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Crystal structure of the cyclomaltohexaose (α-cyclodextrin) complex with isosorbide dinitrate. Guest-modulated channel-type structure

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Abstract

The crystal structure of the 2:1 complex of cyclomaltohexaose (α-cyclodextrin, α-CD) with isosorbide dinitrate was determined by single-crystal X-ray analysis. In the crystal with the space group *C*2, two cyclomaltohexaose molecules form a head-to-head dimer with the secondary hydroxy-group sides facing each other. The dimer unit is stacked along the crystallographic *c*-axis to form a channel-type structure. The isosorbide dinitrate molecule is encapsulated in the cylindrical cavity of the cyclomaltohexaose dimer. The dimeric structure exhibits pseudo twofold symmetry, and the guest molecule is disordered on the local symmetry axis. The isosorbide moiety is located at the center of the dimer cavity, and the nitrate groups penetrate into the cyclomaltohexaose rings. The guest molecule modulates the dimer structure to attain the most stable accommodation into the cavity. The cyclomaltohexaose molecules are laterally shifted away from each other to create the cavity fitted to the shape of the guest molecule. As the result, the intermolecular hydrogen bonds between secondary hydroxy-groups are not fully formed, but the dimeric structure is stabilized by the interaction with the guest molecule. © 2002 Elsevier Science Ltd. All rights reserved.

Keywords: Cyclomaltohexaose; α-Cyclodextrin; Isosorbide dinitrate; Inclusion complex; Crystal structure; Channel-type packing

1. Introduction

Crystals of cyclomaltose complexes have been largely categorized into three types, cage-type, channel-type, and layer-type.[1] In the cage-type structure, cyclomaltose molecules are arranged in a herringbone fashion, and both ends of the cyclomaltose cavity are blocked by adjacent molecules. The guest molecule is limited in its size to be enclosed within the isolated cavity. The channel-type structure is formed by the linear stack of cyclomaltose rings. The column-like structure can include molecules that are longer than the depth of the cyclomaltose cavity and penetrating two or more cyclomaltose rings. Cyclomaltose molecules in the layer-type structure are arranged to form a molecular layer. The end of the cavity of cyclomaltose molecules is open to the intermolecular space of the adjacent layer, which accommodates molecules or groups not included in the host cavity.

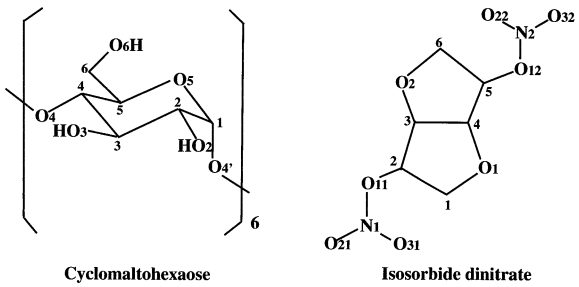

Fig. 1. Atomic numbering of cyclomaltohexaose and isosorbide dinitrate.

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Table 1
Crystallographic data and refinement statistics

Chemical formula	$2(C_{36}H_{60}O_{30})\cdot C_6H_8N_2O_8\cdot 9\ H_2O$
Formula weight	2344.0
Space group	$C2$
Lattice parameters	
a (Å)	13.774(1)
b (Å)	24.139(1)
c (Å)	31.255(3)
β (°)	91.67(1)
V (Å^3)	10389(1)
D_{calcd} (g cm^{-3})	1.499
μ (cm^{-1})	0.237
Minimum and maximum indices	H: 0, 17; K: 0, 30; L: −39, 39
Crystal size (mm)	$0.2\times0.2\times0.6$
Temperature (K)	173
Measured data	11695
Unique data	10882
Parameters	1596
Restraints	323
R (all data)	0.063
wR_2	0.198
Goodness-of-fit	1.316
Mean and maximum shift/esd	0.008, 0.155
Maximum and minimum electron density (e Å^{-3})	0.71, −0.62

Some variation has been observed in each packing mode. The channel-type packing is further classified into two types, the head-to-head and the head-to-tail. In the head-to-tail channel-type structure, cyclomaltose rings are linearly stacked to form a column-like structure,[2] while in the head-to-head channel-type structure the repetition unit is a head-to-head dimer.[3] The cage-type packing structure has been observed in the two types of crystals with the space group $P2_1$[4] and $P2_12_12_1$.[5] In the crystallization process, one of these packing structures is selected so that the guest molecule can be most stably accommodated. However, we still have no general knowledge about how the packing structure is regulated by the guest molecule.

In this paper, we present the crystal structure of the 2:1 complex of cyclomaltohexaose (α-cyclodextrin, α-CD) with isosorbide dinitrate, and discuss the modulation of the host packing structure for the accommodation of the guest molecule. The structure of this complex is expected to provide information about the role of the guest molecule in both the dimer formation of cyclomaltohexaose and in the crystal packing. Isosorbide dinitrate is an organic nitrate vasodilator that has been used as a model drug.[6,7]

2. Results and discussion

The atomic numbering of cyclomaltohexaose and isosorbide dinitrate is shown in Fig. 1. Crystallographic data and the result of the structure refinement are summarized in Table 1. The asymmetric unit contains two cyclomaltohexaose molecules, one isosorbide dinitrate molecule, and nine water molecules distributed over ten sites. The X-ray data were collected at 293 and 173 K. The electron density of the disordered guest molecule was so diffused at 293 K that the guest molecule could not be modeled. The twofold disorder was resolved on the electron density map at 173 K and the structure was successfully refined.

Structure of cyclomaltohexaose.—As shown in Fig. 2, two cyclomaltohexaose molecules form the head-to-head dimer with the secondary hydroxy-group sides facing each other. The two molecules are related with a

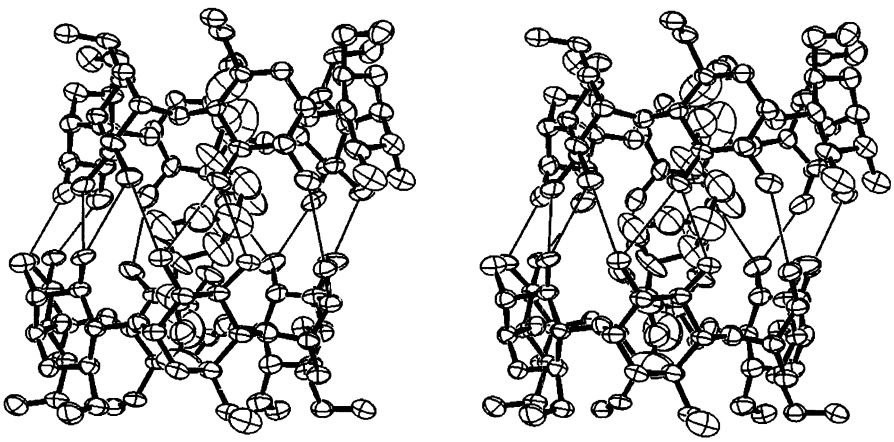

Fig. 2. Stereoview of the structure of the cyclomaltohexaose complex with isosorbide dinitrate. Thermal ellipsoids are drawn with 30% probability.[11] The isosorbide dinitrate molecule is twofold disordered, and only one structure (A) is drawn because of the clarity.

