

## 2. RECIPROCAL SPACE IN CRYSTAL-STRUCTURE DETERMINATION

$$E^2 = \sum_n (F_{HLE} - F_H)^2 / n. \quad (2.4.4.32)$$

2.4.4.7. *Suggested modifications to Blow and Crick formulation and the inclusion of phase information from other sources*

Modifications to the Blow and Crick procedure of phase evaluation have been suggested by several workers, although none represent a fundamental departure from the essential features of their formulation. In one of the modifications (Cullis *et al.*, 1961a; Ashida, 1976), all  $E_i$ 's are assumed to be the same, but the lack-of-closure error  $\xi_{Hi}$  for the  $i$ th derivative is measured as the distance from the mean of all intersections between phase circles to the point of intersection of the phase circle of that derivative with the phase circle of the native protein. Alternatively, individual values of  $E_i$  are retained, but the lack of closure is measured from the weighted mean of all intersections (Ashida, 1976). This is obviously designed to undo the effects of the unduly high weight given to  $F_N$  in the Blow and Crick formulation. In another modification (Raiz & Andreeva, 1970; Einstein, 1977), suggested for the same purpose, the  $F_N$  and  $F_{NHi}$  circles are treated as circular bands, the width of each band being related to the error in the appropriate structure factor. A comprehensive set of modifications suggested by Green (1979) treats different types of errors separately. In particular, errors arising from imperfect isomorphism are treated in a comprehensive manner.

Although the isomorphous replacement method still remains the method of choice for the *ab initio* determination of protein structures, additional items of phase information from other sources are increasingly being used to replace, supplement, or extend the information obtained through the application of the isomorphous replacement. Methods have been developed for the routine refinement of protein structures (Watenpaugh *et al.*, 1973; Huber *et al.*, 1974; Sussman *et al.*, 1977; Jack & Levitt, 1978; Isaacs & Agarwal, 1978; Hendrickson & Konnert, 1980) and they provide a rich source of phase information. However, the nature of the problem and the inherent limitations of the Fourier technique are such that the possibility of refinement yielding misleading results exists (Vijayan, 1980a,b). It is therefore sometimes desirable to combine the phases obtained during refinement with the original isomorphous replacement phases. The other sources of phase information include molecular replacement (see Chapter 2.3), direct methods (Hendrickson & Karle, 1973; Sayre, 1974; de Rango *et al.*, 1975; see also Chapter 2.2) and different types of electron-density modifications (Hoppe & Gassmann, 1968; Collins, 1975; Schevitz *et al.*, 1981; Bhat & Blow, 1982; Agard & Stroud, 1982; Cannillo *et al.*, 1983; Raghavan & Tulinsky, 1979; Wang, 1985).

The problem of combining isomorphous replacement phases with those obtained by other methods was first addressed by Rossmann & Blow (1961). The problem was subsequently examined by Hendrickson & Lattman (1970) and their method, which involves a modification of the Blow and Crick formulation, is perhaps the most widely used for combining phase information from different sources.

The Blow and Crick procedure is based on an assumed Gaussian 'lumped' error in  $F_{NHi}$  which leads to a lack of closure,  $\xi_{Hi}(\alpha)$ , in  $F_{NHi}$  defined by (2.4.4.20). Hendrickson and Lattman make an equally legitimate assumption that the lumped error, again assumed to be Gaussian, is associated with  $F_{NHi}^2$ . Then, as in (2.4.4.20), we have

$$\xi_{Hi}''(\alpha) = F_{NHi}^2 - D_{Hi}^2(\alpha), \quad (2.4.4.33)$$

where  $\xi_{Hi}''(\alpha)$  is the lack of closure associated with  $F_{NHi}^2$  for an assumed protein phase angle  $\alpha$ . Then the probability for  $\alpha$  being the

correct phase angle can be expressed as

$$P_i(\alpha) = N_i \exp[-\xi_{Hi}''(\alpha)/2E_i''^2], \quad (2.4.4.34)$$

where  $E_i''$  is the r.m.s. error in  $F_{NHi}^2$ , which can be evaluated using methods similar to those employed for evaluating  $E_i$ . Hendrickson and Lattman have shown that the exponent in the probability expression (2.4.4.34) can be readily expressed as a linear combination of five terms in the following manner.

