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## Structure Reports

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## Key indicators

Single-crystal X-ray study
$T=293 \mathrm{~K}$
Mean $\sigma(\mathrm{C}-\mathrm{C})=0.002 \AA$
$R$ factor $=0.047$
$w R$ factor $=0.131$
Data-to-parameter ratio $=15.7$
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.
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## 1,6-Bis(5-acetyl-4,7-dimethoxybenzofuran-6-yloxy)hexane

The khellinone dimer, 1,6-bis-(5-acetyl-4,7-dimethoxybenzo-furan-6-yloxy)hexane, $\mathrm{C}_{30} \mathrm{H}_{34} \mathrm{O}_{10}$, was prepared as part of a series of Kv1.3 ion channel blockers. The dimer lies on a centre of symmetry, and adopts an extended structure such that the separation between the benzofuran groups is 9.927 (3) $\AA . \mathrm{C}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds link the molecules into linear chains which lie parallel to the [201] direction.

## Comment

As part of a study into the effect of dimerization of the natural product khellinone on the blockade of Kv1.3 potassium ion channels, we prepared the title compound, (I). We have reported that dimerization of khellinone through atom O5 (as labelled in Fig. 1) substantially increases the level of Kv1.3 blockade (Baell et al., 2004). It was reported that optimal blockade in the alkane linker series occurred for the pentane linker with a distance of approximately $9.82 \AA$ between the benzofuran groups. The distance was calculated using a molecular model of the dimer. The crystal structure of the title compound, which contains the hexane linker, offers further data on the structure-activity relationships of this series. Information about the distance between and the relative orientation of the benzofuran moieties in the crystal structure is especially of interest.

(I)

The molecule lies on a centre of symmetry, and adopts an extended conformation (Fig. 1) such that the separation between the benzofuran groups [C8‥C $8^{\text {i }}$; symmetry code: (i) $-x,-y,-z]$ is 9.927 (3) $\AA$. The two benzofuran groups are, necessarily, parallel, but have a perpendicular separation of 0.98 (8) $\AA$. All nine atoms of the benzofuran ring system are planar, the greatest deviations being 0.0093 (12) $\AA$ for C 2 and 0.0093 (13) $\AA$ for C3. One methoxy group is almost coplanar with the ring, the torsion angle $\mathrm{C} 3-\mathrm{C} 2-\mathrm{O} 3-\mathrm{C} 11$ being $6.9(3)^{\circ}$; for the other methoxy group the torsion angle C6$\mathrm{C} 7-\mathrm{O} 4-\mathrm{C} 12$ is $66.3(2)^{\circ}$, while the dihedral angle between the plane of the acetyl group and the plane of the benzofuran atoms is $89.31(12)^{\circ}$.
$\mathrm{C}-\mathrm{H} \cdots \mathrm{O}$ hydrogen bonds $\left[\mathrm{C} 5-\mathrm{H} 5=0.95 \AA, \mathrm{H} 5 \cdots \mathrm{O} 2^{\mathrm{ii}}=\right.$ $2.35 \AA, \mathrm{C} 5 \cdots \mathrm{O} 2^{\mathrm{ii}}=3.286(2) \AA$ and $\mathrm{C} 5-\mathrm{H} 5 \cdots \mathrm{O}^{\mathrm{ii}}=172^{\circ}$;

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Figure 1
ORTEPII (Johnson, 1976) diagram of (I). Displacement ellipsoids are drawn at the $50 \%$ probability level [symmetry code: (i) $-x,-y,-z$ ].
symmetry code: (ii) $\left.1+x, \frac{1}{2}-y, \frac{1}{2}+z\right]$ link the molecules into linear chains which lie parallel to the [201] direction.