Table 2
Parameters describing the macrocyclic conformation

	O-4(n)–O-4($n+1$) distance		O-2(n)–O-3($n+1$) distance			
	Molecule 1	Molecule 2	Molecule 1	Molecule 2		
G-1–G-2	4.28(1)	4.28(1)	2.82(1)	2.82(1)		
G-2–G-3	4.33(1)	4.19(1)	3.54(1)	2.92(1)		
G-3–G-4	4.18(1)	4.34(1)	3.06(1)	2.86(1)		
G-4–G-5	4.36(1)	4.16(1)	2.82(1)	2.82(1)		
G-5–G-6	4.16(1)	4.31(1)	2.79(1)	3.19(1)		
G-6–G-1	4.25(1)	4.23(1)	3.00(1)	2.77(1)		
Average	4.26(7)	4.25(6)	3.01(26)	2.90(14)		
	O-4 angle [a]		Tilt-angle [b]		O-4–center distance	
	Molecule 1	Molecule 2	Molecule 1	Molecule 2	Molecule 1	Molecule 2
G-1	117.8(3)	119.1(3)	13.0	9.0	4.18	4.21
G-2	119.5(3)	119.3(3)	13.7	12.2	4.17	4.24
G-3	117.5(3)	120.1(3)	21.3	6.3	4.41	4.32
G-4	118.8(3)	117.9(3)	8.1	12.6	4.29	4.17
G-5	118.7(3)	119.1(3)	9.2	10.7	4.18	4.28
G-6	119.9(3)	118.3(3)	9.0	14.9	4.33	4.27
Average	118.7(8)	119.0(7)	12.4(4.5)	11.0(2.8)	4.26(9)	4.25(5)

[a] The angle defined as C-4(n)–O-4(n)–C-1(n-1).
[b] The angle defined made by the plane through six O-4 atoms and the plane C-(n), C-4(n), O-4(n), and O-4($n+1$).

pseudo twofold axis that is nearly parallel to the crystallographic a-axis. Some parameters describing the macrocyclic structure of cyclomaltohexaose are listed in Table 2. These parameter values indicate that the structure of cyclomaltohexaose molecules has no distinct difference from those of previously reported cyclomaltohexaose crystals with the channel-type structure.[2,3,8] The six glycosidic O-4 atoms that are planar within the deviation of 0.078 Å (molecule 1) and 0.068 Å (molecule 2) form the hexagon with the radius and side length of 4.26(9) Å (molecule 1) and 4.25(5) Å (molecule 2). The two cyclomaltohexaose molecules are superimposable with an rms deviation of 0.37 Å for all atoms. A relatively large deviation is observed in the primary hydroxy groups that are in the (−)-gauche conformation. The two cyclomaltohexaose molecules are not identical in their structure, but molecule 1 is less symmetrical than molecule 2. The average tilt angle of the molecule 1 (12.4°(5)) is larger than that of the molecule 2 (11.0°(3)). In molecule 2, intramolecular hydrogen bonds are fully formed between HO-2 and HO-3 of the adjacent glucose unit. Distances between O-2 and O-3 of the adjacent glucose unit are in the range 2.77(1)–3.18(1) Å. In contrast, the HO-2 hydroxyl group of the G2 unit in molecule 1 forms no hydrogen bond with the HO-3 hydroxyl group of the G3 unit (the O-2(2)–O-3(3) distance of 3.54(1) Å) because of the large inclination of the G3 unit (the tilt angle of 21.3°) with its primary hydroxy-group side toward the inside of the macrocycle.

Host–guest interaction.—The isosorbide dinitrate molecule is encapsulated in the cavity of the cyclomaltohexaose dimer. The two cyclomaltohexaose molecules are so arranged as to fully include the bulky guest molecule. The dimeric structure is not an ideal cylindrical shape, but the cyclomaltohexaose molecules are laterally shifted away from each other. These two cyclomaltohexaose molecules are connected by hydrogen bonds between the secondary hydroxyl groups, but the secondary hydroxy groups are not fully hydrogen bonded. The G4 unit of the molecule 2 forms no hydrogen bonds with molecule 1 (Fig. 3). It is clear from the structure of the complex that the lateral shift is caused to create the dimer cavity that is fitted to the shape of the guest molecule.

The isosorbide moiety is located at the center of the dimer cavity while the nitrate groups penetrate the cyclomaltohexaose cavity from the secondary hydroxy-group side. The guest molecule is disordered as designated A and B with the equal occupancy, and the two dispositions are related with the pseudo twofold symmetry of the host dimer. The guest molecule is in van der Waals contact with the inside wall of the cyclomaltohexaose cavity. Short contacts between host and guest molecules are shown in Fig. 4. Most of the contacts less than 3.5 Å are involved with the nitrate

groups, which are located at the center of the cyclomaltohexaose ring. The closest contact (3.23(2) Å) is observed between O-4(6) of molecule 2 and a nitrate oxygen atom of the guest molecule A. The nitrate group of molecule A included in the cyclomaltohexaose molecule 1 closely contacts with O-4(4), C-5(3), and O-4(4), while that included in the cyclomaltohexaose molecule 2 has close contacts with C-5(3) and O-4(6). Similar intermolecular short contacts are observed for molecule B. The nitrate group of the molecule B has close contact with C-5(2), C-5(5), and O-4(6) of molecule 1. The C-5 and O-4 atoms of both G2 and G5 units of molecule 2 are in close contact with the other nitrate group. Since the C-5H bonds point to the center of the cyclomaltohexaose ring, the planar nitrate group is included with such orientation as not to have unfavorably short contacts with hydrogen atoms bonded to C-5 as well as O-4 atoms. A similar mode of host–guest contact has been observed in the cyclomaltohexaose complex with *m*-nitroaniline[8] where the nitro group has close contacts with O-4 atoms and C-5H groups. Such short contact of C-5H groups with the nitrate oxygen atoms suggests the contribution of the C–H–O hydrogen bonds to stabilize the accommodation of the guest molecule.

