Table 2 Solvent flattening and phase extension

Cycle	1*	2†	3‡	4†	5‡	5a§
Resolution (Å)	3.5	3.5	2.5	3.5	3.5	3.5-3.0
Reflection no.	5411	5411	5411	5411	5411	2588
Figure of merit[16]	0.68	0.72	0.87	0.91	0.93	0.61
R-factor	—	—	0.24	—	0.22	0.39
$\Delta\alpha°$	—	33.2	39.8	47.3	48.0	—
Correlation coefficient‖ between:						
molecules 1 and 2	0.51	—	0.84	—	0.87	—
molecules 3 and 4	0.46	—	0.85	—	0.87	—

$R^2 = \Sigma(F_{obs} - F_{calc})^2 / \Sigma F_{obs}^2$. $\Delta\alpha°$ = Average accumulated phase difference.

* Original MIR data.

† After electron density averaging around two local 2-fold axes.

‡ After 2-fold averaging and solvent flattening.

§ After solvent flattening and phase extension, data from 3.5 to 3.0 Å resolution.

‖ $\Sigma(\rho_a - \bar{\rho}_a)\ (\rho_b - \bar{\rho}_b) / (\Sigma(\rho_a - \bar{\rho}_a)^2 \times \Sigma(\rho_b - \bar{\rho}_b)^2)^{1/2}$, where ρ_a is electron density for molecule α; ρ_b, electron density for the symmetry related molecule b; $\bar{\rho}_a$, $\bar{\rho}_b$, average electron densities of the respective molecules.

proteins. Second, at the local level, monellin and thaumatin have only two small regions (both tripeptides), located in exposed, looping regions, sharing sequence and topology. According to the conventional notion, each of these regions is too small by itself to be the complete antigenic determinant. Third, because the separations of these two regions are different in the two proteins (26 Å in monellin and 18 Å in thaumatin), we can rule out the possibility that they jointly form the common single antigenic site. The only remaining possibility is that several smaller regions (shorter than three residues), with or without one of the two above tripeptides, jointly form the common antigenic site.

As for sweet taste, there is no *in vitro* assay and no taste receptor molecule has yet been isolated. However, the *in vitro* immunological cross-reactivity may cast some light on taste. The possible relevance is suggested by the facts that (1) the antibodies of one protein cross-react to the other and vice versa[8-10]; (2) antibody-protein complexes lose their ability to elicit sweet taste (unpublished results); (3) a group of sweet compounds such as aspartame compete for the same antibodies but non-sweet aspartame derivatives do not[8,9]; (4) cross-adaptation of monellin and thaumatin in human taste experiments[23] and electrophysiological experiments[24] suggests they are recognized by the same receptor; (5) because antibody and receptor binding sites are likely to be exposed, one may be a subset of the other.

At present these are the only two proteins with known crystal structures that have immunological cross-reactivity without sequence similarity. Biochemical and immunological studies are in progress to identify the regions which may be responsible for the antibody cross-reactivity and the sweet-taste-receptor binding. High-resolution refinement of both proteins is also in progress. The α-carbon coordinates of the structure will be deposited in the Brookhaven Protein Data Bank.

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Corrigendum

Cloning and sequencing of a cDNA for a ligninase from *Phanerochaete chrysosporium*

Ming Tien & Chen-Pei D. Tu
Nature **326**, 520-523 (1987)

FURTHER work on sequencing of ligninase cDNA clone ML-1 has led to the following corrections in the nucleotide sequence:

a change from CG to GC at positions 125-126;
a change from G to C at position 1,043;
an insertion of a C at position 1,051.

The above changes in the nucleotide sequence result in the following correction in the amino acid sequence:

a change from Ser 14 to Cys 14;
a change from Ser 320 to Thr 320;
a change of amino acids 323-346 to (323)Pro-Thr-Leu-Thr-Thr-Leu-Pro-Gly-Pro-Glu-Thr-Ser-Val-Gln-Arg-Ile-Pro-Pro-Pro-Pro-Gly-Ala-STOP(344).

The new termination codon is TAA at positions 1116-1118. The change in reading frame at nucleotide residue 1051 decreases the total amino acid residues from 346 to 344.

Errata

The surface windfield over the Antarctic ice sheets

Thomas R Parish & David H. Bromwich
Nature **328**, 51-54 (1987).

FIGURES 2 and 3 in this letter were transposed. The upper figure on page 53 is Fig. 3, including arrows to show wind direction.

Electrogenic glutamate uptake is a major current carrier in the membrane of axolotl retinal glial cells

Helen Brew & David Attwell
Nature **327**, 707-709 (1987).

IN the penultimate paragraph of this letter (beginning "Depolarization induced release . . . ") two words were omitted during the proof correction stage. The last sentance in the paragraph should read: "This release, which may be non-vesicular, could be accounted for by the strong voltage-dependence of glutamate transport which we have observed, if the same carrier exists in neurons and if the glutamate concentration in neurons is high enough to allow a net glutamate efflux on depolarization."