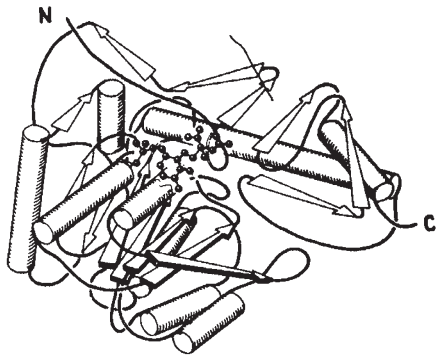
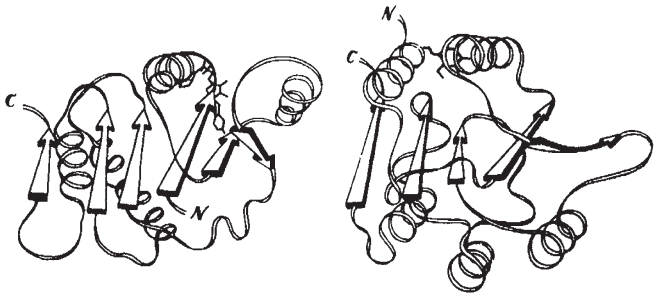


Fig. 2 Schematic drawing of the model of Asp-transaminase subunit built from secondary structure elements. α-Helices are shown as cylinders and β-strands as arrows, those belonging to the 'nucleotide-binding domain' shown as space-filled arrows. The coenzyme is shown covalently linked to α-Me-Asp.

compounds, at 50 mM concentration. Crystals soaked with erythro-β-hydroxyaspartate acquired a gingerish colour after 1 hour, which could be maintained for several months. The X-ray experiments were performed on crystals soaked for 2 h. Crystals soaked with maleate or succinate became a distinctly brighter yellow than the original α-Me-Asp complex. X-ray experiments were done after 1–2 days of soaking. At 5 Å resolution, the difference maps of all three complexes contained some features in the substrate-binding area but no conformational changes. A similar X-ray experiment on the abortive complex of the pyridoxal form of the enzyme with 2-oxoglutarate gave a difference map showing conformational changes localised in the same region as the substrate-free form of the holoenzyme[3], but of opposite sign.

It is of interest that the conformations of the apoenzyme and the α-Me-Asp complex are similar. A number of prominent positive peaks observed near more extended features interpreted as conformational changes, suggest that some of the conformational changes can be ascribed to the interaction of ions. After the removal of α-Me-Asp one such positive peak persists near a position previously occupied by the distal carboxyl. Another is seen in the vicinity of the C-terminal helix. It can be supposed that an anion replacing the substrate carboxyls is a cause of the conformational changes in the substrate-binding area. Also, in relation to the apoenzyme, the absence of negative density for the removed phosphate of the pyridoxal phosphate or substrate analogue may be explained by similar anion replacements. It is possible that the additional space created by removal of the coenzyme allows the anion to bind without causing conformational distortions to the adjacent protein framework.

In the study of Asp-transaminase much attention has been paid to the so-called syncatalytic phenomena observed after the addition of pairs of substrates (such as the L-glutamate/2-oxoglutarate pair)[20–24]. These effects have been treated in terms of conformational changes concomitant with the formation of covalent intermediates in the course of the catalytic process. It is tempting to assume that the conformational changes discussed here are a part of the same picture. However some remarks seem to be relevant: (1) The conformational changes observed by us are concomitant not with catalysis but with binding of substrates or inhibitors. (2) The conformational changes that accompany the transition between substrate-binding, and substrate-free forms are different in two subunits, this asymmetry may be explained by restrictions imposed by crystal packing. (3) The possibility that the observed changes are a property only of the chicken heart cytosol enzyme cannot be excluded. (4) In addition to the gross conformational changes observed at 5 Å resolution, more subtle changes are probably also present which may be of the most important functional meaning. It may be predicted that comparative X-ray studies of different states of Asp-transaminase at higher resolution should soon clarify many of the problems discussed here.



LDH Asp-transaminase

Fig. 3 Comparison of two domains present in the the three-dimensional structure of lactate dehydrogenase and Asp-transaminase.

We thank Yu. V. Nekrasov, A. A. Vagin and V. M. Kochkina for valuable assistance, and L. N. Johnson for the picture of 'nucleotide-binding domain' in phosphorylase *b*. We also thank Professor A. E. Braunstein for valuable advice and discussions.