Crystal structure and packing.—The crystal structure of the complex is shown in Fig. 5. Intermolecular hydrogen bonds are listed in Table 3. The dimer units

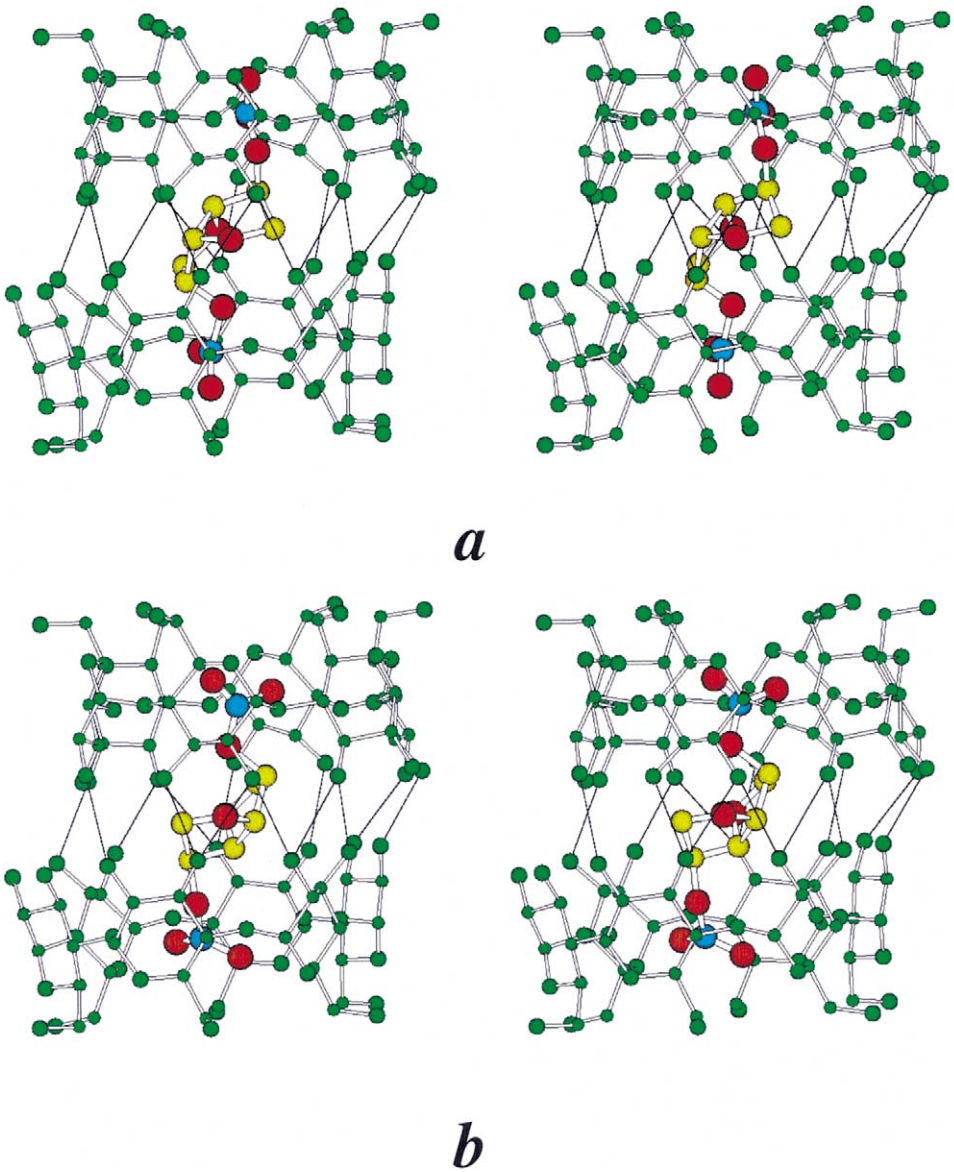

Fig. 3. Stereoview of the structure of the cyclomaltohexaose complex with isosorbide dinitrate showing the disorder of the guest molecule: (a) guest molecule A; (b) guest molecule B. Carbon, oxygen, and nitrogen atoms in the guest molecule are rendered by yellow, red, and blue, respectively. Intermolecular hydrogen bonds between cyclomaltohexaose molecules (green) are shown by thin lines.

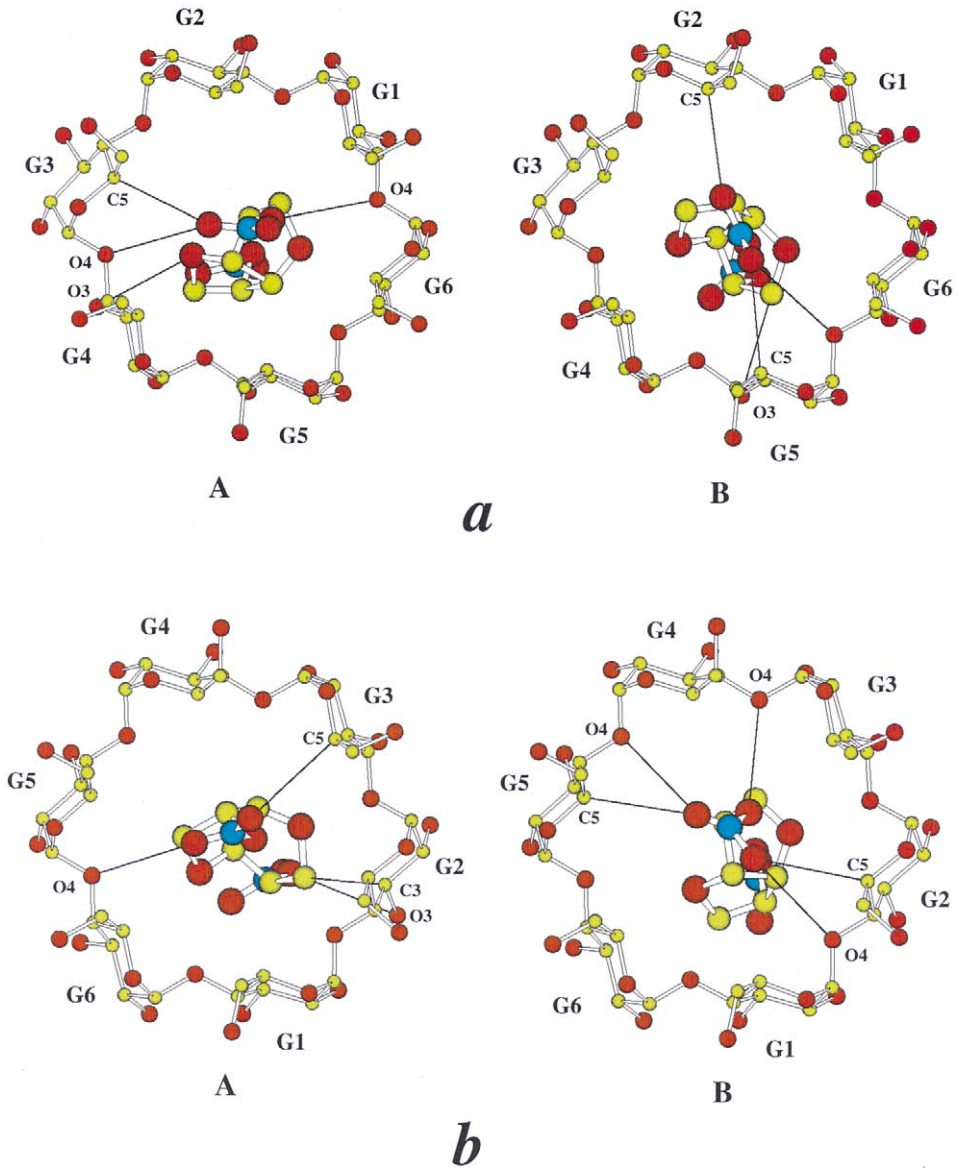

Fig. 4. Intermolecular contacts less than 3.5 Å between host and guest molecules shown by thin lines: (a) cyclomaltohexaose molecule 1 with the guest molecule A (A) and the guest molecule B (B); (b) cyclomaltohexaose molecule 2 with the guest molecule A (A) and the guest molecule B (B).

