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(3*RS*,1*SR*)-3-Bromo-3-(1-phenylpropyl)chroman-2,4-dione

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Key indicators

Single-crystal X-ray study
T = 295 K
Mean σ(C–C) = 0.005 Å
R factor = 0.041
wR factor = 0.115
Data-to-parameter ratio = 14.7

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

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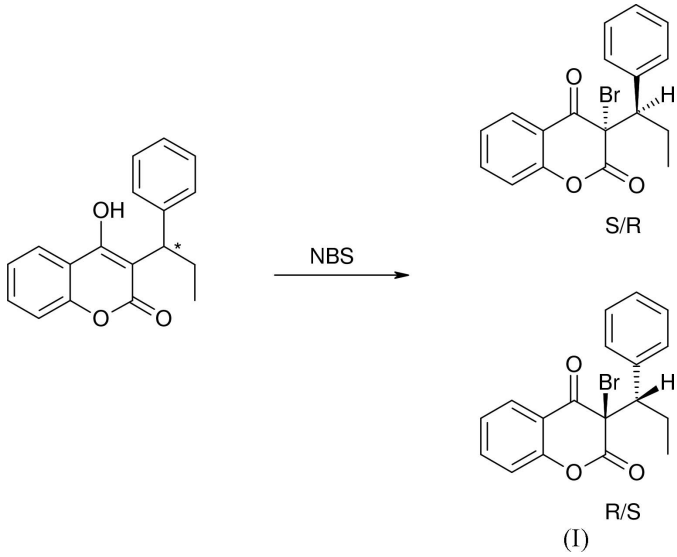
The title compound, $C_{18}H_{15}BrO_3$, was obtained by bromination of phenprocoumone with *N*-bromosuccinimide. The X-ray structure confirms an earlier proposal concerning the regioselectivity of the reaction to introduce the Br atom at the 3-position.

Comment

The title compound, (I), was prepared in an approach to synthesize possible metabolites of phenprocoumon, a well known antithrombotic compound (Hirsh *et al.*, 2001). In order to compare the fragmentation pattern of an unknown metabolite (He *et al.*, 1999) in human urine with a chemically synthesized compound by mass spectrometry (MS) techniques, we decided to introduce bromine into the 3-position of phenprocoumone. Analytical data obtained by TLC, IR, ^{1}H NMR and ^{13}C NMR supported the expected structure of (I). However, by performing gas chromatography(GC)/MS analysis of (I), no isotopic pattern of a bromine-containing compound in the spectrum could be detected in the spectrum. Furthermore, no difference between phenprocoumon and (I) concerning both retention time and fragmentation pattern was observed, indicating decomposition of (I) to the starting material as a measurement artifact. Additionally, use of the electrospray ionization (ESI)–MS technique as a soft ionization method revealed unexpectedly no bromine. We now report the X-ray crystal structure analysis which definitively proved the structure of (I).



(I)

The molecular structure of (I) is shown in Fig. 1, and some geometrical parameters are listed in Table 1. The crystal

structure of (I) consists of enantiomers of one diastereomer. Since the other diastereomer was not detected, we conclude that the approach of bromine to the 3-position of phenprocoumone takes place on the same side as the proton (and opposite to the bulky phenyl group), yielding only the racemic mixture of enantiomers of one possible pair of diastereomers. The molecules are linked by C—H···O hydrogen bonds (Table 2) to form a dimer. This also leads to a rather short C5···Br1($-x$, $-y$, $-z$) contact [3.292 (4) Å].

Experimental

Phenprocoumone (2.5 mmol) was stirred with *N*-bromosuccinimide (2.75 mmol) in dry chloroform for 2 h at room temperature. The mother liquor was evaporated and the residue purified by silica-gel column chromatography (ethyl acetate–hexane = 1:5) to yield (I) quantitatively (Hegedüs, 1958). Crystals of (I) precipitated at 278 K from acetone solution by slow evaporation.