## Experimental

To a suspension of khellinone ( $236 \mathrm{mg}, 1.0 \mathrm{mmol}$ ) and caesium carbonate ( $163 \mathrm{mg}, 0.5 \mathrm{mmol}$ ) in DMF ( 2 ml ) under nitrogen was added 1,6 -dibromohexane $(0.077 \mathrm{ml}, 0.5 \mathrm{mmol})$ and the reaction mixture was stirred at 348 K for 16 h . The reaction mixture was diluted with ethyl acetate ( 10 ml ), washed with $10 \%$ aqueous citric acid $(3 \times 10 \mathrm{ml})$ and brine $(10 \mathrm{ml})$, dried over $\mathrm{MgSO}_{4}$ and concentrated in vacuo. The crude product was purified by flash chromatography, eluting with ethyl acetate/cyclohexane (1:9 to 1:4) to give the title compound ( $215 \mathrm{mg}, 77 \%$ ) as a colourless solid, which was then crystallized from ethyl acetate/cyclohexane (1:4) and analysed by X-ray crystallography (m.p. ${ }^{362-363 ~ K) . ~ S p e c t r o s c o p i c ~ a n a l y s i s, ~}{ }^{1} \mathrm{H}$ NMR ( $\left.\mathrm{CDCl}_{3}, \delta\right): 1.48(m, 4 \mathrm{H}), 1.75(m, 4 \mathrm{H}), 2.52(s, 6 \mathrm{H}), 3.97(s, 6 \mathrm{H})$, $4.06(m, 10 \mathrm{H}), 6.85(d, J=2.4 \mathrm{~Hz}, 2 \mathrm{H}), 7.55(d, J=2.4 \mathrm{~Hz}, 2 \mathrm{H}) ;{ }^{13} \mathrm{C}$

NMR $\left(\mathrm{CDCl}_{3}, \delta\right): 25.6,26.8,32.7,61.0,61.2,75.1,104.6,116.3,124.5$, 134.4, 143.9, 144.4, 144.8, 148.6, 201.8; IR ( KBr , chloroform, $v, \mathrm{~cm}^{-1}$ ): 1702; MS ( $\mathrm{ES}^{+}$) m/z $555\left(M+\mathrm{H}^{+}\right)$; analysis found: C 64.9, H 6.1\%; $\mathrm{C}_{30} \mathrm{H}_{34} \mathrm{O}_{10}$ requires C $65.0, \mathrm{H} 6.2 \%$.

Crystal data
$\mathrm{C}_{30} \mathrm{H}_{34} \mathrm{O}_{10}$
$M_{r}=554.57$
Monoclinic, $P 2_{\mathrm{d}} / c$
$a=7.1937$ (6) А 。
$b=13.8894$ (12) $\AA$
$c=14.3709$ (12) A
$\beta=93.271$ (2) ${ }^{\circ}$
$V=1433.5(2) \AA^{3}$
$Z=2$

$$
\begin{aligned}
& D_{x}=1.285 \mathrm{Mg} \mathrm{~m}^{-3} \\
& \text { Mo } K \alpha \text { radiation } \\
& \text { Cell parameters from } 2418 \\
& \quad \text { reflections } \\
& \theta=2.8-24.2^{\circ} \\
& \mu=0.10 \mathrm{~mm}^{-1} \\
& T=293(2) \mathrm{K} \\
& \text { Plate, colourless } \\
& 0.40 \times 0.40 \times 0.10 \mathrm{~mm}
\end{aligned}
$$

## Data collection

Bruker SMART APEX CCD area-

$$
2408 \text { reflections with } I>2 \sigma(I)
$$

$R_{\text {int }}=0.022$
$\theta_{\text {max }}=27.5^{\circ}$
$h=-9 \rightarrow 9$
$k=-18 \rightarrow 17$
$l=-18 \rightarrow 8$

## Refinement

Refinement on $F^{2}$
$R\left[F^{2}>2 \sigma\left(F^{2}\right)\right]=0.047$
$w=1 /\left[\sigma^{2}\left(F_{o}{ }^{2}\right)+(0.0608 P)^{2}\right.$
$w R\left(F^{2}\right)=0.131$
$S=1.02$
3276 reflections
209 parameters
H -atom parameters constrained
$+0.2628 P]$
where $P=\left(F_{o}{ }^{2}+2 F_{c}^{2}\right) / 3$
$(\Delta / \sigma)_{\max }<0.001$
$\Delta \rho_{\max }=0.20 \mathrm{e}_{\mathrm{max}}{ }_{\circ}^{-3}$
$\Delta \rho_{\min }=-0.19 \mathrm{e}^{-3}$

All H atoms were assigned an individual isotropic displacement parameter. Each methyl group was allowed to rotate freely about its $\mathrm{C}-\mathrm{C}$ bond, while the other H atoms were constrained to ride on their parent atoms. The final $\mathrm{C}-\mathrm{H}$ distances were in the range $0.94-$ 1.03 Å.

Data collection: SMART (Bruker, 2000); cell refinement: SAINT; data reduction: SAINT (Bruker, 2000); program(s) used to solve structure: SHELXS97 (Sheldrick, 1990); program(s) used to refine structure: SHELXL97 (Sheldrick, 1997); molecular graphics: ORTEPII (Johnson, 1976); software used to prepare material for publication: SHELXL97.

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