are aligned parallel to the crystallographic *c*-axis to form the head-to-head channel type structure. Because the dimeric structure is distorted from the ideal cylindrical shape, the column structure formed of such a dimer unit is rather in the zigzag mode. No direct hydrogen bonds are formed between dimer units along the column, but the primary hydroxy-group side is linked by water-mediated hydrogen bonds with the adjacent dimer unit. Therefore, the crystal packing is stabilized by the hydrogen-bond network including water molecules that are distributed in intermolecular space between cyclomaltohexaose columns.

A variety of channel-type packing structures have been reported as shown in Fig. 6. The channel-type structure is classified into the head-to-head type and the head-to-tail type. The head-to-tail structure is formed by the one-dimensional stack of cyclomaltohexaose rings. In the orthorhombic crystal (**5** in Fig. 6),[2] the cyclomaltohexaose ring is perpendicular to the column axis, while its molecular axis inclines against the column axis in the monoclinic crystal (**4**).[8] In the head-to-head channel-type structure, the repetition unit is a dimer structure with the secondary hydroxyl sides facing. In the tetragonal crystal, the two cyclomaltohexaose molecules in the dimer unit are related by the crystallographic twofold axis.[3] The dimer unit is stacked along the fourfold axis; therefore, the next dimer unit is 90° rotated around the column axis. The dimer unit in the triclinic crystal has the pseudo twofold symmetry axis perpendicular to the column axis.[3] Each

cyclomaltohexaose molecule is tilted against the column axis, and as a result, the two molecules are laterally shifted to attain a linear stack.

The present crystal with the space group $C2$ adds another type of the head-to-head channel type structure. The structural variety of the channel-type packing should be caused by the interaction of cyclomaltohexaose with the included guest molecule. However, in spite of a number of channel type structures solved by X-ray analysis, there is still no rational explanation for how the guest molecule selects one of these channel-type structures. The present crystal structure demonstrates that the structure of the dimer unit is formed to accommodate the guest molecule in the most stable fashion. Therefore, the induced-fit mechanism may regulate the formation of the dimeric structure, and as a result, it modulates the crystal packing.

3. Experimental

Crystals of the cyclomaltohexaose complex with isosorbide dinitrate were obtained from an aqueous solution containing the host and guest in 2:1 molar ratio. X-ray diffraction data were measured at 293 and 173 K using the graphite-monochromated Cu K_α radiation on a Nonius CAD4 diffractometer equipped with a FR590 generator. Intensity data were collected up to 157° in 2θ by using a $\theta - 2\theta$ scan mode. The crystal belonged to the monoclinic space group $C2$ and the asymmetric unit contained one dimer unit. Lattice parameters were $a = 13.840(1)$, $b = 24.153(1)$, $c = 31.349(3)$ Å, and $\beta = 91.66(1)°$ at 293 K and $a = 13.774(1)$, $b = 24.139(1)$, $c = 31.255(2)$ Å, and $\beta = 91.67(1)°$ at 173 K. The structure was solved by the direct method using the program SNB[9] and refined by the full-matrix least-squares

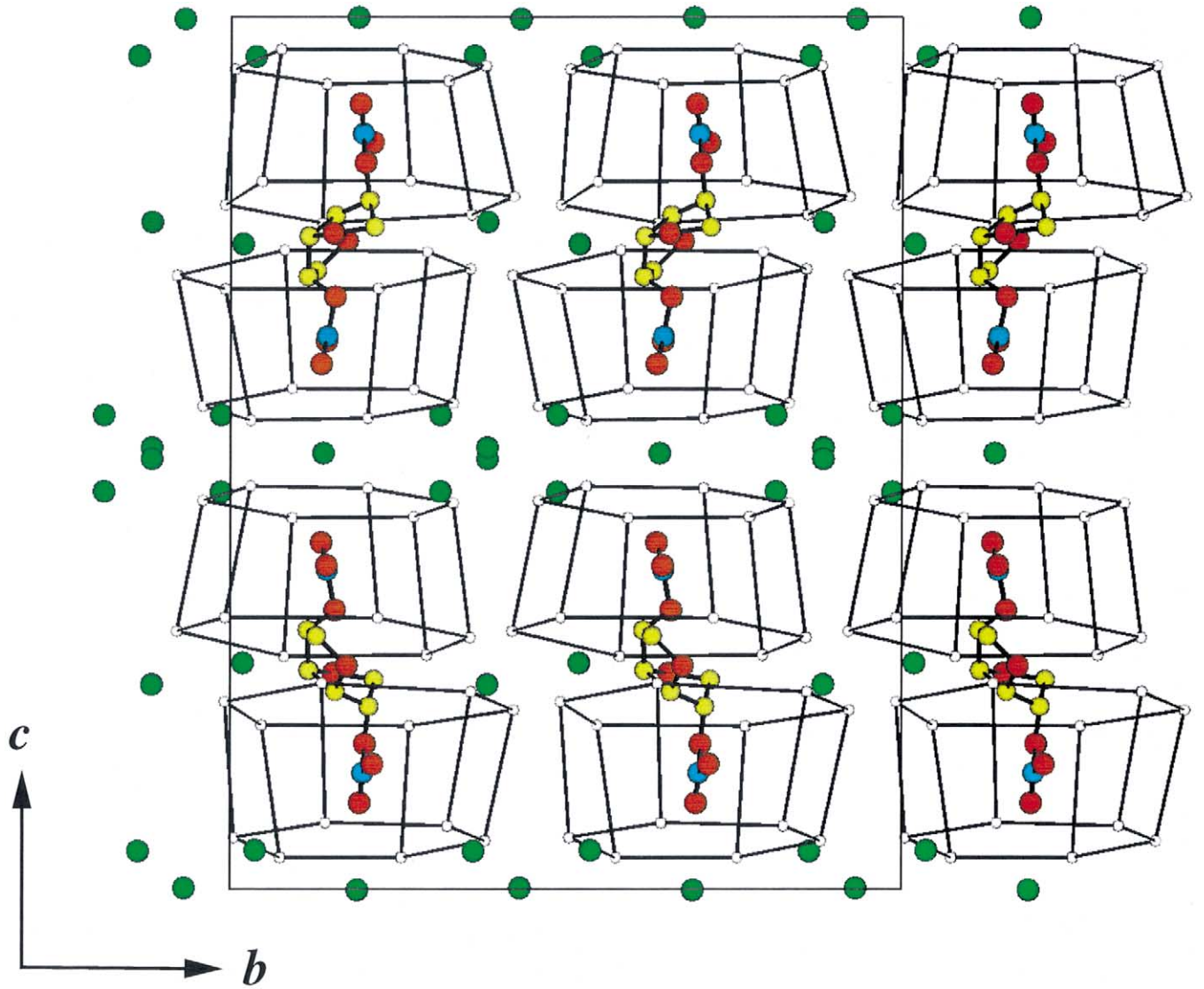

Fig. 5. Crystal structure viewed along the a-axis. The cyclomaltohexaose molecules are represented by truncated hexagonal cone. Water molecules are shown by green colored circles.

