organic papers

Acta Crystallographica Section E Structure Reports Online

ISSN 1600-5368

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Key indicators

Single-crystal X-ray study T = 292 K Mean σ (C–C) = 0.007 Å R factor = 0.035 wR factor = 0.106 Data-to-parameter ratio = 14.2

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

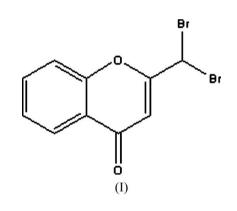
2-(Dibromomethyl)-4H-chromen-4-one

In the crystal structure of the title compound, $C_{10}H_6Br_2O_2$, centrosymmetric hydrogen-bonded dimers are formed *via* C-H···O hydrogen bonds. π - π stacking interactions involving these dimers are also observed.

Received 17 October 2005 Accepted 27 October 2005 Online 31 October 2005

Comment

Chromones are one of the most important groups of biological compounds in nature, and are used as a synthetic lead for drug discovery. Recently, the structural modification of the chromone scaffold, with the introduction of heterocylic substituents at either the 2- or 3-position, has attracted considerable attention. Some chromones bearing a heterocyclic thioether group have been reported to be anticancer agents (Khim *et al.*, 2004). The title compound, (I), is an important intermediate for the synthesis of chromone derivatives.



The molecular structure of (I) is illustrated in Fig. 1. Atom C8, with attached atom H8, forms a hydrogen bond to atom O2 of a symmetry-related molecule. This leads to the formation of hydrogen-bonded dimers, as shown in Fig. 2 (details are given in Table 1). As a result, a ten-membered ring is formed whose topological motif corresponds to the first level graph-set descriptor $R_2^2(10)$ (Bernstein *et al.*, 1995). Weak $\pi - \pi$ stacking is observed, with the distance between the benzene ring centroids, $Cg1\cdots Cg1b$, being 3.672 (3) Å (see Fig. 2 for details). These interactions are very similar to those observed in our previous report on the crystal structure of 3-(4,6-dimethylpyrimidin-2-yl)-2-methylchromen-4-one (Huang *et al.*, 2005).

Experimental

Compound (I) was synthesized according to the literature procedure of Khim *et al.* (2004). Crystals suitable for X-ray analysis were grown from acetone at 277 K.

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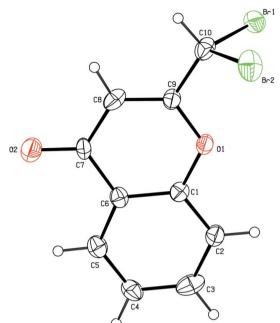


Figure 1

A view of the molecular structure of (I), showing the atom-labelling scheme and with displacement ellipsoids drawn at the 50% probability level. H atoms are represented by circles of arbitrary size.

Crystal data

$C_{10}H_6Br_2O_2$	$D_x = 2.073 \text{ Mg m}^{-3}$
$M_r = 317.97$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/c$	Cell parameters from 2048
a = 8.2343 (14) Å	reflections
b = 10.3445 (18) Å	$\theta = 2.6-25.1^{\circ}$
c = 12.047 (2) Å	$\mu = 7.93 \text{ mm}^{-1}$
$\beta = 96.884 \ (3)^{\circ}$	T = 292 (2) K
V = 1018.7 (3) Å ³	Block, pink
Z = 4	$0.30 \times 0.20 \times 0.10 \text{ mm}$
Data collection	

Data collection

Bruker SMART 4K CCD area-	1802 independent reflections
detector diffractometer	1496 reflections with $I > 2\sigma(I)$
φ and ω scans	$R_{\rm int} = 0.025$
Absorption correction: multi-scan	$\theta_{\rm max} = 25.1^{\circ}$
(SADABS; Sheldrick, 1996)	$h = -9 \rightarrow 9$
$T_{\min} = 0.179, T_{\max} = 0.453$	$k = -11 \rightarrow 12$
5018 measured reflections	$l = -12 \rightarrow 14$

Refinement

Refinement on F^2	$w = 1/[\sigma^2(F_o^2) + (0.0485P)^2]$
$R[F^2 > 2\sigma(F^2)] = 0.035$	+ 1.7251P]
$wR(F^2) = 0.106$	where $P = (F_0^2 + 2F_c^2)/3$
S = 1.13	$(\Delta/\sigma)_{\rm max} = 0.008$
1802 reflections	$\Delta \rho_{\rm max} = 0.56 \ {\rm e} \ {\rm \AA}^{-3}$
127 parameters	$\Delta \rho_{\rm min} = -0.47 \text{ e } \text{\AA}^{-3}$
H-atom parameters constrained	

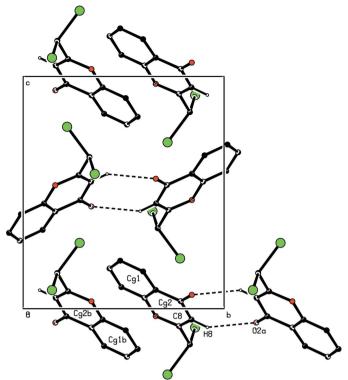
Table 1

Hydrogen-bond geometry (Å, °).

$D - \mathbf{H} \cdot \cdot \cdot A$	$D-\mathrm{H}$	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdot \cdot \cdot A$
$\overline{C8{-}H8{\cdot}\cdot{\cdot}O2^i}$	0.93	2.54	3.342 (6)	145

Symmetry code: (i) -x + 1, -y + 2, -z.

H atoms were placed in calculated positions and treated as riding atoms, with C-H bond distances in the range 0.93-0.98 Å, and with $U_{\rm iso}({\rm H}) = 1.2 U_{\rm eg}({\rm C}).$





A view of the crystal packing in compound (I), showing the formation of the hydrogen-bonded dimers and the π - π stacking. Hydrogen bonds are shown as dashed lines. H atoms not involved in hydrogen bonding have been omitted. [Symmetry codes: (a) -x + 1, -y + 2, -z; (b) 1 - x, 1 - y, -z.]

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.

The authors acknowledge financial support from the National Key Project for Basic Research (grant No. 2002CCA00500), the National Natural Science Foundation of China (grant nos. 20432010, 20476036 and 20172017), the Programme for New Century Excellent Talents in Universities of China and the Programme for Excellent Research Groups of Hubei Province (grant no. 2004ABC002).

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