Note added in proof: Recently similar three-dimensional structure and conformational changes have been described for chicken mitochondrial Asp-transaminase[25].

Received 30 July; accepted 19 December 1979.

1. Braunstein, A. E. *Enzymes* **9**, 379–481 (1973).
2. Arnone, A. *et al. J. molec. Biol.* **12**, 509–513 (1977).
3. Borisov, V. V. *et al. J. molec. Biol.* **125**, 275–292 (1978).
4. Gehring, H. *et al. J. molec. Biol.* **115**, 97–101 (1977).
5. Volkova, G. A. *et al. Kristallografiya* **23**, 823–824 (1978).
6. Borisov, V. V. *et al. Dokl. Akad. Nauk S.S.S.R.* **250**, N4 (1979).
7. Levitt, M. & Chothia, C. *Nature* **261**, 552–558 (1976).
8. Adams, M. J. *et al. Nature* **227**, 1098–1103 (1970).
9. Hill, E., Tsernoglou, D., Webb, L. & Banaszak, L. J. *J. molec. Biol.* **72**, 577–591 (1972).
10. Bränden, C.-I. *et al. Proc. natn. Acad. Sci. U.S.A.* **70**, 2439–2442 (1973).
11. Buchner, M., Ford, G. C., Moras, D., Olsen, K. W. & Rossmann, M. G. *Proc. natn. Acad. Sci. U.S.A.* **70**, 3052–3054 (1973).
12. Banks, R. D. *et al. Nature* **279**, 773–777 (1979).
13. Campbell, J. W., Watson, H. C. & Hodgson, G. I. *Nature* **250**, 301–303 (1974).
14. Ploegman, J. H., Drent, G., Kalk, K. H. & Hol, W. G. J. *J. molec. Biol.* **123**, 557–594 (1978).
15. Fletterick, R. J., Syguch, J., Semple, H. & Madsen, N. B. *J. biol. Chem.* **251**, 6142–6146 (1976).
16. Weber, I. T. *et al. Nature* **274**, 433–437 (1978).
17. Adams, K. J., Ford, G. C., Liljas, A. & Rossmann, M. G. *Biochem. biophys. Res. Commun.* **53**, 46–51 (1973).
18. Chandrasekhar, K., McPherson, A. Jr, Adams, M. J. & Rossmann, M. G. *J. molec. Biol.* **77**, 503–518 (1973).
19. Metzler, C. M. *et al. J. biol. Chem.* **253**, 5251–5254 (1978).
20. Christen, P. & Riordan, J. F. *Biochemistry* **9**, 3025–3054 (1970).
21. Birchmeier, W., Zaoralek, P. E. & Christen, P. *Biochemistry* **12**, 2874–2879 (1973).
22. Birchmeier, W., Wilson, K. J. & Christen, P. *J. biol. Chem.* **248**, 1751–1759 (1975).
23. Gehring, H. & Christen, P. *Biochem. biophys. Res. Commun.* **63**, 441–447 (1975).
24. Pfister, K., Kagi, J. H. R. & Christen, P. *Proc. natn. Acad. Sci. U.S.A.* **75**, 145–148 (1978).
25. Eichele, G., Ford, G. C., Glor, M., Jansonius, J. N., Mavrides, C. & Christen, P. *J. molec. Biol.* **133**, 161–180 (1979).

Corrigendum

In the News and Views item 'Structure and force generation in muscle' by J. M. Squire, *Nature* **281**, 99, lines 14 and 15 in the right-hand column should read '... of 20% of the actin monomers in the thin filaments or to 40% labelling...' (The values 20 and 40% were transposed in the original.)

Erratum

In the review article 'Nuclear weapons and power-reactor plutonium', by A. B. Lovins, *Nature* **283**, 817–822, p. 818 paragraph 1 line 4, should begin '(GWt-d)', paragraph 2 line 6 should read '...27–33 GWt-d/T...'. A line was omitted from the paragraph on p. 822 headed Conclusions. Lines 10–17 should read:
'and "not a valid concept"[31]. (Dilution with UO_2 or other materials requiring chemical or physical[56] separation is a valid concept—it means more material must be diverted and processed[19,25,34]—but does not solve the problem.) Taking all effects on weapons physics into account, a high $^{238,240,242}Pu$ content may reduce expected yield to a level that could devastate only a modest portion of a city rather than all of it, and may make that yield much less predictable, if the bomb is crudely made. But...'. In refs 27 and 55 the title should read '*Nuclear Policies: Fuel Without the Bomb*'.