ATOMIC COORDINATES FOR THE CHLOROPHYLL CORE OF A BACTERIOCHLOROPHYLL a-PROTEIN FROM GREEN PHOTOSYNTHETIC BACTERIA

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Summary: Preliminary atomic coordinates are presented for the seven bacterio-chlorophylls constituting the core of one subunit of the trimeric water soluble bacteriochlorophyll a-protein from the green photosynthetic bacterium Prosthecochloris aestuarii, strain 2K, formerly identified as Chlorobium limicola, strain 2K. The coordinates were derived from a 2.8 Å resolution electron density map based on four isomorphous heavy-atom derivatives, and adjusted to have stereochemically acceptable bond lengths and angles.

The three-dimensional structure of a bacteriochlorophyll a-containing protein from a green photosynthetic bacterium has been determined by X-ray crystallography (1). [The bacterium, previously designated <u>Chlorobium limicola</u>, strain 2K, has now been identified as <u>Prosthecochloris aestuarii</u> (Ref. 2 and personal communication from J. M. Olson and N. Pfennig).] The chlorophyll-protein, which mediates in the transfer of excitation energy from the bulk antenna pigment chlorobium chlorophyll to the photochemical reaction centers (3), consists of three identical subunits, each consisting of a core of seven bacteriochlorophylls enclosed within an envelope of protein (Fig. 1).

Recently the quality of the electron density map used for the initial structure determination has been improved by the inclusion of a fourth isomorphous heavy-atom derivative, permitting the structure to be defined with greater certainty (4). In the absence of the amino acid sequence, it is not possible at this time to present coordinates for the whole molecule. However, the electron density map does show the general arrangement of the chlorophyll core quite clearly, and permits us to present preliminary coordinates for this part of the molecule.

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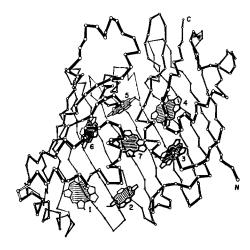


Figure 1. Schematic diagram showing one subunit of the bacteriochlorophyll-protein. For clarity, the magnesium atoms, chlorophyll ring substituents and phytyl chains, except for the first bond, have been omitted. The direction of view is from the three-fold axis, which is horizontal, towards the exterior of the molecule.

The coordinates were obtained by building a skeletal model of the core in a Richards optical comparator (5,6). Because the resolution of the electron density map (2.8 Å) does not permit visualization of individual atoms, the geometry of the model was based, as far as possible, on that of ethyl chlorophyllide \underline{a} (7). The rigid conjugated portion of each porphyrin ring was first aligned to coincide with the electron density map, and then rotations were made about the various single bonds in order to place the ring substituents and the phytyl chains. Buckling was allowed in Ring II which is saturated in bacteriochlorophyll \underline{a} (Fig. 2) but not in ethyl chlorophyllide \underline{a} . Markers were then placed in the electron density map to agree, as well as possible, with both the model and the electron density.

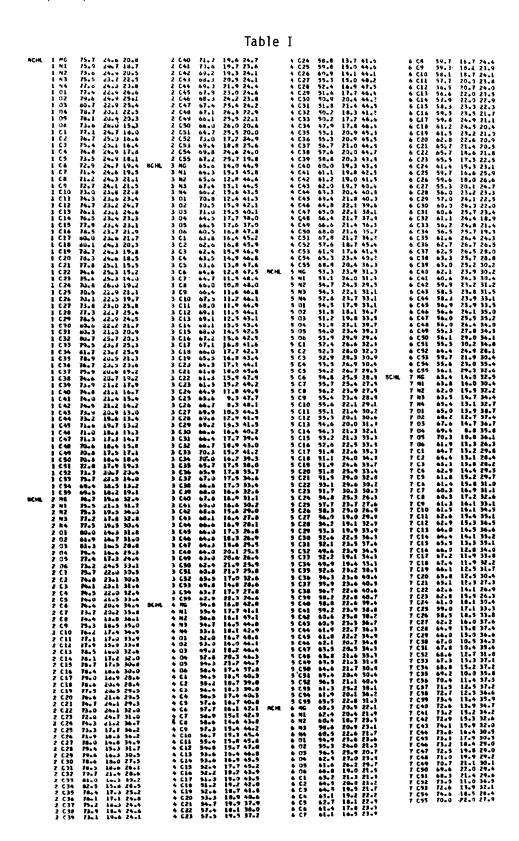
The "raw" coordinates, so obtained, were then checked and idealized by first rotating and translating that part of ethyl chlorophyllide \underline{a} common to bacteriochlorophyll \underline{a} so as to minimize the rms deviation between the corresponding atoms, i.e., C1-C6, C9-C22, C27-C30, C32, C33, N1-N4, and O1. (Rms deviations ranged from 0.14 $\overset{\circ}{A}$ to 0.17 $\overset{\circ}{A}$ for the seven chlorophylls.)

Figure 2. The structure of bacteriochlorophyll \underline{a} showing the atom numbering used in Table I.

The coordinates of all the remaining atoms were then adjusted by a least squares procedure which enforces bond length and angle constraints, and at the same time requires the idealized model to fit as closely as desired to the raw coordinates (8,9). In this application the bond length and angle constraints were weighted ten times as heavily as adherence to the raw coordinates, except for the conjugated portion of the chlorin ring where weights of a thousand were used to force the atoms to coincide with the rotated ethyl chlorophyllide coordinates described above. The "standard" dimensions of the substituent bond lengths and angles were taken from the Handbook of Chemistry and Physics (10). Each magnesium atom was located equidistant from its four nitrogen ligands, and displaced 0.4 Å from the ring plane toward the apparent fifth ligand.

The idealized coordinates for the seven bacteriochlorophylls are given in Table I, where the numbering scheme, shown in Figure 2, is based on that used for ethyl chlorophyllide \underline{a} (7). The coordinates are in Angstroms along the orthogonal crystallographic axes \underline{a}^* , \underline{b} , and \underline{c} .

Crystals of the chlorophyll protein have space group ${\rm P6}_3$ with cell



dimensions $\underline{a} = \underline{b} = 112.4 \text{ Å}$, $\underline{c} = 98.4 \text{ Å}$. The transformation giving the fractional crystallographic coordinates (x,y,z) in terms of the orthogonal coordinates (X,Y,Z) is as follows:

x = 0.01027 X

v = 0.00890 Y + 0.00514 X

z = 0.01016 Z

The three-fold axis relating the subunits of the bacteriochlorophyll-protein molecule is parallel to the Z axis and passes through the point X = 64.89 Å, Y = 0 Å (i.e., x = 2/3, y = 1/3). Rotations of the coordinates in Table I by 120° and 240° about this axis will generate the coordinates of the 21 bacteriochlorophyll molecules contained within a complete trimer.

We estimate that within the conjugated portions of each bacteriochloro-phyll molecule the average error in the coordinates quoted in Table I is about $0.3\ \text{Å}$, and unlikely to exceed $0.5\ \text{Å}$. For the ring substituents, including the phytyl chains, the errors could be twice as large, and the detailed conformations of some of these groups are uncertain.

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