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#### **Key indicators**

Single-crystal X-ray study T = 293 K Mean  $\sigma$ (C–C) = 0.005 Å R factor = 0.050 wR factor = 0.152 Data-to-parameter ratio = 12.2

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

# 2-(4-Chlorobenzyl)-1,2-benzisothiazol-3(2*H*)-one 1,1-dioxide

In the title compound,  $C_{14}H_{10}$ ClNO<sub>3</sub>S, the mean planes of benzisothiazole moiety and the 4-chlorobenzene ring make a dihedral angle of 66.2 (5)°. Weak intermolecular C-H···O hydrogen bonds link molecules into linear chains extending along the *b* axis.

## Comment

Saccharin, one of the earliest synthetic sweeteners, has been widely applied in drug synthesis. Many pharmaceuticals have been made starting from saccharin, for example, the antiinflammatory and antirheumatic drug Meloxicam (Xu *et al.*, 1999). The 4-chlorobenzyl group is an important intermediate in organic synthesis. We report here the crystal structure of the title compound, (I).



In (I) (Fig. 1), all bond lengths and angles (Table 1) within the saccharin group are similar to those observed in the series of *N*-saccharin acids (Feeder & Jones, 1996), *N*-saccharin peracids (Feeder & Jones, 1994) and saccharin (Glidewell *et al.*, 2000). The mean plane of the benzisothiazole (C1–C7/S1/



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N1) moiety and the benzene (C9–C14) ring make a dihedral angle of 66.2 (5)°. Weak intermolecular C–H···O hydrogen bonds (Table 2) link molecules into linear chains extending along the *b* axis.

## **Experimental**

The title compound was prepared by reaction of sodium saccharinate (4.17 g, 0.02 mol) and 4-chlorobenzyl chloride (2.50 g, 0.02 mol) in N,N-dimethylformamide (5 ml) under reflux for 5 h; 4.67 g product was obtained (yield 76.0%). Single crystals of the title compound suitable for X-ray measurements were obtained by recrystallization from ethyl acetate at room temperature.

Z = 2

 $D_x = 1.599 \text{ Mg m}^{-3}$ 

Cell parameters from 5601

Mo  $K\alpha$  radiation

reflections

 $\theta = 1.6 - 27.5^{\circ}$ 

 $\mu = 0.47 \text{ mm}^{-1}$ 

T = 293 (2) K

Plate, colourless

 $0.53\,\times\,0.47\,\times\,0.11$  mm

## Crystal data

 $\begin{array}{l} C_{14}H_{10}\text{CINO}_3\text{S} \\ M_r = 307.74 \\ \text{Triclinic, } P\overline{1} \\ a = 7.2657 \ (15) \ \mathring{A} \\ b = 7.4743 \ (15) \ \mathring{A} \\ c = 13.317 \ (3) \ \mathring{A} \\ \alpha = 97.50 \ (3)^\circ \\ \beta = 102.82 \ (3)^\circ \\ \gamma = 111.25 \ (3)^\circ \\ V = 639.3 \ (3) \ \mathring{A}^3 \end{array}$ 

#### Data collection

Rigaku R-AXIS RAPID IP<br/>diffractometer2201 independent reflections<br/>2065 reflections with  $I > 2\sigma(I)$ pub $\omega$  scans $R_{int} = 0.025$ Absorption correction: multi-scan<br/>(ABSCOR; Higashi, 1995) $h = -9 \rightarrow 9$ <br/> $R = -9 \rightarrow 9$ Ref $T_{min} = 0.753, T_{max} = 0.953$  $k = -8 \rightarrow 8$ 2851 measured reflections $l = -15 \rightarrow 15$ Brul

#### Refinement

Refinement on  $F^2$   $R[F^2 > 2\sigma(F^2)] = 0.050$   $wR(F^2) = 0.152$  S = 1.112201 reflections 181 parameters H-atom parameters constrained  $w = 1/[\sigma^{2}(F_{o}^{2}) + (0.0884P)^{2} + 0.4878P]$ where  $P = (F_{o}^{2} + 2F_{c}^{2})/3 (\Delta/\sigma)_{max} < 0.001 \Delta\rho_{max} = 0.46 \text{ e} \text{ Å}^{-3}$ 

 $\Delta \rho_{\rm min} = -0.55 \ {\rm e} \ {\rm \AA}^{-3}$ 

# Table 1

Selected geometric parameters (Å, °).

Cl1-C12	1.735 (3)	S1-C1	1.748 (3)
S1-O2	1.418 (2)	N1-C7	1.376 (4)
S1-O1	1.421 (2)	N1-C8	1.463 (4)
S1-N1	1.666 (2)		
O2-S1-O1	117.21 (14)	N1-C8-C9	113.3 (2)
C7-N1-S1	115.0 (2)		

#### Table 2

Hydrogen-bond geometry (Å, °).

$D - H \cdots A$	D-H	$H \cdot \cdot \cdot A$	$D \cdots A$	$D - \mathbf{H} \cdots A$
$C2-H2B\cdots O3^{i}$	0.93	2.39	3.300 (4)	165

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

All H atoms were placed in calculated positions, with C–H = 0.93–0.97 Å, and included in the final cycles of refinement using a riding model, with  $U_{iso}(H) = 1.2U_{eq}(C)$ .

Data collection: *RAPID-AUTO* (Rigaku, 1999); cell refinement: *RAPID-AUTO*; data reduction: *RAPID-AUTO*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1999); software used to prepare material for publication: *SHELXTL*.

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