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Key indicators

Single-crystal X-ray study  
T = 293 K  
Mean  $\sigma(\text{C}-\text{C}) = 0.007 \text{ \AA}$   
Disorder in solvent or counterion  
R factor = 0.076  
wR factor = 0.161  
Data-to-parameter ratio = 13.7

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

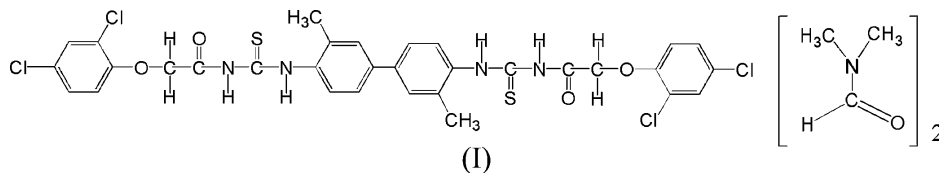
3,3'-Bis(2,4-dichlorophenoxyacetyl)-1,1'-  
(2,2'-dimethylbiphenyl-4,4'-diyl)dithiourea  
N,N-dimethylformamide disolvate

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In the title compound,  $\text{C}_{32}\text{H}_{26}\text{Cl}_4\text{N}_4\text{O}_4\text{S}_2 \cdot 2\text{C}_3\text{H}_7\text{NO}$ , the molecule of 3,3'-bis(2,4-dichlorophenoxyacetyl)-1,1'-(2,2'-dimethylbiphenyl-4,4'-diyl)dithiourea (BT) possesses a crystallographically imposed centre of symmetry at the mid-point of the central C—C bond. Intramolecular N—H···O and C—H···S hydrogen bonds contribute to the essential planarity of the BT skeleton, with a maximum deviation from the mean plane of 0.196 (2) Å for the S atoms.

Comment

The title compound, (I), belongs to the family of aroylthiourea compounds, which exhibit various biological properties such as antiviral, herbicidal, pesticidal, and plant-growth regulating activities (Xu *et al.*, 2003; Sun *et al.*, 2006; Du & Ye, 2002). We present here its crystal structure.



The triclinic unit cell of (I) contains one molecule of 3,3'-bis(2,4-dichlorophenoxyacetyl)-1,1'-(2,2'-dimethylbiphenyl-4,4'-diyl)dithiourea (BT) and two molecules of *N,N*-dimethylformamide (DMF). All bond lengths and angles are normal (Allen *et al.*, 1987). The BT molecule possesses a crystallographically imposed centre of symmetry at the mid-point of the central C—C bond (Fig. 1).

Intramolecular N—H···O and C—H···S hydrogen bonds (Table 1) contribute to the essential planarity of the BT skeleton, with a maximum deviation from the mean plane of 0.196 (2) Å for the S atoms.

Experimental

BT was prepared according to the method of Zhang & Lin (1992). Single crystals suitable for X-ray analysis were obtained by slow evaporation of a DMF solution at 293 K.

Crystal data

$\text{C}_{32}\text{H}_{26}\text{Cl}_4\text{N}_4\text{O}_4\text{S}_2 \cdot 2\text{C}_3\text{H}_7\text{NO}$	$V = 1046.8 (4) \text{ \AA}^3$
$M_r = 882.70$	$Z = 1$
Triclinic, $P\bar{1}$	$D_x = 1.400 \text{ Mg m}^{-3}$
$a = 10.012 (2) \text{ \AA}$	Mo $K\alpha$ radiation
$b = 10.488 (2) \text{ \AA}$	$\mu = 0.44 \text{ mm}^{-1}$
$c = 11.124 (2) \text{ \AA}$	$T = 293 (2) \text{ K}$
$\alpha = 67.78 (3)^\circ$	Prism, yellow
$\beta = 77.92 (3)^\circ$	$0.30 \times 0.20 \times 0.10 \text{ mm}$
$\gamma = 78.07 (3)^\circ$	

## Data collection

Enraf–Nonius CAD-4  
diffractometer  
 $\omega/2\theta$  scans  
Absorption correction:  $\psi$  scan  
(North *et al.*, 1968)  
 $T_{\min} = 0.881$ ,  $T_{\max} = 0.958$   
4104 measured reflections

4104 independent reflections  
1798 reflections with  $I > 2\sigma(I)$   
 $\theta_{\max} = 26.0^\circ$   
3 standard reflections  
every 200 reflections  
intensity decay: none

## Refinement

Refinement on  $F^2$   
 $R[F^2 > 2\sigma(F^2)] = 0.076$   
 $wR(F^2) = 0.161$   
 $S = 1.00$   
4104 reflections  
300 parameters

H-atom parameters constrained  
 $w = 1/[\sigma^2(F_o^2) + (0.047P)^2]$   
where  $P = (F_o^2 + 2F_c^2)/3$   
 $(\Delta/\sigma)_{\max} = 0.001$   
 $\Delta\rho_{\max} = 0.22 \text{ e } \text{\AA}^{-3}$   
 $\Delta\rho_{\min} = -0.24 \text{ e } \text{\AA}^{-3}$

Table 1

Hydrogen-bond geometry ( $\text{\AA}$ ,  $^\circ$ ).

$D-H\cdots A$	$D-H$	$H\cdots A$	$D\cdots A$	$D-H\cdots A$
$N1-H1A\cdots O1$	0.86	2.09	2.558 (5)	114
$N2-H2A\cdots O2$	0.86	1.93	2.669 (5)	143
$C15-H15A\cdots S1$	0.93	2.49	3.182 (5)	131

All H atoms were positioned geometrically ( $C-H = 0.93\text{--}0.97 \text{ \AA}$  and  $N-H = 0.86 \text{ \AA}$ ) and refined as riding, with  $U_{\text{iso}}(\text{H}) = 1.2\text{--}1.5U_{\text{eq}}(\text{C})$  of the parent atom. The DMF solvent molecule was treated as disordered over two positions, with refined occupancies of 0.552 (10) and 0.448 (10).

Data collection: *CAD-4 Software* (Enraf–Nonius, 1989); cell refinement: *CAD-4 Software*; data reduction: *XCAD4* (Harms & Wocadlo, 1995); program(s) used to solve structure: *SHELXS97*

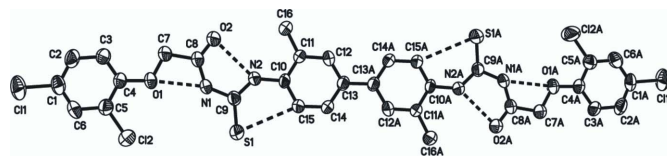


Figure 1

View of the BT molecular structure in (I) showing the atom-labelling scheme [symmetry code: (A)  $-1 - x, 1 - y, 1 - z$ ]. Displacement ellipsoids are drawn at the 50% probability level. The dashed lines denote intramolecular hydrogen bonds. H atoms have been omitted.

(Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Bruker, 1998); software used to prepare material for publication: *SHELXTL*.

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