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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 described¹⁴. Extensive attempts to obtain a second derivative using wild-type AFP, various Cys and His mutants either through cocrystallization or soaking experiments, failed. Therefore, type III AFP was labelled with selenomethionine¹⁵ and crystallized under similar conditions to the wildtype protein, although at lower pH (3.25 rather than 4.50). The 1.25 Åresolution data were collected at beam X11 ($\lambda = 0.91$ 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 DENZO¹⁶ and CCP4¹⁷. 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 method¹⁸, however, enabled all five internal Se atom positions to be determined. The MIRAS phases calculated with MLPHARE¹⁹ were improved by solvent flattening and skeletonization using CCP417, which resulted in a readily interpretable 2.5 Å map. Refinement was performed using X-PLOR²⁰. 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 Nterminal 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.

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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. 2b 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_{IAV} + SDF-1 (left) and 'HIV- 1_{IAV} + RANTES' (right). \square

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.