19.2.4. Data processing

19.2.4.1. *Data sampling*

The principle of three-dimensional reconstruction is based on the central section theorem, which states that the experimental or computed projected diffraction pattern of a three-dimensional object is a plane that intersects the centre of the three-dimensional Fourier space in the direction normal to the direction of the projection (DeRosier & Klug, 1968). Because of the crystallographic symmetry inherent in a protein crystal, only a portion of the entire three-dimensional Fourier space, equivalent to an asymmetric unit of the crystal unit cell, is needed for the reconstruction. The structure factors of a three-dimensional crystal are localized in the three-dimensional reciprocal lattice, whereas the structure factors of a two-dimensional crystal are distributed continuously along the lattice lines, each of which passes through the reciprocal lattice in the zero projection plane (Fig. 19.2.4.1) (Henderson & Unwin, 1975). The assignment of z^* for each observation (h, k, z^*) along the lattice line is determined from the tilt angle and direction of the tilt axis for each image (Shaw & Hills, 1981). In general, the three-dimensional data set is initially built up from low-angle data and is gradually extended to the high-angle data. The angular parameters for each observed reflection are iteratively refined among one another within the whole data set. The

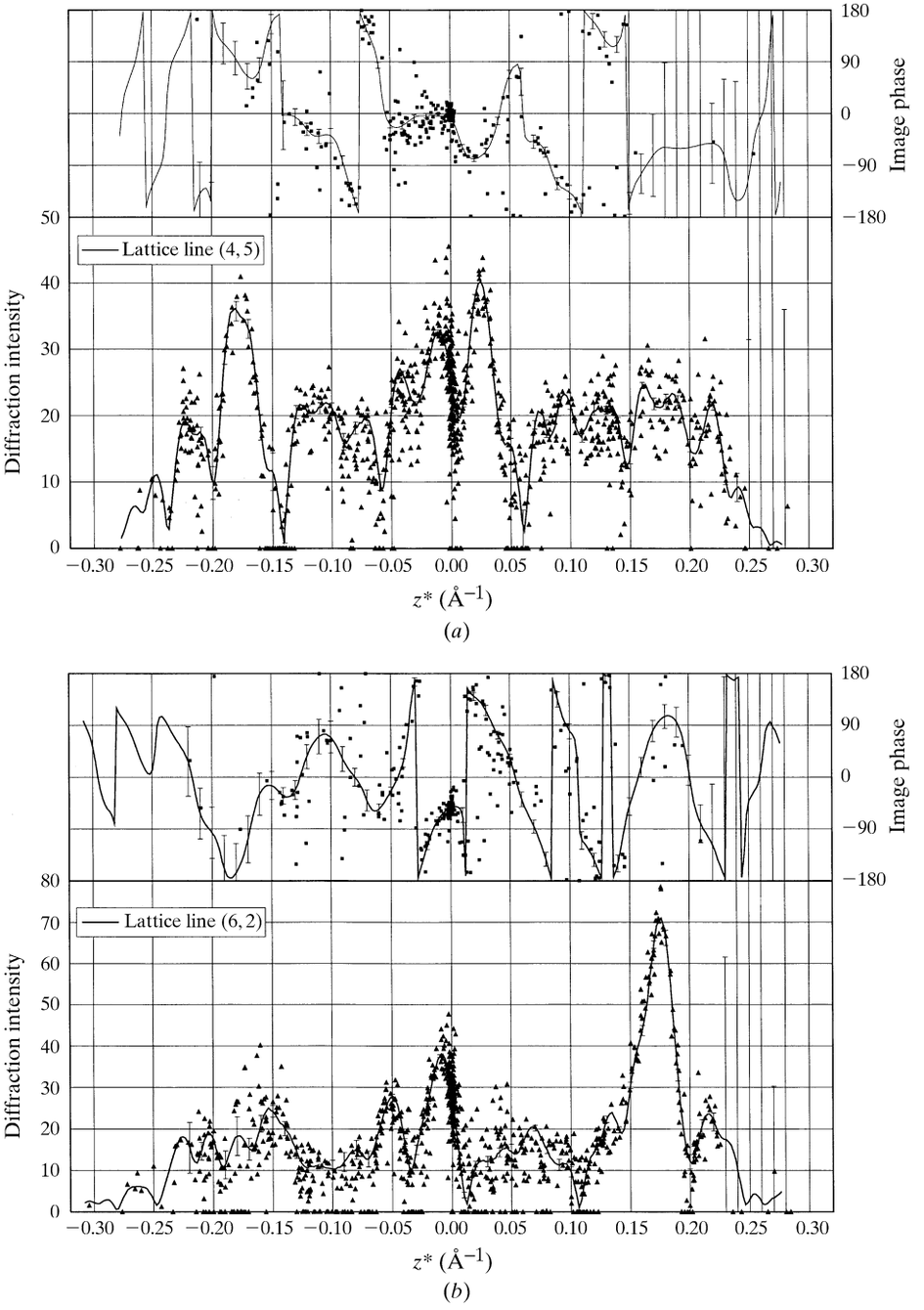

Fig. 19.2.4.2. Experimental intensities from electron diffraction patterns and phases from images of bacteriorhodopsin, recorded from tilted crystals in an electron cryomicroscope. Fitted curves for two representative lattice lines are shown: (*a*) (4, 5, z^*) and (*b*) (6, 2, z^*) (Courtesy of Drs Terushisa Hirai and Yoshinori Fujiyoshi at Kyoto University.)

references