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Key indicators

Single-crystal X-ray study
 $T = 292$ K
Mean $\sigma(\text{C}-\text{C}) = 0.009$ Å
 R factor = 0.058
 wR factor = 0.157
Data-to-parameter ratio = 13.1For details of how these key indicators were
automatically derived from the article, see
<http://journals.iucr.org/e>.Diethyl 6,9-dibromo-1,4-dioxo-1,2,3,4,5,10-
hexahydro-2,3,4a,10a-tetraazabenzo[*g*]-
cyclopenta[*cd*]azulene-2a,10b-dicarboxylateThe title compound, $\text{C}_{18}\text{H}_{18}\text{Br}_2\text{N}_4\text{O}_6$, is an important inter-
mediate for the synthesis of molecular clips. Intermolecular
 $\text{N}-\text{H} \cdots \text{O}$ hydrogen bonds form eight-membered rings. No
 $\pi-\pi$ stacking is observed.

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Comment

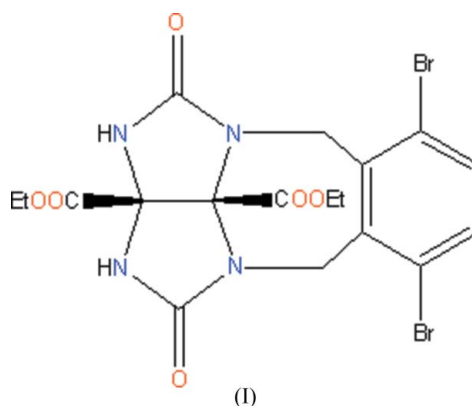
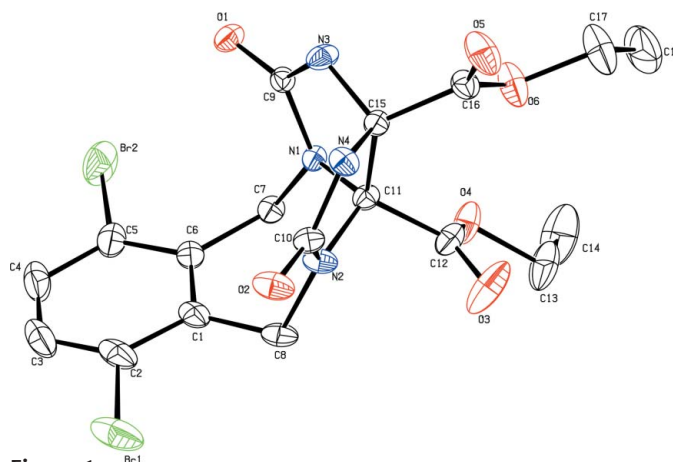
The derivatives of glycoluril are well known in studies of
organic supramolecular structures (Isaacs & Fettinger, 1999;
Burnett *et al.*, 2003; Chakraborty *et al.*, 2002). In addition,
glycoluril derivatives have significant potential in crystal
engineering studies (Wu *et al.*, 2002; Johnson *et al.*, 2002). In
this paper, we present the X-ray crystallographic analysis of
the title compound, (I), which is an important intermediate for
the preparation of S- and C-shaped methylene-bridged
glycoluril dimers (Wu *et al.*, 2002).The molecular structure of (I) is shown in Fig. 1. Selected
bond lengths and angles are given in Table 1. The molecules

Figure 1

The molecule of (I), showing the atom-numbering scheme. Displacement
ellipsoids are drawn at the 50% probability level.

are linked by intermolecular N—H...O hydrogen bonds (Table 2 and Fig. 2), utilizing a carbonyl O atom as acceptor. As a result, an eight-membered ring is formed, the topological motif of which corresponds to the first level graph-set descriptor $R_2^2(8)$ (Bernstein *et al.*, 1995). No π – π stacking is observed.

Experimental

The title compound was synthesized according to the literature method of Wu *et al.* (2002). Crystals appropriate for data collection were obtained by slow evaporation of a chloroform solution at 283 K.

Crystal data

$C_{18}H_{18}Br_2N_4O_6$	$D_x = 1.757 \text{ Mg m}^{-3}$
$M_r = 546.18$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 6947 reflections
$a = 12.0665 (11) \text{ \AA}$	$\theta = 2.33\text{--}23.98^\circ$
$b = 10.3050 (10) \text{ \AA}$	$\mu = 3.97 \text{ mm}^{-1}$
$c = 17.4969 (17) \text{ \AA}$	$T = 292 (2) \text{ K}$
$\beta = 108.371 (2)^\circ$	Block, colorless
$V = 2064.8 (3) \text{ \AA}^3$	$0.40 \times 0.30 \times 0.30 \text{ mm}$
$Z = 4$	