Table 3
Intermolecular contacts

	Distance	Symmetry operator		Distance	Symmetry operator
O-3(1)1–O-3(2)2	2.78		O-3(2)1–O-10(W)	3.04	$(x-1/2,\ y+1/2,\ z)$
O-3(1)1–O-2(2)2	3.09		O-6(2)1–O-8(W)	2.79	$(x-1/2,\ y+1/2,\ z)$
O-2(2)1–O-3(1)2	2.74		O-6(2)1–O-3(W)	2.78	$(-x+1/2,\ y+1/2,\ -z)$
O-2(3)1–O-3(6)2	2.81		O-2(3)1–O-2(2)2	2.83	$(x+1,\ y,\ z)$
O-3(3)1–O-2(6)2	2.84		O-3(3)1–O-2(5)1	2.79	$(x+1/2,\ y+1/2,\ z)$
O-2(4)1–O-3(5)2	2.77		O-3(3)1–O-3(4)2	2.94	$(x+1/2,\ y+1/2,\ z)$
O-3(4)1–O-2(5)2	2.82		O-3(3)1–O-9(W)	3.20	$(x+1/2,\ y+1/2,\ z)$
O-3(4)1–O-3(6)2	3.13		O-6(3)1–O-3(W)	2.78	$(x+1/2,\ y+1/2,\ z)$
O-2(5)1–O-2(3)2	3.04		O-6(3)1–O-4(W)	2.82	$(x+1/2,\ y+1/2,\ z)$
O-2(6)1–O-2(2)2	2.88		O-6(4)1–O-1(W)	2.84	$(x+1,\ y,\ z)$
O-2(6)1–O-3(3)2	3.14		O-6(5)1–O-3(W)	2.74	$(-x+1,\ y,\ -z)$
O-3(6)1–O-3(3)2	2.78		O-6(6)1-O-8(W)	2.76	$(x-1,\ y,\ z)$
O-6(1)1–O-1(W)	2.75		O-6(1)2–O-6(W)	2.79	$(x+1/2,\ y+1/2,\ z)$
O-6(4)1–O-8(W)	2.76		O-6(1)2–O-7(W)	2.78	$(x+1/2,\ y+1/2,\ z)$
O-3(5)1–O-9(W)	2.72		O-3(2)2–O-9(W)	3.17	$(-x-1,\ y,\ -z)$
O-6(5)1–O-4(W)	2.76		O-6(2)2–O-5(W)	2.78	$(x-1/2,\ y+1/2,\ z)$
O-6(6)1–O-3(W)	2.68		O-6(2)2–O-6(W)	2.79	$(-x+1/2,\ y+1/2,\ -z+1)$
O-6(3)2–O-7(W)	2.72		O-3(3)2–O-10(W)	2.74	$(x-1,\ y,\ z)$
O-3(4)2–O-9(W)	2.85		O-6(3)2–O-5(5)2	3.20	$(x-1,\ y,\ z)$
O-2(4)2–O-9(W)	2.73		O-6(3)2–O-2(W)	2.77	$(x-1,\ y,\ z)$
O-6(4)2–O-5(W)	2.78		O-3(4)2–O-2(6)2	3.15	$(x-1/2,\ y-1/2,\ z)$
O-6(4)2–O-6(W)	2.73		O-6(5)2–O-7(W)	2.79	$(x+1,\ y,\ z)$
O-2(5)2–O-10(W)	2.63		O-6(5)2–O-6(W)	2.67	$(-x+1,\ y,\ -z+1)$
O-6(6)2–O-2(W)	2.72		O-6(6)2–O-5(W)	2.81	$(x+1/2,\ y+1/2,\ z)$
O-2(1)1–O-9(W)	2.71	$(x-1/2,\ y+1/2,\ z)$	O-4(W)–O-4(W)	2.79	$(-x+1,\ y,\ -z)$
O-6(1)1–O-1(W)	2.76	$(-x,\ y,\ -z)$	O-5(W)–O-5(W)	2.79	$(-x+1,\ y,\ -z+1)$
O-2(2)1–O-2(3)2	2.73	$(x+1/2,\ y+1/2,\ z)$	O-7(W)–O-7(W)	2.80	$(-x,\ y,\ -z+1)$
O-2(2)1–O-10(W)	3.03	$(x-1/2,\ y+1/2,\ z)$	O-8(W)–O-8(W)	2.81	$(-x+2,\ y,\ -z)$

