as would be expected for the binding site for the basic ribonuclease molecule. The diameter of the cavity formed by the β -sheet is between 18 and 25 Å, with the shortest distance between the terminal repeats of only 13 Å (Fig. 1d). RNase A has dimensions of $20 \times 25 \times 45$ Å and no conformational changes upon binding have been reported. Therefore only a part of the ribonuclease molecule could bind in the cavity formed by the β -sheet. Because most tertiary interactions stabilizing the structure of RI occur between successive β - α building blocks, the two ends of the horseshoe may be able to move substantially relative to each other in solution. The resulting elasticity of the structure may be important in ribonuclease binding. □

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CORRECTION

A protein kinase homologue controls phosphorylation of ganciclovir in human cytomegalovirus-infected cells

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Nature **358**, 162–164 (1992).

FIGURE 3 of this letter contains an error in the numbering of the amino-acid residues of the HCMV UL97 protein. The 4-amino-acid deletion in UL97 should comprise residues 590–593, and not residues 638–641 as indicated in the figure. □

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