frame for the coordinates is 'orthogonal'. If $a = b = c = 1$, but α, β or $\gamma \neq 90°$, then the reference frame is 'axial'.

If the reference frame is 'fractional', then the values obtained for a, b, c, α, β and γ should be those of the crystallographic unit cell. For macromolecular structures, where the number of vectors is large, the statistical significance is high and the cell parameters obtained provide an independent evaluation of the experimentally measured cell parameters.

A Fortran program *ELAST* has been written to perform the above analysis on protein structures, considering only bonds between backbone atoms. For a protein of average size, the number of bonds included is about 2000. The time required for the analysis is approximately 4 s on a Convex C2.

This work was supported in part by NIH grant T32NS07078. This is manuscript No. 5953-MB of the Research Institute of Scripps Clinic.

References

PATTERSON, A. L. (1985). In *International Tables for X-ray Crystallography*, Vol. II, edited by J. S. KASPER & K. LONSDALE, pp. 52–64. Birmingham: Kynoch Press. (Present distributor Kluwer Academic Publishers, Dordrecht.)

SANDS, D. E. (1982). *Vectors and Tensors in Crystallography*. Reading, MA: Addison-Wesley.

Acta Cryst. (1990). A**46**, 626

Bloch waves and multislice in transmission and reflection diffraction. Erratum.

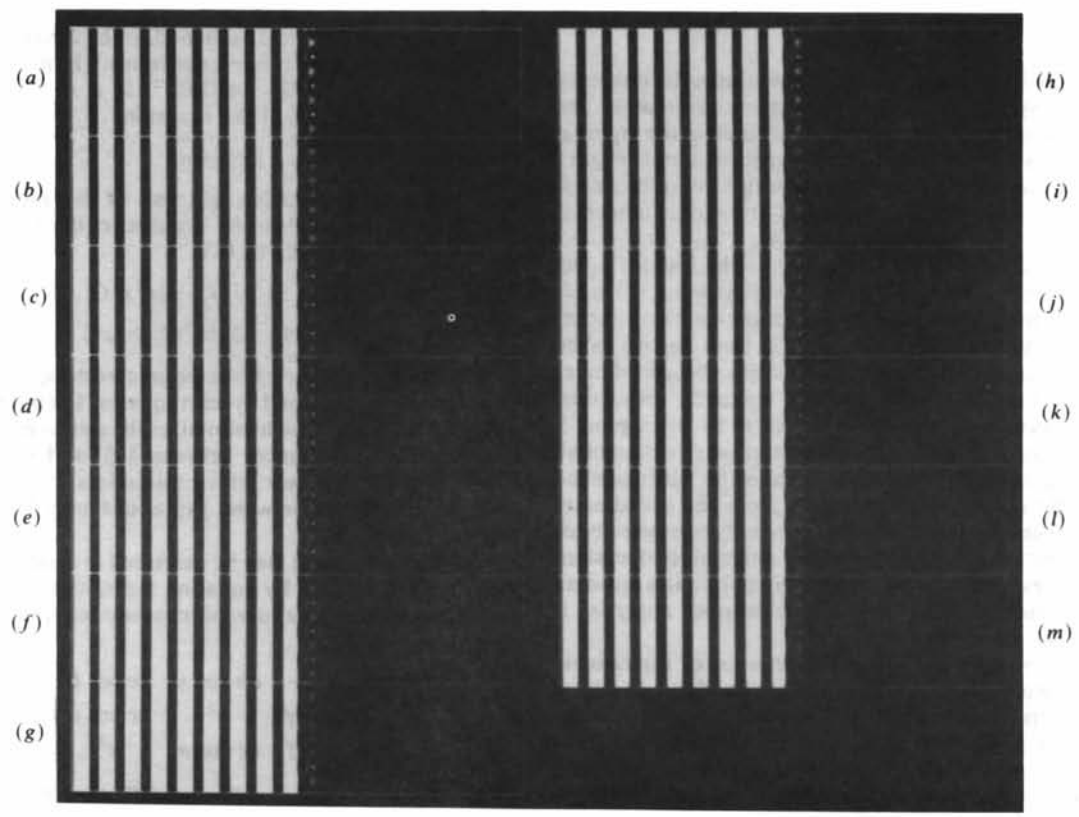
By Y. MA* and L. D. MARKS, *Materials Research Center, Northwestern University, Evanston, IL* 60208, *USA*

(*Received* 14 *April* 1990)

Abstract

Owing to a printer's error, Fig. 11(i) of the paper by Ma & Marks [*Acta Cryst.* (1990). A**46**, 11–32] was published in the wrong orientation. The correct figure is given.

* Present address: Department of Materials Science and Engineering, University of Utah, Salt Lake City, UT 84112, USA.



(i)

Fig. 11. Corresponding results under the same conditions as for Fig. 8, except that the incidence angle is 10 mrad.

0108-7673/90/070626-01$03.00