Data collection

Bruker SMART 4K CCD area-detector diffractometer	3656 independent reflections
φ and ω scans	2925 reflections with $I > 2\sigma(I)$
Absorption correction: multi-scan (SADABS; Sheldrick, 1996)	$R_{\text{int}} = 0.028$
$T_{\text{min}} = 0.238$, $T_{\text{max}} = 0.304$	$\theta_{\text{max}} = 25.1^\circ$
14418 measured reflections	$h = -14 \rightarrow 14$
	$k = -12 \rightarrow 12$
	$l = -20 \rightarrow 20$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0709P)^2 + 5.0818P]$
$R[F^2 > 2\sigma(F^2)] = 0.058$	where $P = (F_o^2 + 2F_c^2)/3$
$wR(F^2) = 0.157$	$(\Delta/\sigma)_{\text{max}} < 0.001$
$S = 1.03$	$\Delta\rho_{\text{max}} = 1.02 \text{ e \AA}^{-3}$
3656 reflections	$\Delta\rho_{\text{min}} = -1.09 \text{ e \AA}^{-3}$
279 parameters	
H atoms treated by a mixture of independent and constrained refinement	

Table 1

Selected geometric parameters (\AA , $^\circ$).

Br1—C2	1.906 (7)	C13—C14	1.488 (8)
C1—C2	1.398 (7)	C17—C18	1.470 (8)
C1—C6	1.403 (8)		
N2—C11—C12	107.8 (4)	C16—C15—C11	119.9 (4)
N3—C15—C11	101.4 (3)		
C8—C1—C6—C7	−1.1 (6)	C12—C11—N2—C8	−69.9 (5)
C6—C7—N1—C9	−76.0 (5)		

Table 2

Hydrogen-bond geometry (\AA , $^\circ$).

$D\text{—}H\cdots A$	$D\text{—}H$	$H\cdots A$	$D\cdots A$	$D\text{—}H\cdots A$
N4—H4A...O1 ⁱ	0.86 (4)	2.13 (5)	2.965 (5)	166 (7)
N3—H3A...O2 ⁱⁱ	0.81 (4)	1.95 (5)	2.750 (5)	170 (8)

Symmetry codes: (i) $-x + 2, y - \frac{1}{2}, -z + \frac{1}{2}$; (ii) $-x + 2, y + \frac{1}{2}, -z + \frac{1}{2}$.

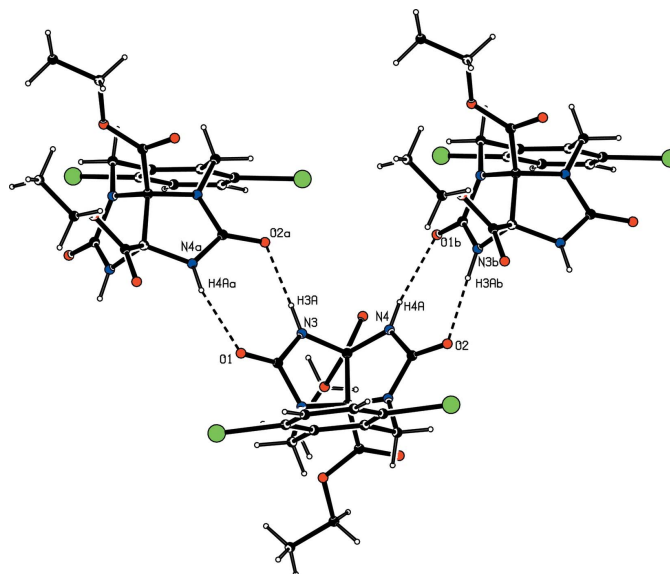


Figure 2

The crystal packing of (I). Dashed lines indicate hydrogen bonds.

The N-bound H atoms were located in a difference map and refined freely [$N\text{—}H = 0.81 (4)\text{--}0.86 (4) \text{ \AA}$]; their displacement parameters were allowed for with $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(N)$. The methyl H atoms were positioned geometrically ($C\text{—}H = 0.96 \text{ \AA}$). The constraint $U_{\text{iso}}(H) = 1.5U_{\text{eq}}(C)$ was applied, but each group was allowed to rotate freely about its C—C bond. All other H atoms were placed in geometrically idealized positions [0.93 (for CH) or 0.97 \AA (for CH_2)], and constrained to ride on their parent atoms, with $U_{\text{iso}}(H) = 1.2U_{\text{eq}}(C)$. The highest peak and deepest hole are located 0.87 and 0.85 \AA , respectively, from atom Br2.

Data collection: SMART (Bruker, 1997); cell refinement: SAINT (Bruker, 1999); data reduction: SAINT; program(s) used to solve structure: SHELXS97 (Sheldrick, 1997); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: SHELXTL (Bruker, 2001); software used to prepare material for publication: SHELXTL.

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