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Key indicators

Single-crystal X-ray study T = 293 K Mean σ (C–C) = 0.002 Å R factor = 0.053 wR factor = 0.145 Data-to-parameter ratio = 23.3

For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

A monoclinic polymorph of 25,27-bis(benzyloxy)-26,28-dihydroxycalix[4]arene

A new polymorph of the title compound, $C_{42}H_{36}O_4$, is reported. It crystallizes in space group $P2_1/c$, whereas the previously known polymorph [Bolte & Sakhaii (2004), *Acta Cryst.* C60, o1360–o1361] crystallizes in space group $P\overline{1}$. The conformations of the molecules differ in the orientation of one benzyl residue.

Comment

A triclinic polymorph (space group $P\overline{1}$), (II), of the title compound has already been described (Bolte & Sakhaii, 2004). In this work, a monoclinic polymorph, (I), of the title compound is reported. It crystallizes in space group $P2_1/c$.



A perspective view of (I) is shown in Fig. 1. Bond lengths and angles can be regarded as normal (Cambridge Structural Database, Version 5.27 plus one update; *MOGUL* Version 1.0; Allen, 2002).

A least-squares fit (Fig. 2) of the central calixarene framework of (I) and (II) (r.m.s. deviation 0.06 Å) reveals that the two molecules differ only in the orientation of one of the two benzyl residues (Table 3).

Two intramolecular hydrogen bonds stabilize the molecular conformation. The different orientations of the benzyl residue in (I) and (II) do not affect these hydrogen bonds.

Experimental

The title compound was synthesized according to the procedure described by Casnati *et al.* (1991). Colourless crystals suitable for X-ray diffraction were grown from a methanol-chloroform solution (1:1) of the title compound.

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The molecular structure of (I), with displacement ellipsoids drawn at the 30% probability level. H atoms bonded to C atoms have been omitted. Dashed lines indicate hydrogen bonds.



Figure 2

A least-squares fit of the two polymorphs of the title compound. Full lines indicate polymorph (I) and dashed lines indicate polymorph (II). H atoms have been omitted.

Crystal data

$C_{42}H_{36}O_4$	$D_x = 1.252 \text{ Mg m}^{-3}$
$M_r = 604.71$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 8192
a = 11.250 (1) Å	reflections
b = 15.380 (1) Å	$\theta = 3.5 - 25.0^{\circ}$
c = 18.616 (2) Å	$\mu = 0.08 \text{ mm}^{-1}$
$\beta = 95.31 \ (1)^{\circ}$	T = 293 (2) K
V = 3207.2 (5) Å ³	Block, colourless
Z = 4	$0.50 \times 0.50 \times 0.30 \text{ mm}$

Data collection

Siemens SMART CCD three-circle 5	829 reflecti
diffractometer I	$R_{int} = 0.046$
ω scans θ	$P_{\rm max} = 31.9^{\circ}$
Absorption correction: none h	$n = -15 \rightarrow$
27936 measured reflections k	$z = -23 \rightarrow$
9849 independent reflections <i>l</i>	$= -27 \rightarrow 2$

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.053$ $wR(F^2) = 0.145$ S = 1.019849 reflections 423 parameters H atoms treated by a mixture of independent and constrained refinement 5829 reflections with $I > 2\sigma(I)$ $R_{int} = 0.046$ $\theta_{max} = 31.9^{\circ}$ $h = -15 \to 16$ $k = -23 \to 22$ $l = -27 \to 27$

$$\begin{split} &w = 1/[\sigma^2(F_{\rm o}^2) + (0.0587P)^2 \\ &+ 0.609P] \\ &where \ P = (F_{\rm o}^2 + 2F_{\rm c}^2)/3 \\ (\Delta/\sigma)_{\rm max} < 0.001 \\ \Delta\rho_{\rm max} = 0.16 \ {\rm e} \ {\rm \AA}^{-3} \\ \Delta\rho_{\rm min} = -0.20 \ {\rm e} \ {\rm \AA}^{-3} \end{split}$$

Table 1Selected bond lengths (Å).

O5-C22	1.4046 (15)	O6-C6	1.4671 (18)
O5-C5	1.4516 (17)	C12-O12	1.3668 (17)
O6-C42	1.3974 (17)	O32-C32	1.3650 (16)

Table 2

Hydrogen-bond geometry (Å, °).

$\overline{D-\mathrm{H}\cdots A}$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - H \cdots A$
O12-H12···O6	0.96 (2)	1.85 (2)	2.8077 (15)	173 (2)
O32-H32···O5	0.90 (2)	1.93 (2)	2.8056 (14)	163.7 (19)

Table 3

Comparison of torsion angles (°) for the two polymorphs, (I) and (II).

	(I)	(II)
C42-O6-C6-C61	75.91 (18)	-160.16 (16)
O6-C6-C61-C62	-88.8 (2)	-166.37(18)
O6-C6-C61-C66	88.20 (19)	14.4 (3)
C41-C42-O6-C6	99.91 (15)	87.4 (2)
C43-C42-O6-C6	-83.46 (16)	-95.22 (19)

H atoms were located in a difference map, but refined with fixed individual isotropic displacement parameters $[U_{\rm iso}({\rm H}) = 1.2U_{\rm eq}({\rm C})]$ using a riding model, with C–H = 0.93 and 0.97 Å, for C_{aromatic} and C_{methylene}, respectively. The hydroxyl H atoms were refined isotropically.

Data collection: *SMART* (Siemens, 1995); cell refinement: *SAINT* (Siemens, 1995); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1990); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *XP* in *SHELXTL-Plus* (Sheldrick, 1991); software used to prepare material for publication: *SHELXL97*.

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