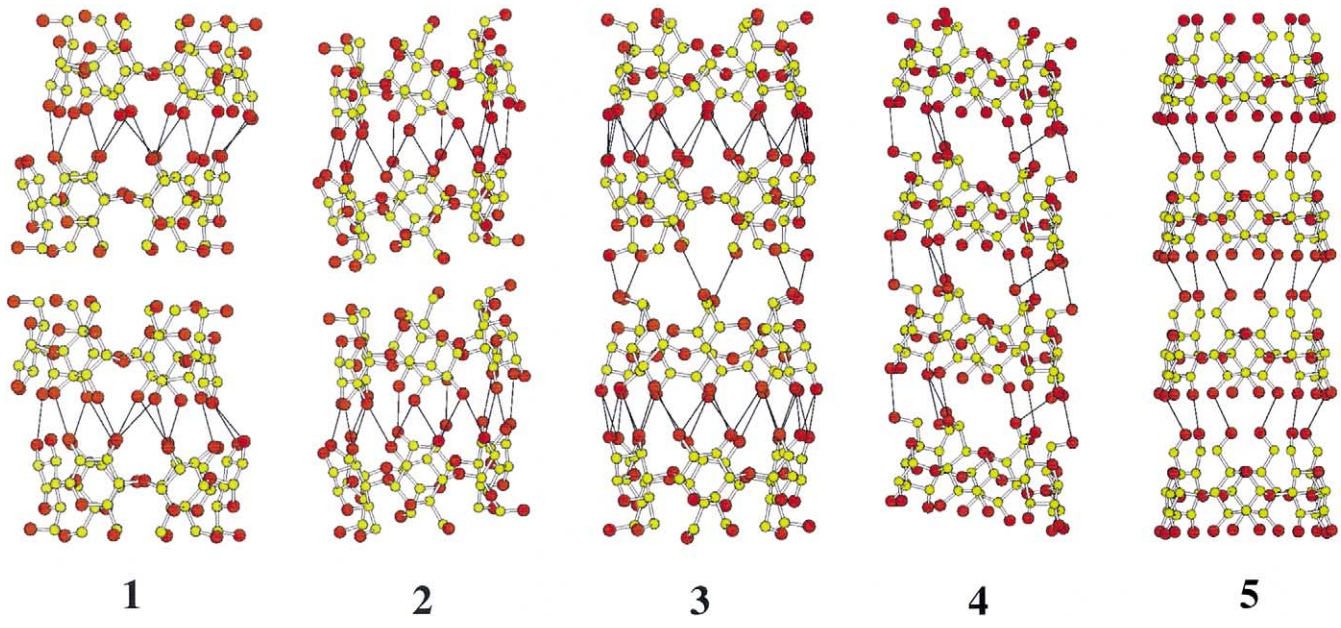

Fig. 6. Comparison of the packing mode in the channel-type structure: the present *C*2 crystal (1), triclinic crystal of the head-to-head type (2), tetragonal crystal of the head-to-head type (3), monoclinic crystal of the head-to-tail type (4), orthorhombic crystal of the head-to-tail type (5).

Table 4
Atomic parameters

Atom	x	y	z	Occupancy	U_{eq} (Å^2)
C-1(1)1	0.2724(3)	0.3647(1)	0.1158(1)	1.000	0.027(1)
C-2(1)1	0.2002(3)	0.3481(1)	0.1494(1)	1.000	0.027(1)
C-3(1)1	0.2072(3)	0.2862(1)	0.1577(1)	1.000	0.027(1)
C-4(1)1	0.1895(2)	0.2557(1)	0.1157(1)	1.000	0.025(1)
C-5(1)1	0.2566(3)	0.2772(1)	0.0806(1)	1.000	0.028(1)
C-6(1)1	0.2282(3)	0.2555(2)	0.0366(1)	1.000	0.033(1)
O-2(1)1	0.2227(2)	0.3795(1)	0.1871(1)	1.000	0.034(1)
O-3(1)1	0.1383(2)	0.2669(1)	0.1869(1)	1.000	0.030(1)
O-4(1)1	0.2105(2)	0.1983(1)	0.1233(1)	1.000	0.027(1)
O-5(1)1	0.2514(2)	0.3366(1)	0.0772(1)	1.000	0.029(1)
O-6(1)1	0.1318(2)	0.2704(1)	0.0243(1)	1.000	0.038(1)
C-1(2)1	0.6462(3)	0.4088(1)	0.1491(1)	1.000	0.026(1)
C-2(2)1	0.5728(3)	0.4296(2)	0.1815(1)	1.000	0.028(1)
C-3(2)1	0.4786(3)	0.3964(1)	0.1785(1)	1.000	0.027(1)
C-4(2)1	0.4400(2)	0.3923(1)	0.1327(1)	1.000	0.023(1)
C-5(2)1	0.5194(2)	0.3758(1)	0.1021(1)	1.000	0.025(1)
C-6(2)1	0.4838(3)	0.3795(2)	0.0557(1)	1.000	0.032(1)
O-2(2)1	0.6125(2)	0.4313(1)	0.2235(1)	1.000	0.037(1)
O-3(2)1	0.4089(2)	0.4219(1)	0.2053(1)	1.000	0.034(1)
O-4(2)1	0.3666(2)	0.3513(1)	0.1321(1)	1.000	0.028(1)
O-5(2)1	0.6019(2)	0.4116(1)	0.1077(1)	1.000	0.027(1)
O-6(2)1	0.4386(2)	0.4305(1)	0.0470(1)	1.000	0.038(1)
C-1(3)1	0.8914(2)	0.2405(2)	0.1534(1)	1.000	0.028(1)
C-2(3)1	0.9051(3)	0.2813(2)	0.1901(1)	1.000	0.031(1)
C-3(3)1	0.8130(3)	0.3158(2)	0.1958(1)	1.000	0.030(1)
C-4(3)1	0.7732(3)	0.3395(1)	0.1536(1)	1.000	0.026(1)
C-5(3)1	0.7767(3)	0.2978(2)	0.1167(1)	1.000	0.027(1)
C-6(3)1	0.7631(3)	0.3241(2)	0.0729(1)	1.000	0.031(1)
O-2(3)1	0.9283(3)	0.2525(2)	0.2286(1)	1.000	0.049(1)
O-3(3)1	0.8343(4)	0.3588(1)	0.2258(1)	1.000	0.053(1)
O-4(3)1	0.6743(2)	0.3552(1)	0.1606(1)	1.000	0.027(1)
O-5(3)1	0.8697(2)	0.2711(1)	0.1155(1)	1.000	0.029(1)
O-6(3)1	0.8221(2)	0.3711(1)	0.0670(1)	1.000	0.034(1)
C-1(4)1	0.7560(3)	0.0357(2)	0.1518(1)	1.000	0.032(1)
C-2(4)1	0.7979(3)	0.0563(2)	0.1947(1)	1.000	0.034(1)
C-3(4)1	0.7919(3)	0.1179(2)	0.1978(1)	1.000	0.035(1)
C-4(4)1	0.8375(3)	0.1447(1)	0.1586(1)	1.000	0.027(1)
C-5(4)1	0.7912(3)	0.1211(2)	0.1173(1)	1.000	0.032(1)
C-6(4)1	0.8310(3)	0.1426(2)	0.0763(1)	1.000	0.036(1)
O-2(4)1	0.7484(2)	0.0295(1)	0.2285(1)	1.000	0.041(1)
O-3(4)1	0.8397(3)	0.1367(1)	0.2356(1)	1.000	0.050(1)
O-4(4)1	0.8181(2)	0.2029(1)	0.1625(1)	1.000	0.033(1)
O-5(4)1	0.8024(2)	0.0621(1)	0.1174(1)	1.000	0.033(1)
O-6(4)1	0.9332(2)	0.1343(1)	0.0732(1)	1.000	0.037(1)
C-1(5)1	0.3863(2)	−0.0109(1)	0.1188(1)	1.000	0.025(1)
C-2(5)1	0.4293(3)	−0.0318(2)	0.1614(1)	1.000	0.028(1)
C-3(5)1	0.5124(3)	0.0065(2)	0.1745(1)	1.000	0.029(1)
C-4(5)1	0.5877(3)	0.0060(1)	0.1397(1)	1.000	0.026(1)
C-5(5)1	0.5416(3)	0.0189(1)	0.0956(1)	1.000	0.027(1)
C-6(5)1	0.6102(3)	0.0058(2)	0.0595(1)	1.000	0.031(1)
O-2(5)1	0.3571(2)	−0.0349(1)	0.1927(1)	1.000	0.031(1)
O-3(5)1	0.5572(2)	−0.0075(2)	0.2146(1)	1.000	0.047(1)
O-4(5)1	0.6555(2)	0.0487(1)	0.1509(1)	1.000	0.030(1)
O-5(5)1	0.4570(2)	−0.0146(1)	0.0870(1)	1.000	0.027(1)
O-6(5)1	0.6406(2)	−0.0499(1)	0.0616(1)	1.000	0.034(1)
C-1(6)1	0.1416(3)	0.1593(1)	0.1095(1)	1.000	0.026(1)

