

the average nonuniformity of the chamber is less than 5%.

The new multiwire area detector is used routinely to collect data from crystals of a complex of dihydrofolate reductase and metho-trexate (a cancer drug) (Poe, Greenfield, Hirshfield, Williams & Hoogsteen, 1972). This work is done in collaboration with Drs D. Matthews, R. Alden, S. Freer and J. Kraut of the UCSD Chemistry Department. The data-collection method using a series of 'stationary pictures' has been described elsewhere (Cork *et al.*, 1974; Xuong, Vernon, Hamlin, Freer, Cork & Anh, 1974). With one DHFR crystal (space symmetry  $P6_1$  with  $a=b=93$  Å and  $c=74$  Å), a standard diffractometer can measure about 6000 reflection intensities (in 120 h) before the intensities have decreased by 15% in average. The new high-speed data collection system can measure about 168 000 reflection intensities in the same time. However, we usually make only 40 000 intensity measurements (out to 2.5 Å resolution) per crystal, after which the crystal reflection intensities have decreased only about 7%. The precision of the chamber data is also better with an intensity reliability  $R$  of 5% as compared with 6.7% from the diffractometer data. The two sets of data also agree with each other ( $R=5.7\%$ ). We have measured more than 200 000 reflection intensities for one parent and four heavy-atom derivative crystals. The difference Patterson maps between parent and heavy-atom derivative data show very clearly the positions of the heavy atoms. Difference Patterson maps between parent data collected by the diffractometer and the heavy-atom derivative data collected with the multiwire area detector show exactly the same heavy-atom peaks. These maps prove then that the chamber data are of at least the same quality as the data collected with the standard diffractometer.

Our experience shows therefore that a flat xenon-filled multiwire area detector is relatively simple to build and that it can collect protein intensity data quite efficiently and with higher precision than has so far been achieved with an area detector composed of phosphorescent screen, image intensifier and TV camera (Minor, Milch & Reynolds, 1974; Arndt & Ambrose, 1968).

Charpak, Hajduk, Jeavons, Stubbs & Khan (1974) have suggested the building of a spherical drift multiwire chamber as an area detector for protein crystallography. This

chamber is more difficult to build than a flat chamber and requires a fixed crystal-to-detector distance that would impose an upper limit on the crystal parameters. A flat chamber can always be positioned at an optimum crystal-to-detector distance depending on the parameters and the size of the reflection spots on the chamber. To reduce the elongation effect of the reflection spots at high incident angles due to the thickness of the chamber, and to improve the data collection rate further, one can use a system of two or more flat chambers.

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#### The measurement of anomalous scattering factors near the Ga $K$ absorption edge in GaP: erratum.

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A correction is given to Fukamachi & Hosoya [*Acta Cryst.* (1975). A31, 215-220]. On p. 216 special position  $(\frac{3}{4}, \frac{3}{4}, \frac{3}{4})$  should read  $(\frac{1}{4}, \frac{1}{4}, \frac{1}{4})$ .

In Fukamachi & Hosoya (1975) the following correction should be made. Page 216, line 7 of §3:  $(\frac{3}{4}, \frac{3}{4}, \frac{3}{4})$  should read  $(\frac{1}{4}, \frac{1}{4}, \frac{1}{4})$ .

#### Reference

- FUKAMACHI, T. & HOSOYA, S. (1975). *Acta Cryst.* A31, 215-220.