that exclude most globular proteins from binding to ice. □

Methods

The crystallization of type III antifreeze protein and preparation of its platinum derivative have been described[14]. Extensive attempts to obtain a second derivative using wild-type AFP, various Cys and His mutants either through co-crystallization or soaking experiments, failed. Therefore, type III AFP was labelled with selenomethionine[15] and crystallized under similar conditions to the wild-type protein, although at lower pH (3.25 rather than 4.50). The 1.25 Å-resolution data were collected at beam X11 (λ = 0.91 Å), DESY, EMBL Hamburg Outstation. All other data were collected using a Mar Research imaging plate equipped with an Rigaku rotating-anode generator. Data were processed using DENZO[16] and CCP4[17]. The difference Patterson map of the seleno-methionyl protein was not interpretable, nor was the difference map cross-phased by the Pt derivative. The direct method[18], however, enabled all five internal Se atom positions to be determined. The MIRAS phases calculated with MLPHARE[19] were improved by solvent flattening and skeletonization using CCP4[17], which resulted in a readily interpretable 2.5 Å map. Refinement was performed using X-PLOR[20]. All data were used (no σ cut) in the refinement, in which 5% randomly chosen data were set aside for R_{free} calculation. All residues are in the allowed Ramchandran regions and all side chains are visible, except for one or two N-terminal residues. Multiple rotamers were observed for residues 2, 24, 25 and 55 in the native model, but not for any of the ice-binding residues. Further refinement involving anisotropic temperature factor and hydrogen atoms for the native protein model is in progress.

Received 13 June; accepted 14 October 1996.

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ACKNOWLEDGEMENTS. We thank Q. Ye and S. Gauthier for technical assistance; F. Sönnichsen for NMR coordinates from his ongoing refinement, for his help in modelling the ice planes, and for discussions; T. G. Flynn for his support and encouragement; C. A. Knight for comments on our manuscript; and L. Johnson and other members of the Laboratory of Molecular Biophysics, University of Oxford, for their help in the early stages of this project. This work was supported by the Faculty of Medicine, Queen's University (Z.J.) and the MRC of Canada (Z.J. and P.L.D.). Z.J. is an MRC scholar and C.I.D. was recipient of an MRC Studentship. Access to Hamburg Outstation, DESY, is gratefully acknowledged.

CORRESPONDENCE and requests for materials should be addressed to Z.J. (e-mail: jia@crystal.biochem.queensu.ca). The coordinates of type III AFP have been deposited in the Brookhaven Protein Data Bank, accession code 1MSI. For an animation of AFP binding to ice, visit the World-Wide Web site: http:// crystal.biochem.queensu.ca/nature.

ERRATA

The CXC chemokine SDF-1 is the ligand for LESTR/fusin and prevents infection by T-cell-line-adapted HIV-1

Estelle Oberlin, Ali Amara, Françoise Bachelerie, Christine Bessia, Jean-Louis Virelizier, Fernando Arenzana-Seisdedos, Olivier Schwartz, Jean-Michel Heard, Ian Clark-Lewis, Daniel F. Legler, Marcel Loetscher, Marco Baggiolini & Bernhard Moser

Nature **382,** 833–835 (1996)

THE labelling of the two lower panels of Fig. 2*b* was accidentally omitted. These panels showed inhibition (left panel) or lack of inhibition (right panel) of syncytia formation by 100 nM SDF-1 or RANTES, respectively. The labels should thus have read 'HIV-1_{LAV} + SDF-1 (left) and 'HIV-1_{LAV} + RANTES' (right). □

Specific cytotoxic T cells eliminate cells producing neutralizing antibodies

Oliver Planz, Peter Seiler, Hans Hengartner & Rolf M. Zinkernagel

Nature **382,** 726–729 (1996)

THE title shown above is incomplete and should read "Specific cytotoxic T cells eliminate B cells producing virus-neutralizing antibodies". □

ADDENDUM

Three-dimensional structure of human cytomegalovirus protease

Huey-Sheng Shieh, Ravi G. Kurumbail, Anna M. Stevens, Roderick A. Stegeman, Eric J. Sturman, Jina Y. Pak, Arthur J. Wittwer, Mark O. Palmier, Roger C. Wiegand, Barry C. Holwerda & William C. Stallings

Nature **383,** 279–282 (1996)

THIS letter contains six additional figures as Supplementary Information. These are available on *Nature*'s World-Wide Web site (http://www.nature.com) or as paper copy from Mary Sheehan at the London editorial office of *Nature*. □