Table 4 (*Continued*)

Atom	*x*	*y*	*z*	Occupancy	U_{eq} (Å^2)
C-2(6)1	0.1289(3)	0.1184(1)	0.1461(1)	1.000	0.027(1)
C-3(6)1	0.2248(3)	0.0892(1)	0.1562(1)	1.000	0.026(1)
C-4(6)1	0.2611(3)	0.0615(1)	0.1158(1)	1.000	0.026(1)
C-5(6)1	0.2637(3)	0.1029(2)	0.0788(1)	1.000	0.030(1)
C-6(6)1	0.2826(3)	0.0749(2)	0.0365(1)	1.000	0.038(1)
O-2(6)1	0.0925(2)	0.1458(1)	0.1826(1)	1.000	0.030(1)
O-3(6)1	0.2150(2)	0.0469(1)	0.1877(1)	1.000	0.032(1)
O-4(6)1	0.3589(2)	0.0445(1)	0.1253(1)	1.000	0.029(1)
O-5(6)1	0.1725(2)	0.1304(1)	0.0725(1)	1.000	0.029(1)
O-6(6)1	0.2073(3)	0.0377(2)	0.0248(1)	1.000	0.048(1)
C-1(1)2	0.3583(3)	0.3535(1)	0.3515(1)	1.000	0.028(1)
C-2(1)2	0.4267(3)	0.3698(2)	0.3155(1)	1.000	0.034(1)
C-4(1)2	0.5647(3)	0.3390(1)	0.3636(1)	1.000	0.026(1)
C-3(1)2	0.5196(3)	0.3372(2)	0.3188(1)	1.000	0.033(1)
C-5(1)2	0.4899(3)	0.3255(2)	0.3972(1)	1.000	0.029(1)
C-6(1)2	0.5285(3)	0.3321(2)	0.4429(1)	1.000	0.034(1)
O-2(1)2	0.3756(2)	0.3604(1)	0.2760(1)	1.000	0.042(1)
O-3(1)2	0.5856(2)	0.3573(2)	0.2883(1)	1.000	0.050(1)
O-4(1)2	0.6393(2)	0.2985(1)	0.3649(1)	1.000	0.028(1)
O-5(1)2	0.4062(2)	0.3612(1)	0.3916(1)	1.000	0.031(1)
O-6(1)2	0.5742(2)	0.3840(1)	0.4489(1)	1.000	0.045(1)
C-1(2)2	0.1045(2)	0.1898(1)	0.3431(1)	1.000	0.025(1)
C-2(2)2	0.1093(3)	0.2278(1)	0.3042(1)	1.000	0.028(1)
C-3(2)2	0.2088(3)	0.2540(1)	0.3034(1)	1.000	0.027(1)
C-4(2)2	0.2327(3)	0.2830(1)	0.3456(1)	1.000	0.026(1)
C-5(2)2	0.2164(3)	0.2446(2)	0.3838(1)	1.000	0.026(1)
C-6(2)2	0.2267(3)	0.2729(2)	0.4268(1)	1.000	0.031(1)
O-2(2)2	0.0894(2)	0.1965(1)	0.2658(1)	1.000	0.033(1)
O-3(2)2	0.2100(2)	0.2925(1)	0.2685(1)	1.000	0.036(1)
O-4(2)2	0.3323(2)	0.2983(1)	0.3447(1)	1.000	0.027(1)
O-5(2)2	0.1198(2)	0.2215(1)	0.3811(1)	1.000	0.026(1)
O-6(2)2	0.1716(2)	0.3222(1)	0.4302(1)	1.000	0.032(1)
C-1(3)2	0.2401(2)	−0.0167(1)	0.3522(1)	1.000	0.027(1)
C-2(3)2	0.1962(3)	0.0017(2)	0.3090(1)	1.000	0.028(1)
C-3(3)2	0.1978(3)	0.0639(1)	0.3048(1)	1.000	0.027(1)
C-4(3)2	0.1539(2)	0.0923(1)	0.3436(1)	1.000	0.024(1)
C-5(3)2	0.2035(3)	0.0694(1)	0.3849(1)	1.000	0.026(1)
C-6(3)2	0.1640(3)	0.0924(2)	0.4257(1)	1.000	0.031(1)
O-2(3)2	0.2519(2)	−0.0231(1)	0.2761(1)	1.000	0.033(1)
O-3(3)2	0.1475(2)	0.0805(1)	0.2664(1)	1.000	0.034(1)
O-4(3)2	0.1768(2)	0.1494(1)	0.3389(1)	1.000	0.025(1)
O-5(3)2	0.1926(2)	0.0102(1)	0.3859(1)	1.000	0.029(1)
O-6(3)2	0.0619(2)	0.0834(1)	0.4285(1)	1.000	0.033(1)
C-1(4)2	0.6114(3)	−.0599(2)	0.3847(1)	1.000	0.030(1)
C-2(4)2	0.5659(3)	−.0852(2)	0.3444(1)	1.000	0.030(1)
C-3(4)2	0.4776(3)	−.0514(2)	0.3299(1)	1.000	0.033(1)
C-4(4)2	0.4076(2)	−0.0452(1)	0.3660(1)	1.000	0.027(1)
C-5(4)2	0.4569(3)	−.0291(1)	0.4087(1)	1.000	0.029(1)
C-6(4)2	0.3899(3)	−.0408(2)	0.4457(1)	1.000	0.036(1)
O-2(4)2	0.6363(2)	−0.0890(1)	0.3126(1)	1.000	0.037(1)
O-3(4)2	0.4297(2)	−0.0794(2)	0.2957(1)	1.000	0.049(1)
O-4(4)2	0.3404(2)	−0.0031(1)	0.3533(1)	1.000	0.027(1)
O-5(4)2	0.5429(2)	−0.0611(1)	0.4177(1)	1.000	0.033(1)
O-6(4)2	0.3603(2)	−0.0971(1)	0.4436(1)	1.000	0.041(1)
C-1(5)2	0.8605(3)	0.1079(1)	0.3853(1)	1.000	0.028(1)
C-2(5)2	0.8700(3)	0.0634(2)	0.3504(1)	1.000	0.032(1)
C-3(5)2	0.7730(3)	0.0358(2)	0.3418(1)	1.000	0.030(1)

Table 4 (*Continued*)

