Spadafora's work may well prove to be a storm in a teacup, since the basic idea was recorded nearly 20 years ago but remained unnoticed by cell biologists and animal breeders, possibly because no minireview accompanied it. The belated rediscovery of the work of Brackett *et al.* vindicates the findings of the Spadafora group. We are happy to learn that recently at least one other group has been able to repeat Spadafora's experiments.

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Structure of *ras* Protein

During the structure refinement at 2.2 Å resolution of the catalytic domain of human c-H-*ras* protein, an alternative tracing (Fig. 1, top left) of the backbone structure was recognized (*1*). The new tracing involves the switching of two β strands, β1 and β3, of the original tracing (Fig. 1, bottom left), which was derived from a 2.7 Å resolution multiple isomorphous replacement (MIR) map (*2*). Residues affected by the switch are 1 to 11 and 46 to 65. All the other residues remain in the same place as in the original model. Most of the biochemical and biological interpretations and conclusions we described previously are not affected by the switch except for those relating to residue 61, which is located in weak electron density. The new model better defines the conformation of residues 10 and 11 (as reflected by lower temperature factors) at the beginning of the phosphate binding loop L1 and brings the conserved Asp^{57} close to the magnesium ion. The overall topology is now more similar to that of the G-binding domain of bacterial elongation factor EFTu (*3*), and the conformation of the phosphate binding loop L1, in particular, is very similar to those of EFTu and adenylate kinase (*4*). The evidence for the correctness of the new tracing is listed below:

1) The residual (*R* factor) of refinement by X-PLOR (*5*) and TNT (*6*) programs for the structure excluding both L4 (which is located in a region of very weak electron density) and bound water molecules was 0.234 for the new structure and 0.268 for the earlier structure. The new model for the complete structure refines to a current *R* factor of 0.19.

2) We have constructed a mutant at residue 59, which could be used to distinguish the two structural models. The difference electron density map between the Thr^{59} mutant and the normal protein (Ala^{59}) shows a positive peak at the position expected in the new structure, but not in the old one.

3) The new structure also fits the original MIR map with the exception of residues 61 to 65, which are located in very weak electron density. Furthermore, the heavy atoms (*2*) are located in the same positions relative to the liganding residues in both structures: Cys^{80} and Met^{111} near heavy-atom site A, Cys^{118} near site B, and Met^{67} and Met^{72} near site C.

4) The difference electron density map between another mutant (Val^{12}) and normal protein (Gly^{12}) shows a strong peak corresponding to the side chain of Val at the location expected in the new as well as the old structures, consistent with both structures having the same L1 location and conformation beginning at residue 12.

Two views of the new backbone structure are shown in Fig. 1, top right and bottom right. A short α helix in L4 revealed during the refinement is also indicated in the figures. The α-carbon coordinates of the new structure have been deposited at the Brookhaven Data Bank. New figures and photographs are available on request.

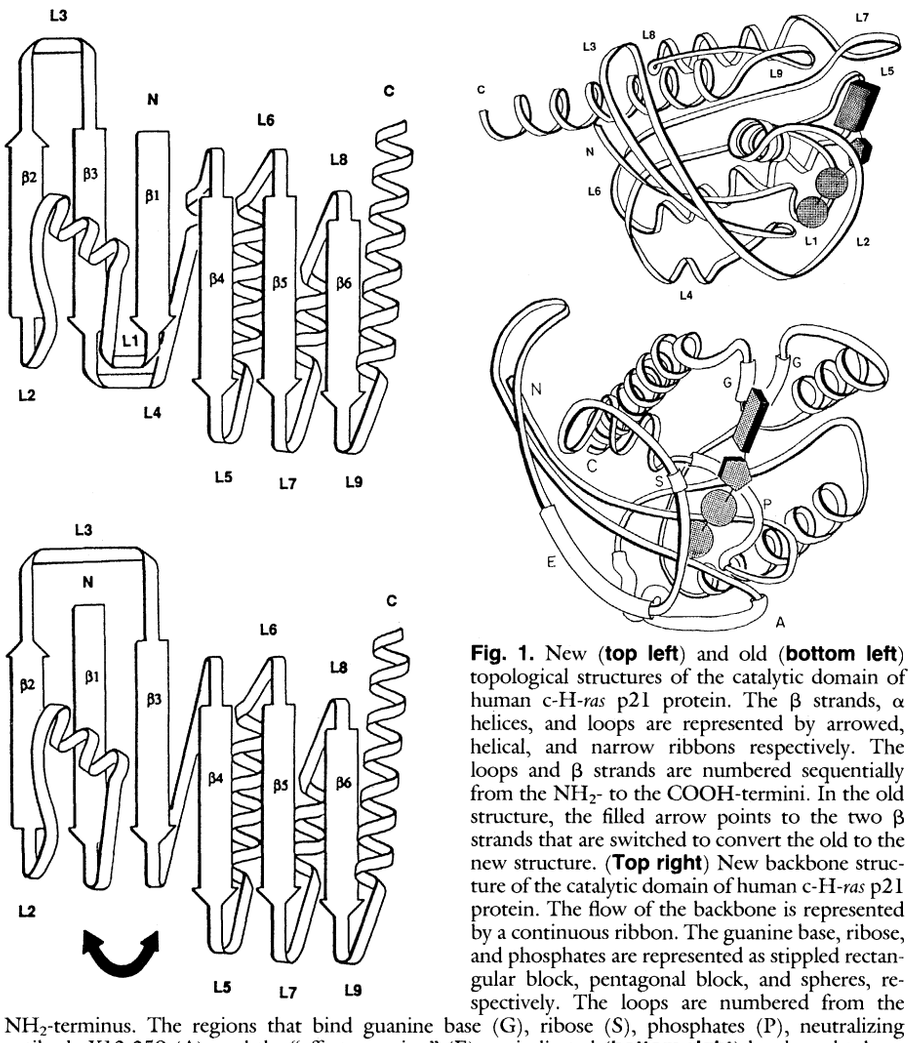

Fig. 1. New (**top left**) and old (**bottom left**) topological structures of the catalytic domain of human c-H-*ras* p21 protein. The β strands, α helices, and loops are represented by arrowed, helical, and narrow ribbons respectively. The loops and β strands are numbered sequentially from the NH_2- to the COOH-termini. In the old structure, the filled arrow points to the two β strands that are switched to convert the old to the new structure. (**Top right**) New backbone structure of the catalytic domain of human c-H-*ras* p21 protein. The flow of the backbone is represented by a continuous ribbon. The guanine base, ribose, and phosphates are represented as stippled rectangular block, pentagonal block, and spheres, respectively. The loops are numbered from the NH_2-terminus. The regions that bind guanine base (G), ribose (S), phosphates (P), neutralizing antibody Y13-259 (A), and the "effector region" (E) are indicated (**bottom right**) by sleeved tubes.

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REFERENCES AND NOTES

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Erratum: In the Table of Contents of the 24 March 1989 issue, the title of the report "Histamine is an intracellular messenger mediating platelet aggregation" by S. P. Saxena *et al.* appearing on page 1596 was incorrectly printed.