$$-\xi_{Hi}''(\alpha)/2E_i''^2 = K_i + A_i \cos \alpha + B_i \sin \alpha + C_i \cos 2\alpha + D_i \sin 2\alpha, \quad (2.4.4.35)$$

where  $K_i, A_i, B_i, C_i$  and  $D_i$  are constants dependent on  $F_N, F_{Hi}, F_{NHi}$  and  $E_i''$ . Thus, five constants are enough to store the complete probability distribution of any reflection. Expressions for the five constants have been derived for phase information from anomalous scattering, tangent formula, partial structure and molecular replacement. The combination of the phase information from all sources can then be achieved by simply taking the total value of each constant. Thus, the total probability of the protein phase angle being  $\alpha$  is given by

$$P(\alpha) = \prod_s P_s(\alpha) = N \exp \left( \sum_s K_s + \sum_s A_s \cos \alpha + \sum_s B_s \sin \alpha + \sum_s C_s \cos 2\alpha + \sum_s D_s \sin 2\alpha \right), \quad (2.4.4.36)$$

where  $K_s, A_s$  etc. are the constants appropriate for the  $s$ th source and  $N$  is the normalization constant.

 2.4.4.8. *Fourier representation of anomalous scatterers*

It is often useful to have a Fourier representation of only the anomalous scatterers in a protein. The imaginary component of the electron-density distribution obviously provides such a representation. When the structure is known and  $F_N(+)$  and  $F_N(-)$  have been experimentally determined, Chacko & Srinivasan (1970) have shown that this representation is obtained in a Fourier synthesis with  $i[F_N(+) + F_N^*(-)]/2$  as coefficients, where  $F_N^*(-)$ , whose magnitude is  $F_N(-)$ , is the complex conjugate of  $F_N(+)$ . They also indicated a method for calculating the phase angles of  $F_N(+)$  and  $F_N^*(-)$ . It has been shown (Hendrickson & Sheriff, 1987) that the Bijvoet-difference Fourier synthesis proposed earlier by Kraut (1968) is an approximation of the true imaginary component of the electron density. The imaginary synthesis can be useful in identifying minor anomalous-scattering centres when the major centres are known and also in providing an independent check on the locations of anomalous scatterers and in distinguishing between anomalous scatterers with nearly equal atomic numbers (Sheriff & Hendrickson, 1987; Kitagawa *et al.*, 1987).

**2.4.5. Anomalous scattering of neutrons and synchrotron radiation. The multiwavelength method**

The multiwavelength anomalous-scattering method (Ramaseshan, 1982) relies on the variation of dispersion-correction terms as a function of the wavelength used. The success of the method therefore depends upon the size of the correction terms and the availability of incident beams of comparable intensities at different appropriate wavelengths. Thus, although this method was used as early as 1957 (Ramaseshan *et al.*, 1957) as an aid to structure solution employing characteristic X-rays, it is, as outlined below, ideally suited in structural work employing neutrons and synchrotron radiation. In principle,  $\gamma$ -radiation can also be used for phase

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determination (Raghavan, 1961; Moon, 1961) as the anomalous-scattering effects in  $\gamma$ -ray scattering could be very large; the wavelength is also easily tunable. However, the intensity obtainable for  $\gamma$ -rays is several orders lower than that obtainable from X-ray and neutron sources, and hence  $\gamma$ -ray anomalous scattering is of hardly any practical value in structural analysis.

### 2.4.5.1. Neutron anomalous scattering

Apart from the limitations introduced by experimental factors, such as the need for large crystals and the comparatively low flux of neutron beams, there are two fundamental reasons why neutrons are less suitable than X-rays for the *ab initio* determination of crystal structures. First, the neutron scattering lengths of different nuclei have comparable magnitudes whereas the atomic form factors for X-rays vary by two orders of magnitude. Therefore, Patterson techniques and the related heavy-atom method are much less suitable for use with neutron diffraction data than with X-ray data. Secondly, neutron scattering lengths could be positive or negative and hence, in general, the positivity criterion (Karle & Hauptman, 1950) or the squarability criterion (Sayre, 1952) does not hold good for nuclear density. Therefore, the direct methods based on these criteria are not strictly applicable to structure analysis using neutron data, although it has been demonstrated that these methods could be successfully used in favourable situations in neutron crystallography (Sikka, 1969). The anomalous-scattering method is, however, in principle more powerful in the neutron case than in the X-ray case for *ab initio* structure determination.

