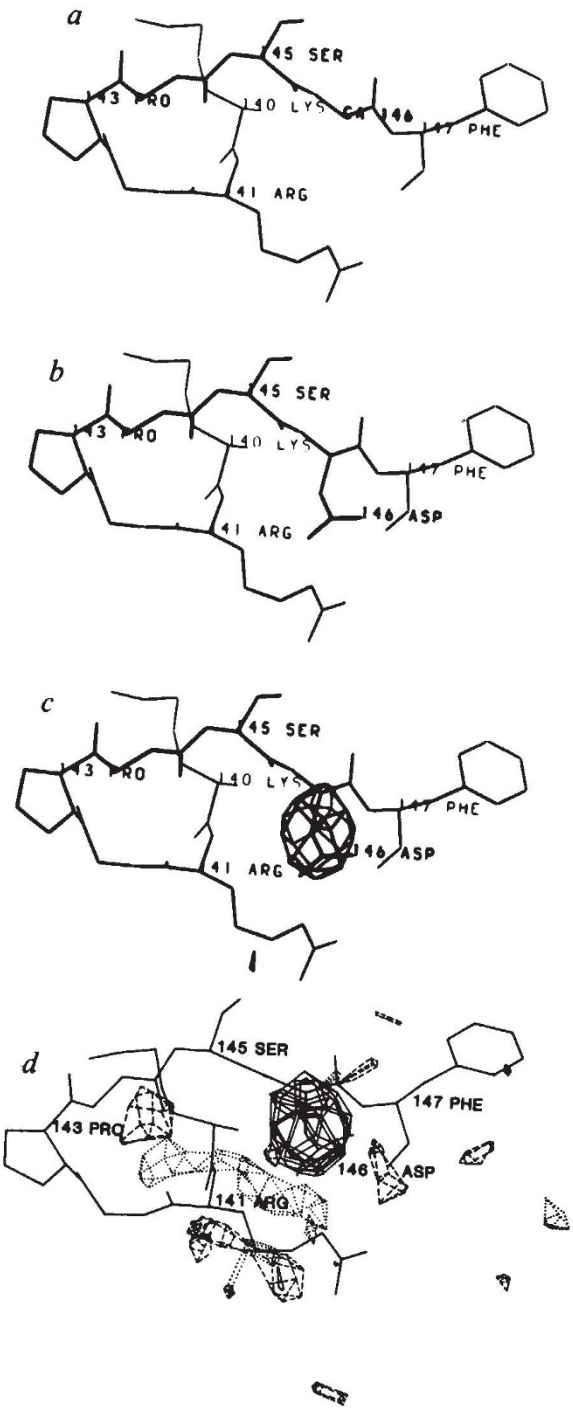

Fig. 2 *a*, Structure of the amino acid 140–147 loop which contains a glycine at position 146 in the parent HA. Atomic coordinates for the parent structure[15] were obtained by model building (I. A. Wilson and D.C.W.) on a version of the BILDER program[20] modified by Robert Ladner. These were refined to an R factor of 0.26 after six cycles of restrained least-squares refinement[21] where the contribution of the structure factor to the least-squares equation was evaluated by the gradient-curvature method on a difference map (ref. 22 and M. Lewis and D. Rees, personal communication). ($R = \Sigma|siI_{hi} - \bar{I}_h|/\Sigma\bar{I}_h$) where si = scale factor (including film temperature factor) for crystal i, and I_{hi} = intensity of reflection h of crystal i.) Exact 3-fold symmetry was imposed on the HA trimer in the crystallographic asymmetric unit by refining only a monomer's coordinates from 3-fold averaged difference maps. An overall B factor of 14 was used. Details of the refinement will be published elsewhere. *b*, The coordinates of the 140–147 loop of the antigenic variant V3a showing the location of the Asp (for Gly) substitution. Note that no conformational changes are observed between *a* and *b*. The V3a loop coordinates were obtained from model building on a $2F_0 - F_c$ map after refining the X31 coordinates (minus the loop) against the V3a data. *c*, The V3a difference map (F_{obs} V3a $- F_{obs\ X31}$) showing the 12σ peak at Asp 146. The only significant difference is at the position expected by the addition of the Asp 146 side chain instead of Gly 146 in the wild type. The difference Fourier was calculated using observed parent and variant structure factors with the refined phases described for *a*. *d*, The same as *c* with additional positive (dashed) and negative (dotted) contours at the noise level, 3σ. The interpretable 3σ peaks are a ridge of difference density indicating a small shift in the position of the side chain of Arg 141, which is within hydrogen bonding distance of Asp 146. (This figure was produced with an Evans and Sutherland PS-300 on the version of FRODO written by J. W. Pflugrath, M. A. Saper, B. Bush and A. Jones.)

in the position of Arg 141 to improve the hydrogen bond to the carboxyl group of Asp 146 led to our finding its displacement in the experimental difference map. Details of the method and results will be given separately.