Atom	*x*	*y*	*z*	Occupancy	U_{eq} (Å^2)
C-4(5)2	0.7365(3)	0.0114(2)	0.3830(1)	1.000	0.027(1)
C-5(5)2	0.7373(3)	0.0553(2)	0.4188(1)	1.000	0.029(1)
C-6(5)2	0.7187(3)	0.0304(2)	0.4622(1)	1.000	0.035(1)
O-2(5)2	0.9063(3)	0.0892(1)	0.3132(1)	1.000	0.047(1)
O-3(5)2	0.7824(3)	−.0076(1)	0.3113(1)	1.000	0.042(1)
O-4(5)2	0.6382(2)	−0.0057(1)	0.3750(1)	1.000	0.029(1)
O-5(5)2	0.8309(2)	0.0814(1)	0.4230(1)	1.000	0.031(1)
O-6(5)2	0.7887(2)	−0.0098(1)	0.4743(1)	1.000	0.044(1)
C-1(6)2	0.7329(3)	0.3137(2)	0.3805(1)	1.000	0.031(1)
C-2(6)2	0.8044(3)	0.2980(2)	0.3456(1)	1.000	0.033(1)
C-3(6)2	0.8029(3)	0.2356(2)	0.3383(1)	1.000	0.031(1)
C-4(6)2	0.8172(3)	0.2047(1)	0.3803(1)	1.000	0.028(1)
C-5(6)2	0.7504(3)	0.2263(1)	0.4148(1)	1.000	0.030(1)
C-6(6)2	0.7749(3)	0.2048(2)	0.4598(1)	1.000	0.036(1)
O-2(6)2	0.7748(2)	0.3269(1)	0.3080(1)	1.000	0.048(1)
O-3(6)2	0.8759(2)	0.2200(1)	0.3107(1)	1.000	0.043(1)
O-4(6)2	0.7952(2)	0.1480(1)	0.3713(1)	1.000	0.034(1)
O-5(6)2	0.7571(2)	0.2858(1)	0.4185(1)	1.000	0.031(1)
O-6(6)2	0.8720(2)	0.2177(1)	0.4726(1)	1.000	0.043(1)
C-1A	0.6049(9)	0.1285(8)	0.2905(4)	0.500	0.084(4)
C-2A	0.4948(11)	0.1130(7)	0.2952(4)	0.500	0.075(5)
C-3A	0.4447(10)	0.1177(5)	0.2505(4)	0.500	0.067(3)
C-4A	0.5211(8)	0.1564(6)	0.2291(3)	0.500	0.072(3)
C-5A	0.4694(11)	0.2075(6)	0.2095(3)	0.500	0.076(4)
C-6A	0.3934(14)	0.2147(7)	0.2507(6)	0.500	0.116(7)
O-1A	0.5984(8)	0.1710(6)	0.2553(4)	0.500	0.072(3)
O-2A	0.3637(8)	0.1549(6)	0.2494(4)	0.500	0.065(3)
N-1A	0.4774(15)	0.1465(10)	0.3612(5)	0.500	0.157(11)
N-2A	0.5009(12)	0.2006(7)	0.1342(3)	0.500	0.052(3)
O-11A	0.4558(10)	0.1581(6)	0.3177(3)	0.500	0.094(4)
O-21A	0.4363(13)	0.1345(7)	0.3917(4)	0.500	0.103(4)
O-31A	0.5616(13)	0.1499(12)	0.3681(7)	0.500	0.174(12)
O-12A	0.4389(8)	0.2000(6)	0.1666(3)	0.500	0.072(2)
O-22A	0.4710(10)	0.1935(10)	0.0994(3)	0.500	0.114(6)
O-32A	0.5830(8)	0.2129(9)	0.1431(5)	0.500	0.110(5)
C-1B	0.5941(12)	0.2299(6)	0.2232(6)	0.500	0.121(7)
C-2B	0.4852(14)	0.2221(8)	0.2075(5)	0.500	0.118(7)
C-3B	0.4302(10)	0.2050(6)	0.2483(4)	0.500	0.096(4)
C-4B	0.5137(11)	0.1854(5)	0.2775(4)	0.500	0.097(4)
C-5B	0.4959(12)	0.1245(7)	0.2930(4)	0.500	0.077(4)
C-6B	0.4432(19)	0.1043(6)	0.2453(6)	0.500	0.113(8)
O-1B	0.6044(10)	0.1880(8)	0.2582(6)	0.500	0.119(6)
O-2B	0.3807(12)	0.1518(8)	0.2399(5)	0.500	0.093(5)
N-1B	0.5064(14)	0.1898(8)	0.1407(5)	0.500	0.075(5)
N-2B	0.4749(8)	0.1398(5)	0.3677(3)	0.500	0.047(2)
O-11B	0.4874(9)	0.1736(5)	0.1833(3)	0.500	0.081(3)
O-21B	0.5080(14)	0.1575(5)	0.1146(4)	0.500	0.097(4)
O-31B	0.5219(16)	0.2380(6)	0.1319(5)	0.500	0.113(5)
O-12B	0.4342(7)	0.1227(5)	0.3311(3)	0.500	0.068(2)
O-22B	0.4285(14)	0.1764(10)	0.3873(5)	0.500	0.141(10)
O-32B	0.5410(11)	0.1178(8)	0.3773(4)	0.500	0.113(6)
O-1W	0.0000(0)	0.1900(2)	0.0000(0)	0.500	0.036(1)
O-2W	1.0000(0)	0.1391(2)	0.5000(0)	0.500	0.034(1)
O-3W	0.2321(2)	−0.0682(1)	0.0020(1)	1.000	0.034(1)
O-4W	0.5170(2)	−0.1373(1)	0.0440(1)	1.000	0.044(1)
O-5W	0.4818(2)	−0.1876(1)	0.4559(1)	1.000	0.044(1)
O-6W	0.2319(2)	−0.1168(1)	0.5063(1)	1.000	0.036(1)
O-7W	−0.0157(3)	−.0135(1)	0.4558(1)	1.000	0.050(1)
O-8W	1.0141(3)	0.0375(2)	0.0445(1)	1.000	0.057(1)
O-9W	0.5614(3)	−0.1171(2)	0.2338(1)	1.000	0.049(1)
O-10W	0.9810(3)	0.0191(2)	0.2589(1)	1.000	0.072(1)

method using the program SHELX-97.[10] The isosorbide dinitrate molecule was disordered, and the electron density map at 293 K was too diffused to construct the structure model. The disorder was resolved on the electron density map at 173 K; therefore, the structure was refined for the low-temperature data. The restraints were applied for the refinement of the guest molecule to maintain normal bond distances and angles. Coordinates of hydrogen atoms in methine and methylene groups were calculated and they were included in the structure factor calculation. The results of the refinement are summarized in Table 1 and atomic parameters are listed in Table 4.

4. Supplementary data

Full crystallographic details, excluding structure factors, have been deposited with the Cambridge Crystallographic Data Center (CCDC 176956). These data may be obtained on request, from The Director, CCDC, 12 Union Road, Cambridge CB2 1EZ, UK (Tel.: +44-1223-336408; fax: +44-1223-336033; e-mail: deposit@ccdc.cam.ac.uk or www: http//www.ccdc.cam.ac.uk).

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