Thermal neutrons are scattered anomalously at appropriate wavelengths by several nuclei. In a manner analogous to (2.4.3.1), the neutron scattering length of these nuclei can be written as

$$b_0 + b' + ib'' = b + ib'' \quad (2.4.5.1)$$

The correction terms  $b'$  and  $b''$  are strongly wavelength-dependent. In favourable cases,  $b'/b_0$  and  $b''/b_0$  can be of the order of 10 whereas they are small fractions in X-ray anomalous scattering. In view of this pronounced anomalous effect in neutron scattering, Ramaseshan (1966) suggested that it could be used for structure solution. Subsequently, Singh & Ramaseshan (1968) proposed a two-wavelength method for unique structure analysis using neutron diffraction. The first part of the method is the determination of the positions of the anomalous scatterers from the estimated values of  $F_Q$ . The method employed for estimating  $F_Q$  is analogous to that using (2.4.4.9) except that data collected at two appropriate wavelengths are used instead of those from two isomorphous crystals. The second stage of the two-wavelength method involves phase evaluation. Referring to Fig. 2.4.3.2 and in a manner analogous to (2.4.3.5), we have

$$\sin \psi_1 = \frac{F_{N1}^2(+)-F_{N1}^2(-)}{4F_{N1}F_{Q1}''}, \quad (2.4.5.2)$$

where  $\psi = \alpha_N - \alpha_Q$  and subscript 1 refers to data collected at wavelength  $\lambda_1$ . Singh and Ramaseshan showed that  $\cos \psi_1$  can also be determined when data are available at wavelength  $\lambda_1$  and  $\lambda_2$ . We may define

$$F_m^2 = [F_N^2(+) + F_N^2(-)]/2 \quad (2.4.5.3)$$

and we have from (2.4.3.3), (2.4.3.4) and (2.4.5.3)

$$F_N = (F_m^2 - F_Q^2)^{1/2}. \quad (2.4.5.4)$$

Then,

$$\cos \psi_1 = \frac{F_{m1}^2 - F_{m2}^2 - [(b_1^2 + b_1'^2) - (b_2^2 + b_2'^2)]x^2}{2(b_1 - b_2)F_{N1}x} + \frac{F_{Q1}}{F_{N1}}, \quad (2.4.5.5)$$

where  $x$  is the magnitude of the temperature-corrected geometrical part of  $\mathbf{F}_Q$ .  $\psi_1$  and hence  $\alpha_{N1}$  can be calculated using (2.4.5.2) and (2.4.5.5).  $\alpha_{N2}$  can also be obtained in a similar manner.

During the decade that followed Ramaseshan's suggestion, neutron anomalous scattering was used to solve half a dozen crystal structures, employing the multiple-wavelength methods as well as the methods developed for structure determination using X-ray anomalous scattering (Koetzle & Hamilton, 1975; Sikka & Rajagopal, 1975; Flook *et al.*, 1977). It has also been demonstrated that measurable Bijvoet differences could be obtained, in favourable situations, in neutron diffraction patterns from protein crystals (Schoenborn, 1975). However, despite the early promise held by neutron anomalous scattering, the method has not been as successful as might have been hoped. In addition to the need for large crystals, the main problem with using this method appears to be the time and expense involved in data collection (Koetzle & Hamilton, 1975).

### 2.4.5.2. Anomalous scattering of synchrotron radiation

The most significant development in recent years in relation to anomalous scattering of X-rays has been the advent of synchrotron radiation (Helliwell, 1984). The advantage of using synchrotron radiation for making anomalous-scattering measurements essentially arises out of the tunability of the wavelength. Unlike the characteristic radiation from conventional X-ray sources, synchrotron radiation has a smooth spectrum and the wavelength to be used can be finely selected. Accurate measurements have shown that values in the neighbourhood of 30 electrons could be obtained in favourable cases for  $f'$  and  $f''$  (Templeton, Templeton, Phillips & Hodgson, 1980; Templeton, Templeton & Phizackerley, 1980; Templeton *et al.*, 1982). Schemes for the optimization of the wavelengths to be used have also been suggested (Narayan & Ramaseshan, 1981). Interestingly, the anomalous differences obtainable using synchrotron radiation are comparable in magnitude to the isomorphous differences normally encountered in protein crystallography. Thus, the use of anomalous scattering at several wavelengths would obviously eliminate the need for employing many heavy-atom derivatives. The application of anomalous scattering of synchrotron radiation for macromolecular structure analysis began to yield encouraging results in the 1980s (Helliwell, 1985). Intensity measurements from macromolecular X-ray diffraction patterns using synchrotron radiation at first relied primarily upon oscillation photography (Arndt & Wonacott, 1977). This method is not particularly suitable for accurately evaluating anomalous differences. Much higher levels of accuracy began to be achieved with the use of position-sensitive detectors (Arndt, 1986). Anomalous scattering, in combination with such detectors, has developed into a major tool in macromolecular crystallography (see IT F, 2001).

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