We thank David Stevens and Rose Gonsalves for assistance, Eugene Brown of Genetic Institute for synthesizing one of the oligonucleotide primers, and acknowledge support from NIH AI 13654 (D.C.W.). M.K. was the recipient of fellowship DRG-542 from the Damon Runyon-Walter Winchell Cancer Fund. We also thank Henry H.-L. Shih, John Brady and Martin Karplus for allowing us to quote from their unpublished results predicting the structure of the single-site mutant

Received 25 April; accepted 14 June 1984.

1. Webster, R. G. & Laver, W. G. in *Influenza Viruses and Influenza* (ed. Kilbourne, E. D.) 270–314 (Academic, New York, 1975).
2. Wiley, D. C., Wilson, I. A. & Skehel, J. J. *Nature* **289**, 373–378 (1981).
3. Caton, J. J., Brownlee, C. C., Yewdell, C. A. & Gerhard, W. *Cell* **31**, 417–427 (1982).
4. Daniels, R. S., Douglas, A. R., Skehel, J. J. & Wiley, D. C. *J. gen. Virol.* **64**, 1657–1662 (1983).
5. Daniels, R. S. *et al.* in *The Origin of Pandemic Influenza Viruses* (eds Laver, G. W. & Chu, C. M.) (Elsevier, New York, in the press).
6. Colman, P. M., Varghese, J. N. & Laver, W. D. *Nature* **303**, 41–44 (1983).
7. Evans, D. M. A., Minor, P. D., Schild, G. S. & Almond, J. W. *Nature* **304**, 459–462 (1983).
8. Laver, W. G., Air, G. M. & Webster, R. G. in *Genetic Variation Among Influenza Viruses* (ed. Nayak, D. P.) 283–295 (Academic, New York, 1981).
9. Webster, R. G. & Laver, W. G. *Virology* **104**, 139–148 (1980).
10. *Bull. Wld Hlth Org.* **45**, 119–124 (1971).
11. Laver, W. G., Air, G. M., Dophiede, T. A. & Ward, C. W. *Nature* **283**, 454–457 (1980).
12. Skehel, J. J. *et al. Proc. natn. Acad. Sci. U.S.A.* (in the press).
13. Rogers, G. N. *et al. Nature* **304**, 76–78 (1983).
14. Wiley, D. C. & Skehel, J. J. *J. molec. Biol.* **112**, 343–347 (1977).
15. Wilson, I. A., Skehel, J. J. & Wiley, D. C. *Nature* **289**, 368–373 (1981).
16. Winkler, F. K., Schutt, C. E. & Harrison, S. C. *Acta crystallogr.* **A35**, 901–911 (1979).
17. Sanger, F., Nicklen, S. & Coulson, A. R. *Proc. natn. Acad. Sci. U.S.A.* **74**, 5463–5467 (1977).
18. Patel, T. P. *et al. Nucleic Acids Res.* **10**, 5605–5620 (1982).
19. Verhoeyen, M. *et al. Nature* **286**, 771–776 (1980).
20. Diamond, R. in *Biomolecular Structure, Conformation, Function and Evolution* Vol. 1 (ed. Srinivasan, R.) 567–588 (Pergamon, Oxford, 1980).
21. Hendrickson, W. A. & Konnert, J. in *Biomolecular Structure, Function, Conformation, and Evolution* Vol. 1 (ed. Srinivasan, R.) 43–47 (Pergamon, Oxford, 1980).
22. Cochran, W. *Acta crystallogr.* **4**, 408–411 (1951).
23. Brooks, B. *et al. J. comp. Chem.* **4**, 187–217 (1983).
24. Gelin, B. R. & Karplus, M. *Biochemistry* **18**, 1256–1268 (1979).

Errata

A general circulation model of water isotope cycles in the atmosphere

S. Joussaume, J. Jouzel & R. Sadourny

Nature **311**, 24–29 (1984)

IN this article, the order of the authors was incorrect. It appears correctly above.

Sequential late Cenozoic structural disruption of the northern Himalayan foredeep

D. W. Burbank & R. G. H. Raynolds

Nature **311**, 114–118 (1984)

THE above article was published with the name of the third author spelt incorrectly as Reynolds.