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Key indicators

Single-crystal X-ray study T = 173 K Mean σ (C–C) = 0.008 Å R factor = 0.036 wR factor = 0.077 Data-to-parameter ratio = 15.1

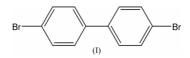
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

Redetermination of 4,4'-dibromobiphenyl

The title compound, $C_{12}H_8Br_2$, previously reported by Kronebusch, Gleason & Britton [*Cryst. Struct. Commun.* (1976), **5**, 839–842] has been rerefined against new intensity data. Geometric parameters agree quite well. However, the positions of the hydroxyl H atoms could be determined employing our new data. Furthermore, the results of the present structure determination are of significantly higher precision. There are two almost identical molecules in the asymmetric unit, which show close intermolecular $Br \cdots Br$ contacts less than 3.48 Å.

Comment

A perspective view of the title compound, (I), is shown in Fig. 1. The original structure was reported by Kronebusch et al. (1976) in space group $P2_1/c$. We have retained the atom numbering of these authors, but we have decided to describe the structure in $P2_1/n$, since the β angle then decreases from 116.6 (2) to 97.32 (3)°. The geometric parameters of both determinations agree quite well (Table 1). However, the present work is of significantly improved precision and we were able to determine the positions of the H atoms. There are two almost identical molecules in the asymmetric unit, which show rather close intermolecular $Br \cdots Br$ contacts: $Br 1 \cdots Br 2^{i}$ = 3.4316 (10) Å and $Br1' \cdots Br2'^{i}$ = 3.4782 (10) Å [symmetry code: (i) x, 1 + y, z]. Furthermore, it is interesting to note that the structure of (I) is isostructural with 4,4'-dichlorobiphenyl (Brock et al., 1978), but not with 4,4'-difluorobiphenyl (Halstead et al., 1976).



Experimental

Our aim was to synthesize a long-chain metallosiloxane containing an Si-O-Si framework by mixing $CoCl_2$, 4,4'-dibromobiphenyl and tetrasodium bis(1,1,3,3,5,5,7,7-octaphenyltetrasiloxanediolate) in pyridine solution. From the product mixture, we isolated suitable single crystals; unfortunately, these proved to be the starting material.

Crystal data

$C_{12}H_8Br_2$	$D_x = 1.955 \text{ Mg m}^{-3}$
$M_r = 312.00$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 9816
$a = 9.7007 (19) \text{\AA}$	reflections
b = 14.114 (3) Å	$\theta = 3.4-25.2^{\circ}$
c = 15.610 (3) Å	$\mu = 7.60 \text{ mm}^{-1}$
$\beta = 97.32 \ (3)^{\circ}$	T = 173 (2) K
V = 2119.8 (7) Å ³	Block, colourless
Z = 8	$0.18 \times 0.16 \times 0.11 \text{ mm}$

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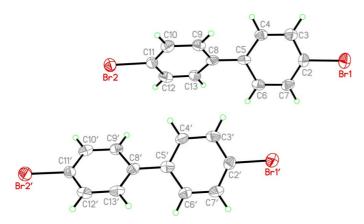


Figure 1

Perspective view of the asymmetric unit of the title compound, with the atom numbering. Displacement ellipsoids are shown at the 50% probability level.

Data collection

Stoe IPDS-II two-circle	3820 independent reflections
diffractometer	2578 reflections with $I > 2\sigma(I)$
ω scans	$R_{\rm int} = 0.078$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.3^{\circ}$
(MULABS; Spek, 1990; Blessing,	$h = -11 \rightarrow 11$
1995)	$k = -16 \rightarrow 16$
$T_{\min} = 0.241, \ T_{\max} = 0.433$	$l = -18 \rightarrow 18$
17434 measured reflections	

Refinement

Refinement on F^2 $R[F^2 > 2\sigma(F^2)] = 0.036$ $wR(F^2) = 0.077$ S = 0.873820 reflections 253 parameters H-atom parameters constrained $w = 1/[\sigma^2(F_o^2) + (0.0364P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$ $(\Delta/\sigma)_{max} = 0.001$ $\Delta\rho_{max} = 0.59 \text{ e } \text{Å}^{-3}$ $\Delta\rho_{min} = -0.86 \text{ e } \text{Å}^{-3}$

Table 1

Comparison of the geometric parameters (°, Å) of the present structure, (I), with those of Kronebusch *et al.* (1976), (II).

	(I)	(II)
C2-C7···C8-C13	38.5 (2)	38.7
$C2' - C7' \cdots C8' - C13'$	42.3 (1)	41.4
C2-Br1	1.909 (5)	1.893
C11-Br2	1.910 (5)	1.916
C2'-Br1'	1.918 (5)	1.886
C11′-Br2′	1.912 (5)	1.899
C5-C8	1.472 (7)	1.496
C5'-C8'	1.491 (7)	1.453

All H atoms could be located unequivocally by difference Fourier synthesis. They were refined with fixed individual displacement parameters $[U_{iso}(H) = 1.2U_{eq}(C)]$, using a riding model with C-H = 0.99 Å.

Data collection: X-AREA (Stoe & Cie, 2001); cell refinement: X-AREA; data reduction: X-AREA; 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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