Crystal data

$C_{18}H_{15}BrO_3$
M_r = 359.21
Triclinic, $P\overline{1}$
a = 6.2769 (16) Å
b = 8.6095 (10) Å
c = 14.775 (3) Å
α = 91.154 (12)°
β = 90.796 (18)°
γ = 103.908 (14)°
V = 774.7 (3) Å^3
Z = 2
D_x = 1.540 Mg m^{-3}
Cu $K\alpha$ radiation
Cell parameters from 25 reflections
θ = 60–71°
μ = 3.70 mm^{-1}
T = 295 (2) K
Plate, colourless
0.38 × 0.28 × 0.02 mm

Data collection

Enraf–Nonius CAD-4 diffractometer
$\omega/2\theta$ scans
Absorption correction: numerical (de Meulenaer & Tompa, 1965)
T_{min} = 0.353, T_{max} = 0.926
3234 measured reflections
3109 independent reflections
2812 reflections with $I > 2\sigma(I)$
R_{int} = 0.043
θ_{max} = 73.1°
$h = -7 \rightarrow 7$
$k = -10 \rightarrow 10$
$l = -18 \rightarrow 0$
3 standard reflections
frequency: 60 min
intensity decay: 10%

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)]$ = 0.041
$wR(F^2)$ = 0.115
S = 1.12
3109 reflections
212 parameters
Only H-atom U's refined
$w = 1/[\sigma^2(F_o^2) + (0.0656P)^2 + 0.3708P]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max}$ = 0.57 e Å^{-3}
$\Delta\rho_{min}$ = −0.57 e Å^{-3}

Table 1
Selected geometric parameters (Å, °).

Br1—C1	1.992 (3)		
C2—C1—Br1	100.32 (18)	C10—C1—Br1	101.28 (18)
C13—C1—Br1	111.1 (2)		
Br1—C1—C13—C14	−175.2 (2)		

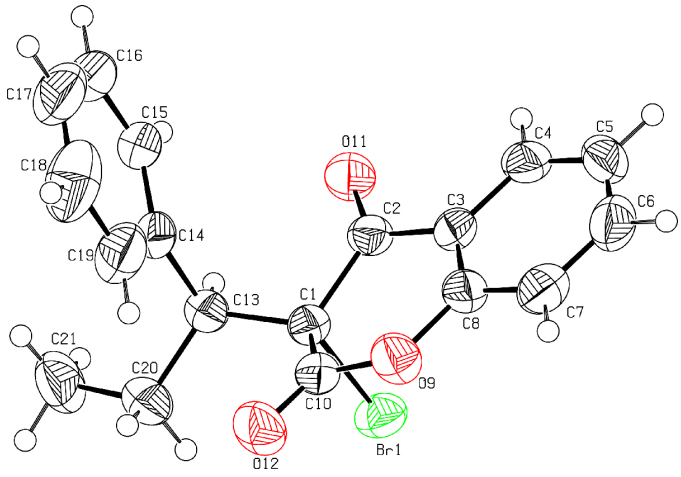


Figure 1
The molecular structure of (I), showing displacement ellipsoids at the 50% probability level.

Table 2
Hydrogen-bonding geometry (Å, °).

D—H···A	D—H	H···A	D···A	D—H···A
C4—H4···O11^{i}	0.93	2.54	3.372 (4)	150

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

H atoms were positioned geometrically and allowed to ride during subsequent refinement, with C—H = 0.93–0.96 Å and with torsional freedom for the methyl group. The U_{iso}(H) parameters were refined without restraints. For methyl and methylene H atoms one U_{iso} parameter per group was refined. The methyl group could rotate around the C—C bond.

Data collection: *CAD-4 Software* (Nonius, 1998); cell refinement: *CAD-4 Software*; data reduction: *CORINC* (Dräger & Gattow, 1971); program(s) used to solve structure: *SIR92* (Altomare *et al.*, 1994); 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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